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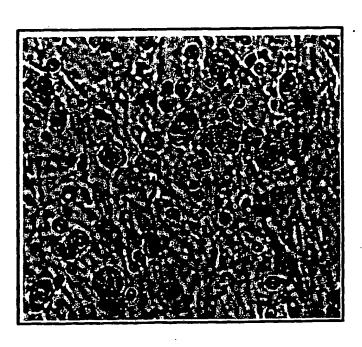
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(54) Title: HUMAN MESENCHYMAL PROGENITOR CELL



(57) Abstract: Pluri-differentiated human mesenchymal progenitor cells (MPCs) are isolated. A method isolates and purifies human mesenchymal progenitor cells from Dexter-type cultures for characterization of and uses, particularly therapeutic uses for such cells. Specifically, isolated MPCs can be used for diagnostic purposes, to enhance the engraftment of hematopoietic progenitor cells, enhance bone marrow transplantation, or aid in the treatment or prevention of graft versus host disease.

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# HUMAN MESENCHYMAL PROGENITOR CELL FIELD OF THE INVENTION

The present invention generally relates to pluri-differentiated mesenchymal progenitor cells and therapeutic uses for the same. More specifically, the isolated mesenchymal progenitor cells are isolated from hematopoietic cells and macrophages in Dexter-type cultures cells.

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#### **BACKGROUND OF THE INVENTION**

Bone marrow, the site of blood cell production and home to various leukemia and lymphoma cells, comprises a complex cellular population including hematopoietic progenitor or stem cells and the stromal cells that support them. Hematopoietic stem cells have the capacity for self-regeneration and for generating all blood cell lineages while stromal stem cells have the capacity for self-renewal and for producing the hematopoietic microenvironment.

Two bone-marrow culture systems introduced in the mid-1970's have evolved as favored media for the *in vitro* analysis of mesengenesis and hematopoiesis. The Friedenstein culture system was introduced in 1976 as a media for the analysis and study of mesengenesis. (Friedenstein, et al, in *Exp Hematol* 4,267-74 (1976). In order to obtain mesenchymal stem cells (MSCs) for expansion in the culture medium, it is necessary to first isolate rare pluripotant mesenchymal stem cells from other cells in the bone marrow. In the Friedenstein culture system, isolating the nonhematopoietic cells is achieved by utilizing their tendency to adhere to plastic. Once isolated, a monolayer of homogeneous, undifferentiated stromal cells is then grown in the culture medium, in the <u>absence</u> of hematopoietic cells. The stromal cells from this system have the potential to differentiate into discrete mesenchymal tissues, namely bone, cartilage, adipose tissue and muscle depending on specific growth supplements. These MSCs have been the target of extensive investigation including exploration of their potential clinical utility in repair or replacement of genetically damaged mesenchymal tissues.

In 1977, Dexter, et al. developed another bone marrow culture system for the study of hematopoiesis. (Dexter et al. *J Cell Physiol 91*, 335-44 (1977). The Dexter culture does not require isolation of the mesenchymal cells before culturing. Thus, the monolayer of stromal cells is grown in the <u>presence</u> of hematopoietic cells. Greenberger later modified the Dexter system by the addition of hydrocortisone to

the culture medium, making it more reproducible (Greenberger, *Nature 275*, 752-4 (1978).

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Based on the Dexter system's ability to support sustained growth and preservation of hematopoietic progenitor cells, it has become the standard *in vitro* model for the study of hematopoiesis. Although the Dexter-type stromal cells and the MSCs in Friedenstein-type cultures express similar cytokine/growth factor profiles, the Dexter cultures have been found to be more efficient at maintaining preservation of hematopoietic progenitor cells. Over the last 23 years, questions have remained as to whether the cells from the Dexter cultures retained the potential to differentiate, like the MSCs in the Friedenstein culture, or whether they have differentiated into another and discrete phenotype due to their interaction with the hematopoietic cells (Prockop, *Science* v276 n5309, p71(4)(April 1997)). It has been widely believed that the stromal cells of the Dexter cultures are a heterogeneous mixture of adipocytes, osteoblasts, fibroblasts, muscle cells, and vascular endothelial cells.

The *in vitro* analysis and study of hematopoiesis in Friedenstein and Dexter culture systems has been of great importance in both veterinary and human medicine. A number of diseases and immune disorders, as well as malignancies, appear to be related to disruptions within the hematopoietic system.

Allogeneic bone marrow transplantation is the preferred treatment for a variety of malignant and genetic diseases of the blood and blood-forming cells. The success rate of allogeneic bone marrow transplantation is, in large part, dependent on the ability to closely match the major histocompatibility complex of the donor cells with that of the recipient cells to minimize the antigenic differences between the donor and the recipient, thereby reducing the frequency of host-versus-graft responses and graft-versus-host disease (GvHD). Unfortunately, only about 20% of all potential candidates for bone marrow transplantation have a suitable family member match.

Bone marrow transplantation can be offered to those patients who lack an appropriate sibling donor by using bone marrow from antigenically matched, genetically unrelated donors (identified through a national registry), or by using bone marrow from a genetically related sibling or parent whose transplantation antigens differ by one to three of six human leukocyte antigens from those of the patient. Unfortunately, the likelihood of fatal GvHD and/or graft rejection increases from 20%

for matched sibling donors to 50% in the cases of matched, unrelated donors and un-matched donors from the patient's family.

The potential benefits of bone marrow transplantation have stimulated research on the cause and prevention of GvHD. The removal of T cells from the bone marrow obtained from matched unrelated or unmatched sibling donors results in a decreased incidence of graft versus host reactions, but an increased incidence of rejection of the allogeneic bone marrow graft by the patient.

Current therapy for GvHD is imperfect, and the disease can be disfiguring and/or lethal. Thus, risk of GvHD restricts the use of bone marrow transplantation to patients with otherwise fatal diseases, such as severe immunodeficiency disorders, severe aplastic anemia, and malignancies.

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The potential to enhance engraftment of bone marrow or stem cells from antigenically mis-matched donors to patients without graft rejection or GvHD would greatly extend the availability of bone marrow transplantation to those patients without an antigenically matched sibling donor.

Thus, it would be useful to develop methods of improving and/or enhance bone marrow transplantation by enhancing the engraftment of bone marrow or hematopoietic progenitor cells and/or decreasing the occurrence of graft rejection or GvHD in allogenic transplants.

Studies of hematopoiesis and mesengenesis and the urgent need for improved methods of treatment in the field of bone marrow transplants have led to the isolation of MSCs from bone marrow stroma. These MSCs are the same pluripotential cells that result from expansion in Friedenstein type cultures. Several patents describe the isolation and therapeutic uses of these MSCs.

U.S. Patent No. 5,486,359, to Caplan, et al., discloses isolated human MSCs, and a method for their isolation, purification, and culturing. Caplan, et al. also describes methods for characterizing and using the purified mesenchymal stem cells for research, diagnostic, and therapeutic purposes. The invention in `359, to Caplan, et al., describes pluri-potential cells that remain pluri-potential, even after cultural expansion. Caplan, et al. also teaches that it is necessary to first isolate the pluri-potent MSCs from other cells in the bone marrow and then, in some applications, uses culture medium to expand the population of the isolated MSCs. The Caplan et al. patent fails to disclose the use of Dexter-type cultures, pluri-

differentiated mesenchymal progenitor cells, or the isolation of cells from Dexter-type cultures.

U.S. Patent No. 5,733,542, to Haynesworth, et al., discloses methods and preparations for enhancing bone marrow engraftment in an individual by administering culturally expanded MSC preparations and a bone marrow graft. U.S. Patent 6,010,696, to Caplan, et al., discloses methods and preparations for enhancing hematopoietic progenitor cell engraftment in an individual by administering culturally expanded MSC preparations and hematopoietic progenitor cells. The cells utilized in the Haynesworth, et al. patent and the `696 patent to Caplan, et al. are the pluri-potential cells described in U.S. Patent 5,486,359. Neither patent discloses the use of Dexter-type cultures, pluri-differentiated mesenchymal progenitor cells, or the isolation of cells from Dexter-type cultures.

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Mesenchymal stem cells that are isolated from bone marrow are further described by Prockop, in *Science* v276 n5309, p71 (4)(1997) and Pittenger, et al. in *Science* v284 i5411, p143 (1). These articles also describe pluri-potential but undifferentiated MSCs and fail to teach or disclose a pluri-differentiated mesenchymal cell or the isolation of mesenchymal cells from Dexter- type cultures.

While the cells disclosed in the prior art may provide some benefit, the isolated MSCs in the prior art have not solved the problems associated with engraftment of hematopoietic progenitor cells or bone marrow. Consequently, there exists a need in the art for methods of improving engraftment of hematopoietic progenitor cells and bone marrow in mammals in need of such treatment. There also exists a need in the art for treating and preventing the occurrence of GvHD in mammals that receive allogeneic bone marrow transplants.

#### SUMMARY OF THE INVENTION

According to the present invention there is provided isolated pluridifferentiated mesenchymal progenitor cells, a method of isolation, diagnostic uses, and therapeutic uses relating to enhancing the engraftment of human bone marrow or hematopoietic progenitor cells and treating GvHD.

The present invention provides an isolated mesenchymal progenitor cell that is pluri-differentiated.

Accordingly, the present invention also provides a method for purifying pluri-differentiated mesenchymal progenitor cells including the steps of: providing a

cell culture preparation by the Dexter method, treating the cells to obtain a cell suspension, removing macrophages, fractionating the cells, and collecting the fraction of pluri-differentiated mesenchymal progenitor cells.

The present invention also provides a method for enhancing bone marrow engraftment in a mammal in need thereof which includes administering to the mammal (i) isolated pluri-differentiated mesenchymal progenitor cells and (ii) a bone marrow graft, wherein the pluri-differentiated mesenchymal progenitor cells are administered in an amount effective to promote engraftment of the bone marrow in the mammal.

The present invention provides a method for enhancing engraftment of hematopoietic progenitor cells in a mammal in need thereof which includes the step of administering to the mammal (i) isolated pluri-differentiated mesenchymal progenitor cells and (ii) hematopoietic progenitor cells, wherein the pluri-differentiated mesenchymal progenitor cells are administered in an amount effective to promote engraftment of the hematopoietic progenitor cells in the mammal.

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Another embodiment of the present invention provides a method for treating graft-versus-host disease (GvHD) in a mammal about to undergo bone marrow or organ transplantation or suffering from GvHD caused by bone marrow or organ transplantation, by administering to the mammal an effective amount of isolated pluri-differentiated mesenchymal progenitor cells.

Yet another embodiment of the present invention provides a method for diagnosing a disease state by: a) establishing gene expression patterns of normal state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells; b) establishing gene expression patterns of various leukemic state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells; c) identifying gene sets that are unique to a given state; and d) comparing a profile of bone marrow derived isolated mesenchymal progenitor cell of unknown state to the gene sets.

Additionally, the present invention provides a method for identifying therapeutic targets for treatment of hematopoietic function by: a) determining the median gene expression profile of bone marrow isolated pluri-differentiated mesenchymal progenitor cells associated with each disease state of interest; b)

identifying gene groups that are up-regulated, down regulated, and common to each disease state; and c) identifying gene sets that are unique to a given state.

The present invention also includes therapeutic compositions including isolated pluri-differentiated mesenchymal progenitor cells and a pharmaceutically acceptable carrier, wherein the pluri-differentiated mesenchymal progenitor cells are present in an amount effective to enhance bone marrow engraftment in a mammal in need thereof; enhance hematopoietic progenitor cell engraftment in a mammal in need thereof; or treat GvHD in a mammal about to undergo bone marrow or organ transplantation or suffering from GvHD caused by bone marrow or organ transplantation.

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#### **BRIEF DESCRIPTION OF THE FIGURES**

Other advantages of the present invention can be readily appreciated as the same becomes better understood by reference to the following detailed description when considered in connection with the accompanying drawings. The following is a brief description of the drawings which are presented only for the purposes of further illustrating the invention and not for the purposes of limiting same. Referring to the drawing figures, like reference numerals designate identical or corresponding elements throughout the several figures.

Figure 1 is a photograph showing the phase contrast photomicrograph view of a Dexter-type stromal cell monolayer reflecting on cellular complexity.

Figure 2 is a photograph showing the percoll gradient centrifugation technique of the present invention that purifies the MPCs (2) in large quantities to greater than 95% purity.

Figure 3 is a photograph showing the Wright-Giemsa staining of Dexter-type stromal cell cultures depicting three morphologically identifiable cell populations, macrophages (5), hematopoietic cells (3), and the mesenchymal progenitor cells (4) of the present invention.

Figures 4A-H show a series of photomicrographs showing the morphologic and phenotypic characteristics of the MPCs of the present invention, as uncovered by staining for representative mesenchymal cell lineage markers. The methods applied are shown in parentheses. (Figure 4A) Wright-Giemsa (Harleco stain using HMS Series Programmable Slide Stainer, Carl Zeiss, Inc.). (Figure 4B) Immunostain using anti-CD68 antibody (Immunotech, Clone PG-M1; Vector,

Vectastain Elite ABC Kit). (Figure 4C) Immunostain using anti-CD45 antibody (Dako, Clone PD7/26 & 2B11; ABC Kit). (Figure 4D) Periodic acid-Schiff (Sigma). (Figure 4E) Nile Red (Sigma), counterstained with DAPI (Vector). (Figure 4F) Alkaline phosphatase (Sigma Kit No. 85), counterstained with Nuclear Fast Red (Baker). (Figure 4G) Immunostain using antibody to fibronectin (Immunotech, Clone 120.5; ABC Kit). (Figure 4H) Immunostain using anti-muscle actin antibody (Ventana, clone HUC 1-1; Ventana system using a section of formalin-fixed, paraffin-embedded cell block, instead of a cytospin). Appropriate positive controls and isotype-matched negative controls were employed to ascertain antibody staining-specificity. All parts of figure as shown, except 4E and 4H, have clearly identifiable built-in cell controls. The morphological features of the cells are listed in row 1 of Table 1.

Figure 5 is a photograph which shows a transmission electron micrograph of an MPC of the present invention bearing microvilli, irregular nucleus, and pools of glycogen (6) in the ectoplasm (x 4,600).

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Figure 6A-M are photographs which show Northern blot analysis of bone marrow stromal cell RNAs for expression of genes specific for multiple mesenchymal cell lineages. Figures 6A-M represent different gene probes used for hybridization. The following outlines the sources of the gene probes employed and the approximate sizes of the major transcripts observed (shown in parentheses): Figure 6A) CD68 (Clone ID 3176179, Genome Systems, Inc (GSI); 2-3 kb); Figure 6B) Cathepsin B (Clone ID 2806166, GSI; 2-3 kb); Figure 6C) GAPDH probe (generated using PCR primers from R&D Systems, Inc; ~2 kb) hybridized to same blot as A and B; Figure 6 D) Adipsin (probe generated using PCR primers as described, Ref 20; 0.5-1 kb); Figure 6E) Osteoblast-specific cadherin-11 (Clone ID 434771, GSI; ~3 kb); Figure 6F) Chondroitin sulfate proteoglycan 2 (Clone ID 1623237, GSI; >10 kb); Figure 6G) Collagen type I alpha 1 (Clone ID 782235, GSI; >10 kb); Figure 6H) Decorin (Clone ID 3820761, GSI; 2-3 kb); Figure 6I) GAPDH probe hybridized to same blot as D-H; Figure 6J) Fibronectin (Clone ID 3553729, GSI; >10 kb); Figure 6K) Caldesmon (Clone ID 1319608, GSI; ~4 kb); Figure 6L) Transgelin (Clone ID 4049957, GSI; ~1.5 kb); and Figure 6M) GAPDH probe hybridized to same blot as J-L.

Figure 7 is a photograph which shows RT-PCR analysis for expression of representative hematopoietic growth factors (G-CSF and SCF) and extracellular

matrix receptors (ICAM-1, VCAM-1, and ALCAM) by the MPCs of the present invention.

Figure 8 is a graph comparing of the ability to support *in vitro* hematopoiesis by the purified MPCs (heavy fraction represented by gray) of the present invention vs. unfractionated bone marrow stromal cells (represented by black).

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Figures **9A** and Figure **9B** are graphs showing flow cytometric evidence of human hematopoietic cell engraftment in a SCID mouse cotransplanted with the MPCs of the present invention. Figure **9A** shows CD45+/CD34+ progenitors in the marrow. Figure **9B** shows CD45/CD34- mature hematopoietic cells circulating in the blood.

Figures 10A-H are photographs which show engraftment of human hematopoietic cells in a SCID mouse cotransplanted with the purified marrow MPCs of the present invention. Figure 10A shows a serial section of a mouse spleen stained with H & E. Figure 10B shows a serial section of a mouse spleen stained with immunoperoxidase stain for CD45. Figure 10C shows bone marrow stained for CD45. Figure 10D shows a serial section of the mouse liver stained with H&E depicting involvement of periportal areas. Figure 10E shows a serial section of the mouse stomach stained with H&E showing transmural infiltration. Figure 10F shows a serial section of the mouse lung stained with H&E showing involvement of peribronchial area. Figure 10G shows a serial section of the mouse pancreas stained with H&E. Figure 10H shows a serial section of the mouse paravertebral ganglia stained with H&E.

Figure 11A is a photomicrograph of a serial section of the spleen of a normal BALB/C mouse showing white pulp populated by darkly staining lymphocytes (H&E). Figure 11B is a photomicrograph of the spleen of a SCID mouse showing white pulp largely consisting of lightly staining stromal framework (H&E). Figure 11C is a photomicrograph of the spleen of a SCID mouse cotransplanted with human bone marrow MNC and the purified bone marrow MPCs of the present invention showing homing (engraftment) of human B cells to white pulp.

Figures 12A-C are photographs which show Southern blotting data. Figure 12A shows that hybridization of sample DNA using a DNA probe specific for human chromosome 17 alpha satellite DNA (p17H8) results in a 2.7 Kb band (7)

(arrow; autoradiogram exposed for only 45 minutes). Figure 12B shows EcoR1 digest of thymic genomic DNA from SCID mice. Figure 12C shows EcoR1 digest of lymph node genomic DNA from SCID mice. Figure 13A and Figure 13 B show graphs comparing the survival rate and engraftment of human hematopoietic cells in SCID mice cotransplanted with the purified bone marrow MPCs of the present invention vs. unpurified bone marrow stromal cells. In the line graphs provided the line with diamonds represents MPCs and bone marrow mononuclear cells, squares represents bone marrow mononuclear cells only, triangles represents unfractionated bone marrow stromal cells, the Xs represent MPCs only, and the circles represent the control. In the bar graphs, the gray bars represent mice that survived and the black bars represent mice with engraftment. Figures 14A-C are photographs which demonstrate apoptosis by TUNEL assay in organs of SCID mice that died after transplantation. Figure 14A shows a serial section of the liver of the mouse that survived. Figure 14B shows a serial section of the liver of the mouse that died. Figure 14C shows a serial section of the spleen of the mouse that survived. Figure 14D shows a serial section of the spleen of the mouse that died.

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Figure 15 shows photomicrographs of single-cell MPCs that were isolated by laser capture microdissection (LCM) and subsequently targeted for microarray analysis.

Figure 16 shows a Venn diagram displaying the stromal-cell gene-list. Stromal cell genes are operationally defined as being active in at least 9 out of 10 single cell MPCs AND 4 out of 5 collective MPC samples AND 7 out of 8 collective USC samples, i.e., 20 of 23 samples tested. This criterion was very stringent and automatically excluded the outliers, independently of filtering for genes with weak expressions on the basis of control strength (referred to as C or CS). The stromal cell gene list of 2755 includes 13 AFFX microarray-assay positive controls.

Figure 17 shows a two-dimensional hierarchical clustering of 2755 stromal cell genes based on the expression profiles of 23 samples. The gene tree is displayed on top and the experiment or sample tree is shown on left. Accordingly, each column represents a particular gene on the chip and each row represents a separate stromal cell sample.

Figure 18 shows composite gene-expression plots of 2755 stromal cell genes comparing collective purified stromal cell samples (cMPC), collective

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unpurified stromal cell samples (cUSC) and single-cell stromal cell samples (sMPC). Individual samples are represented on X-axis. Normalized intensity of gene expression is shown on Y-axis in log scale.

Figures 19 A & B show gene-expression plots of diverse mesenchymal lineage-associated genes and housekeeping genes by collective MPCs and single-cell MPCs. Individual samples are represented on X-axis. Signal intensity of a transcript in log scale normalized across samples is shown on Y-axis. Note the differing log scales, particularly the wide range of log scale for ACTB. Representative lineage markers are shown as follows. Osteoblast markers: osteoblast-specific factor 2 (probe ID 1451\_s-at), osteoblast cadherin 11 (ID 2087\_s\_at) and collagen 1 alpha 2 (ID 32306\_g\_at). Muscle markers: caldesmon (ID 41738 at), transgelin-2 (ID 36678\_at) and smooth muscle myosin heavy chain (ID 32838\_at). Fibroblast markers: fibronectin (ID 31719\_at) and prolyl 4-hydroxylase (ID 37037 at). Adipocyte markers: adipsin (ID 40282\_at) and adipocyte-specific ECM protein (ID 39673\_i\_at). Housekeeping genes: GAPD (ID 35905\_s\_at) and ACTB (ID 32318\_s\_at). Samples 1-5, respectively, represent MPC A, MPC B R2, MPC C R2, MPC D R1, MPC D R2. Samples 6-15, respectively, represent SCA1, SCA2, SCA3, SCB1, SCB3, SCC1, SCC3, SCD1, SCD2, SCD3.

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Figure 20 shows gene-expression plots of representative precursor Blymphocyte-associated genes by collective MPCs and single-cell MPCs. Individual samples are represented on X-axis. Signal intensity of a transcript in log scale normalized across samples is shown on Y-axis. Note that the CD markers that are traditionally associated with hematopoietic cells, CD45 (probe ID 40518\_at), CD19 (ID 1116\_at) and CD34 (ID (538\_at), are expressed by sMPCs. CD45, when present, is more abundantly detected in single MPCs than in collective MPCs, and is particularly noticeable by wide range of log scale for CD45. The other pre-B cell associated markers that are expressed by sMPCs are CD10 (ID 1389\_at), HLA-Dr (ID 33261 at) and CD79A (ID 34391\_at). Samples 1-5, respectively, represent MPC A. MPC B R2, MPC C R2, MPC D R1, MPC D R2. Samples 6-15, respectively, represent SCA1, SCA2, SCA3, SCB1, SCB3, SCC1, SCC3, SCD1, SCD2, SCD3.

Figure 21 shows the master stromal cell table.

#### **DETAILED DESCRIPTION OF THE INVENTION**

Generally, the present invention provides isolated and purified mesenchymal progenitor cells that are pluri-differentiated. Also provided by the present invention is a therapeutic composition including an effective amount of isolated and purified pluri-differentiated mesenchymal progenitor cells and a pharmaceutically acceptable carrier.

The terms "enhance" or "improve" as used herein are intended to indicate that the there is a more beneficial end result. In other words, the product provides a more effective result.

The term "pluri-differentiated" as used herein refers to cells that are a single cell type co-expressing genes specific for multiple lineages. The term "pluri-potential" as used herein refers to cells that are undifferentiated and have the potential to be differentiated into discrete mesenchymal tissues.

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Dexter-type cultures contain stromal cells that co-express multiple message lineage markers. These pluri-differentiated cells are referred to by the inventor as mesenchymal progenitor cells (MPCs). Disclosed herein is a process for isolating and purifying MPCs from Dexter-type cultures. Purified MPCs provide a sufficiently defined system to permit detailed elucidation of the role of bone marrow in normal and leukemic hematopoiesis.

The present invention also provides various methods for using MPCs to enhance bone marrow transplantation, enhance hematopoietic progenitor cell engraftment, for diagnostic purposes, or for the treatment of GvHD.

The exact cell types in Dexter cultures have been identified. No evidence was found for the existence of discrete cellular populations, such as adipocytes, osteoblasts, fibroblasts, smooth muscle cells and endothelial cells, notwithstanding the abundance of literature and wide spread belief (*See*, J.L. Liesveld *et al.*, *Blood* 73, 1794 (1989); A.K. Sullivan, D. Claxton, G. Shematek *et al.*, *Lab Invest* 60, 667 (1989); K. Dorshlind, *Ann Rev Immunol* 8, 126 (1990); S. Perkins, R.A. Fleischman, *Blood* 75, 620 (1990); I.A. Denkers, R.H. Beelen, G.J. Ossenkoppele *et al.*, *Ann Hematol* 64, 210 (1992); P.E. Penn, D.Z. Jiang, R.G. Fei *et al.*, *Blood* 81, 1205 (1993); E. de Wynter *et al.*, *J Cell Sci* 106, 761 (1993); A. Ferrajoli *et al.*, *Stem Cells (Dayt)* 12, 638 (1994); B.R. Clark, A. Keating, *Ann NY Acad Sci* 770, 70 (1995); B.S. Wilkins, D.B. Jones, *Br J Haematol* 90, 757 (1995); S. Gronthos, P.J. Simmons, *J Hematother* 5, 15 (1996); D. Soligo *et al.*, Abstract

#3926, Blood 94, Supplement 1 (Part 2 of 2), p. 168b, Forty 1st Annual Meeting of the American Society of Hematology, New Orleans, LA, December 3-7, 1999, M-A. Dorheim et al., J Cell Physiol 154, 317 (1993), M.K. Majumdar, M.A. Thiede, J.D. Mosca et al., J Cell Physiol. 176, 57 (1998), D.J. Prockop, Science 276, 71 (1997), R.S. Taichman, S.G. Emerson, J Exp Med 179, 1677 (1994); R.S. Taichman, M.J. Reilly, S.G. Emerson, Blood 87, 518 (1996); C.M. Verfaillie, in HEMATOLOGY: Basic Principles and Practice, R. Hoffman, et al., Eds. (Churchill Livingstone, New York, 2000), pp. 140-142.), A.J. Henderson, A. Johnson, K. Dorshkind, J Immunol 145, 423 (1990); M.W. Long, J.L. Williams, K.G. Mann, J Clin Invest 86, 1387 (1990); P.J. Simmons, S. Gronthos, A. Zannettino et al., Prog Clin Biol Res 389, 271 1994); B.A. Roecklein, B. Torok-Storb, Blood 85, 997 (1995); J. Wineman, K. Moore, 1. Lemischka et al., Blood 87, 4082 (1996); K.A. Kelly, J.M. Gimble, Endocrinology 139, 2622 (1998); K.C. Hicok et al., J Bone Miner Res 13, 205 (1998); S.R. Park, R.O. Oreffo, J.T. Triffitt, Bone 24, 549 (1999); J.E. Dennis et al., J Bone Miner Res 14, 700 (1999); and B. Torok-Storb et al., Ann NY Acad Sci 872, 164 (1999)). Instead, the inventor determined that there are only three types of cells in Dextertype cultures, namely, macrophages (~35%), hematopoietic cells (~5%), and a type applicant calls "nonhematopoietic cells" (~60%)(Figure 3, Figure 4A, and Table 1).

Bone marrow mesenchymal cells, the nonhematopoietic cells in Dexter type cultures, possess distinctive features that have previously gone unrecognized. There is both direct visual (Figures 4A-E and Figure 5) and molecular biological (Figure 6) evidence to support the existence of this unique cell type. These findings challenge the prevailing belief that stromal cells derived from Dexter cultures comprise multiple singly-differentiated mesenchymal cell types. Because Dexter cultures represent a primary cell culture system, and not a cell line, these studies indicate that cells in these primary cultures themselves are pluri-differentiated, which has been previously unsuspected. The nonhematopoietic cells of the present invention (MPCs) simultaneously express marker genes specific for multiple mesenchymal cell lineages, including adipocytes, osteoblasts, fibroblasts and smooth muscle cells. As shown in the present disclosure, MPCs can also differentiate into B cells and therefore be useful in affecting the functionality of the immune system.

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The MPCs in Dexter type cultures were characterized using a variety of techniques. Cytospins were prepared using aliquots of unfractionated cells for performance of various cytological, cytochemical and immunocytochemical stains. Reactivity patterns of the bone marrow culture cells are outlined in Table 1. Figures 4A-E illustrate morphologic and phenotypic characteristics, as uncovered by staining for representative cell lineage markers.

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Only rarely have investigators in this field taken the approach of preparing a cell suspension and staining cells on cytospins as was done to characterize the cells of the present invention (Simmons, et al., Nature 328, p429-32 (1987)) and no other group has used this method to address the issue of pluridifferentiation by bone marrow stromal cells. Almost all of the published studies in the field, with a rare exception (Simmons, et al., Nature, 328, p429-32 (1987)), conducted cytochemical and immunocytochemical staining on layers of stromal cells grown to confluence on coverslips. In this situation, the stromal cultures appear very complex especially in the areas of hematopoietic activity, so-called "cobblestones" with macrophages and hematopoietic cells enmeshed in them. Macrophages and nonhematopoietic cells spread themselves and assume varied shapes when they adhere to and grow on plastic or glass. This spreading further contributes to the The complexity precludes a clear perceived heterogeneity and complexity. morphological visualization of the nonhematopoietic cells and consequently interferes with the determination of what percent of what cell type is positive for any given marker.

In terms of lineage markers, up to 100% of the nonhematopoietic cells or MPCs of the present invention expressed two fat cell markers (Nile Red (Figure 4E) and Oil Red O); an osteoblast marker (alkaline phosphatase (Figure 4F)); and two fibroblast markers (fibronectin (Figure 4G) and prolyl-4-hydroxylase). Greater than 85% of the MPCs were also positive for a muscle marker, actin (Figure 4H). There was no evidence of expression of endothelial cell differentiation, as judged by immunohistochemical staining for CD34 and CD31.

In addition, the Dexter type stromal cells had not previously been subjected to Periodic Acid-Schiff (PAS) staining, which revealed a strong and uniform positivity by almost 100% of the MPCs studied. This indicates the presence of large stores of glycogen (Figure 4D). The presence of glycogen (6) was confirmed

by electron microscopy (see Figure 5). In this respect, MPCs are reminiscent of the glycogen-laden reticular cells in the developing bone marrow of human fetuses (observed by L-T. Chen, L.Weiss, *Blood* 46, 389 (1975)). Glycogen deposition is viewed to be a developmentally regulated process during morphogenesis (H. Ohshima, J. Wartiovaara, I. Thesleff, *Cell Tissue Res.* 297, 271 (1999)).

The MPCs also exhibited cytoplasm compartmentalization into endoplasm and ectoplasm. This morphologic finding sheds light on their internal architecture because of correlation of restricted localization of glycogen and smooth muscle actin to ectoplasm; and the restricted localization of acid phosphatase, alkaline phosphotase, Nile Red, Oil Red O, fibronectin, and prolyl-4-hydrolase to endoplasm.

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Additional sets of multiple mesenchymal lineage markers were assessed by Northern blotting of unfractionated cells and purified MPCs to eliminate any observer bias that might be inherent in morphological assessment. Figures 6A-M represent different gene probes used for hybridization.

Compared to unfractionated cells, the purified nonhematopoietic cells expressed significantly higher levels of markers representing fat cells (adipsin, Figure 6D); osteoblasts (osteoblast-specific cadherin-11, chondroitin sulfate, collagen type 1 and decorin, Figures 6E-H); fibroblasts (fibronectin, Figure 6J); and smooth muscle cells (caldesmon and transgelin, Figures 6K-L).

Taken together, the morphologic, cytochemical, and immunocytochemical results (Figure 4A-H and Table 1), and the Northern blotting data (Figure 6A-M) indicate that the nonhematopoietic stromal cells of the Dexter cultures co-express markers specific for at least four different mesenchymal cell lineages. Using a variety of techniques, applicant has demonstrated that the MPCs co-express multilineage mesenchymal cell phenotypes, and in this respect the multi-or pluri-differentiated MPCs are distinct from the pluri-potential, but undifferentiated, MSCs of Friedenstein cultures (Prockop, Science 276, 71-74 (1997).

The nonhematopoietic cells of the present invention were purified from the macrophages, the dominant "contaminating" cell type, using a Percoll gradient method developed by applicant. MPCs were purified by the following process: cells from a Dexter-type culture were treated to obtain a cell suspension, the macrophages were removed, and the cells were fractionated using discontinuous

Percoll gradient centrifugation (Figure 2). The isolated MPCs were then collected and washed.

The purity of the nonhematopoietic cells was demonstrated by a near complete absence of two macrophage markers, CD68 and cathepsin B (as shown by Northern blotting data, Figure 6A and 6B). As a positive control, bone marrow mononuclear cells rich in myelomonocytic cells abundantly expressed CD68 (lanes 5 & 6, Figure 6A). The Northern blot results are consistent with a purity estimate of ~95% (vs. 60% in unfractionated samples) based on morphology and immunocytochemical staining for CD68.

A purified source of MPCs is desirable for a number of reasons. The relative ease with which large numbers of the MPCs can be purified and their distinctive phenotypic characteristics make them valuable targets for future investigations. Purified MPCs provide a sufficiently defined system to permit detailed elucidation of the role of bone marrow in normal and leukemic hematopoiesis in addition to aiding in bone marrow transplantation.

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Another major reason that purified cells are desirable is that Dexter cultures also contain a significant percentage of highly immunogenic macrophages that can cause onset of GvHD after transplantation. The MPCs of the present invention are purified to ~95% free of macrophages and hematopoietic cells. Note the increased survival rate in Severe Combined Immunodeficiency Disease (SCID) mice that received purified MPCs versus those that received unfractionated bone marrow stromal cells in Figure 13B. This data establishes that stromal cells in combination with engraftment or other similar procedures enhances the effectiveness of the treatment.

The present invention also provides methods of enhancing the engraftment of hematopoietic cells and of enhancing the engraftment of bone marrow. The hematopoietic support capacity of the Dexter-type cultures has been repeatedly demonstrated by a number of investigators. RT-PCR analysis showed that Dexter cultures and Friedenstein cultures expressed a similar pattern of cytokine and growth factor mRNAs; yet, Dexter cultures were found to be more efficient than Friedenstein cultures in achieving preservation of hematopoietic progenitors (Majumdar, et al., J.Cell.Physiol., 176, 57-66.). The pluri-differentiated MPC is capable of supporting hematopoiesis, as shown by its ability to express

representative hematopoietic growth factors/cytokines, i.e., G-CSF and SCF as well as matrix receptors/hematopoietic cell adhesion molecules, i.e., ICAM-1, VCAM-1 and ALCAM (Figure 7).

Clarification of the nature of the stromal cells and the ability to purify these cells makes it possible to use them as an adjuvant in bone marrow transplantation following high-dose chemotherapy and radiation therapy. These treatment modalities not only cause damage to the hematopoietic stem cells but also to the supportive stromal cells. However, because the bone marrow microenvironment is destroyed, hematopoietic progenitor cell engraftment is delayed until the stromal environment is restored. As a result, a critical aspect of the current invention is directed to the advantages of transplanting isolated mesenchymal progenitor cells to accelerate the process of stromal reconstruction and ultimately bone marrow engraftment. The stromal cells present in the standard bone marrow transplant are not sufficient in number and can be supplemented with the cultured MPCs of the present invention.

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Yet another embodiment of the current invention provides the use of MPC transplantation to major leukemic conditions, such as acute myeloid leukemia (AML), myelodysplastic syndromes (MDS), chronic myeloid leukemia (CML) and multiple myeloma (MM). This is based on applicant's determination that bone marrow stromal cells in a leukemia patient are functionally and structurally defective, regardless of the damage caused by chemotherapy and radiation therapy. Such defects in bone marrow stromal cells are likely to aid and abet leukemia development. Alternatively, stromal cell defects could be secondarily induced by surrounding leukemia cells, thus contributing to the loss of hematopoietic support function of stromal cells and hematopoietic failure, which is an invariable feature in leukemia. Regardless whether the observed stromal cell defects are primary or secondary to the leukemic process, by reason of their indisputable impact on normal hematopoiesis, these defects remain to be corrected to improve the hematopoietic function.

Stromal cells have never been carefully investigated in terms of genomics in view of the widespread belief that they represent a heterogeneous mixture of cell types. Tissue or cellular heterogeneity presents a major challenge for the application of microarray technology. The purified stromal cells of the present

invention represent a single pluridifferentiated MPC which allows for genomic study of the stromal cells and the development of new, more objective diagnostic tools for patients suffering from leukemia conditions.

The present invention provides a comprehensive phenotype of cultured bone marrow stromal cells at single cell level for the first time. These findings pave the road for ultimate identification and investigation of these cells in fresh samples of marrow, normal as well as diseased, in which they occur at a low frequency and are extremely difficult to study at the present time. The development of this phenotype forms the basis for various diagnostic tests including a comprehensive test that can be used to screen for different abnormalities of bone marrow stromal cells in various hematologic diseases and other diseases effecting stromal cells.

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Results show that isolated single stromal cells simultaneously express transcripts for osteoblasts, fibroblasts, muscle cells and adipocytes. Furthermore, there is shown that isolated single stromal cells simultaneously express transcripts for epithelial cells and neural/glial cells as well as transcripts for CD45, CD19, CD10, CD79a, and representative proto-oncogenes and transcription factors, typically known to be affiliated with normal and neoplastic hematopoietic cells. These findings are evidence of existence of a progenitor cell that is common to nonhematopoietic mesenchymal cells and hematopoietic cells, particularly B-lymphocytes. "Lineage burst" characterized by simultaneous activation of diverse differentiation pathways within the same cell appears to be the signature profile of a stromal cell, indicating that a "pluripotent" cell is "pluridifferentiated" at the molecular level. That is, prior to a selective and full-fledged lineage differentiation, progenitors express genes associated with multiple lineages to which they might possibly commit, thus providing insight into the molecular basis of cellular plasticity.

Transcriptomic analysis has been undeniably contributing to the molecular definition of new disease categories with demonstrable therapeutic benefit. The present invention contributes to the further definition of the stromal cell by refining its molecular signature. The *in vivo* identification of the stromal cell and its possible ontogenic variants as they might occur in different hematological diseases and subsequent targeting of these cells holds the key to ultimately treating some, if not all, of these diseases.

By comprehensively defining the gene expression profile of these cells, the present invention demonstrates the technical applicability of single-cell genomics toward understanding the physiology and pathology of both hematopoietic and nonhematopoietic microenvironments. Classically, the adventitial reticular cells located on the abluminal side of the vascular endothelium within the bone marrow microenvironment were thought to represent the stromal cells or their precursors. As with hematopoietic stem or progenitor cells, the stromal progenitor cells are rare in bone marrow occurring at an estimated frequency of 1 in 10<sup>5</sup> nucleated cells. Cultured stromal cells represent the progeny of the stromal cell, and not necessarily the stromal cell itself, for which no *in vivo* assay exists as yet. The technology of single-cell genomics and the blueprint as described in the present invention allows screening for the abnormalities of bone marrow stromal cells in fresh marrow samples that reflect on the ultimate *in vivo* context.

The ability to purify culture-expanded MPCs from both normal individuals and patients afflicted with various leukemias also allows testing of the hematopoietic supportive role of MPCs in mice models. These systems provide an *in vivo* model in which to examine the role of human bone marrow microenvironment in normal and leukemic hematopoiesis.

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The SCID mouse model is an ideal system in which to investigate MPC function. Engraftment of human hematopoietic progenitors in SCID mice has required either coadministration of exogenous human cytokines, or cotransplantation of human bone marrow plugs or bone fragments. As disclosed herein MPCs are a convenient, new source for human bone marrow stromal cells for enhancing transplantation that does not require cytokines, bone fragment, or marrow.

Unlike prior methods, the isolated MPCs of the present invention support human hematopoiesis in the SCID mouse model as effectively as whole marrow stroma. The transplantation of human marrow mononuclear cells combined with purified MPCs results in dramatically vigorous engraftment of human cells in spleen, bone marrow, liver, pancreas, lungs, stomach, and paravertebral neuronal ganglia of SCID mice (Figures 10A-H and Figures 11A-C). By contrast, mice receiving human bone marrow mononuclear cells alone or MPCs alone expectedly showed no detectable evidence of human hematopoietic cell engraftment (Figure 13A and Figure 13B).

The present invention also provides for a method of preventing or treating GvHD. The highest mortality rate, Figure 13B, was observed in mice receiving the unpurified whole marrow stroma and the bone marrow mononuclear cells. The increased mortality observed is related to the presence of highly immunogenic macrophages and consequent GvHD. The mice with the highest survival rate, shown in Figure 13A, were the mice receiving purified MPCs and bone marrow mononuclear cells.

Notably, there is discrete TUNEL-positive nuclei in the liver of the expired mouse in Figure 14B and complete absence of staining in the liver of the surviving mouse ( see Figure 14A). While some ill-defined globules of staining are observed in the spleen of the mouse that survived, the nuclear integrity of most of the cells is well preserved suggesting minimal or no apoptosis (Figure 14C). In contrast, the dead mouse spleen (Figure 14D) showed extensive TUNEL positivity precluding accurate interpretation. Control mouse liver and spleen showed results similar to those of the mouse that survived.

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The above results indicate that purified MPCs can support human hematopoiesis in SCID mice as effectively as whole marrow stroma. Equally important is that the purified MPCs increased the survival rate. The evidence shows that the increased survival is due to a reduction in GvHD.

Allogeneic bone marrow transplantation is the preferred method of treatment for a variety of malignant and genetic diseases of the blood and blood forming cells. However, failure of hematopoietic cell engraftment can occur for a number of reasons. These include, microenvironmental defects as part of the underlying disease itself (e.g., aplastic anemia), and/ or stromal cell damage caused by chemoradiotherapy and/ or microenvironmental damage as part of GvHD which is a dreaded complication following bone marrow transplantation. In GvHD, donor T cells present in the hematopoietic cell graft destroy host tissues. GvHD can involve multiple organs such as skin, liver, GI system etc. The current treatment modalities for preventing or treating graft failure or GvHD are cumbersome, costly and involve some form of immunosuppression. Stromal cell lesions, either primary to the disease process or secondarily induced by allogeneic bone marrow transplantation, play a prominent role in the success or failure of the hematopoietic cell graft. Cotransplantation of MPC not only enhances hematopoietic cell engraftment but

also prolongs the life of graft recipients by minimizing GvHD. Co-transplantation of healthy, culture-expanded MPC is a viable option in these situations.

The human bone marrow used in the Dexter-type cultures of the present invention can be obtained from a number of different sources in accordance with the procedures known in the art, including from plugs of femoral head cancerous bone pieces or from aspirated marrow. The cells used in the Dexter culture can be autologous, from the tissue donor, or from other individuals.

Modes of administration of MPCs include, but are not limited to, systemic intravenous injection and injection directly to the intended site of activity. The MPCs can be administered by any convenient route, for example by infusion or bolus injection, and can be administered together with other biologically active agents. Administration is preferably systemic.

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The methods of the present invention can be altered, particularly by (1) increasing or decreasing the time interval between administering MPCs and implanting the tissue, cells, or implanting the organs; (2) increasing or decreasing the amount of MPCs administered; (3) varying the number of MPC administrations; (4) varying the method of delivery of the MPCs; and/or (5) varying the source of MPCs.

The MPC preparations are used in an amount effective to promote engraftment of hematopoietic progenitor cells or bone marrow cells; or for the treatment or prevention of GvHD in the recipient. The pharmaceutically effective amount for the purposes herein is thus determined by such considerations as are known in the art. In general, such amounts are typically at least 1x10<sup>4</sup> MPCs per kg of body weight and most generally need not be more than 7x10<sup>5</sup> MPCs/kg.

The present invention also provides pharmaceutical compositions. Such compositions comprise a therapeutically effective amount of MPCs and a pharmaceutically acceptable carrier or excipient. Such a carrier includes but is not limited to McCoy's medium, saline, buffered saline, dextrose, water, and combinations thereof. The formulation should suit the method of administration as is known by those of skill in the art.

In one embodiment, the MPC preparation or composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous

administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition can also include a local anesthetic to ameliorate any pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a cryopreserved concentrate in a hermetically sealed container such as an ampoule indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients can be mixed prior to administration.

The present invention paves the way for applications of mesenchymal progenitor cells in the field of transplantation with respect to hematopoietic support, immunoregulation, and graft facilitation. MPCs can be used as a supporting cell type in bone marrow transplantation, particularly in diseases where defects in the hematopoietic stromal microenvironment are believed to prevail, such as aplastic anemia, myelofibrosis, and bone marrow failure following high dose chemotherapy and radiation therapy.

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Another aspect of the invention provides a method for diagnosing various disease states in mammals by identifying new diagnostic markers, specifically the classification and diagnosis of leukemia. Prior to the present invention, stromal cells were not carefully investigated in terms of genomics because of the widespread belief that they represent a heterogeneous mixture of cell types and cellular heterogeneity presents significant challenges for the application of genetic analysis such as microarray technology. The isolated MPCs of the present invention represent a single cell type and allow for genomic study of the stromal cells.

Using the methods of the present invention, it has been determined that bone marrow stromal cells in leukemia patients are functionally and structurally defective regardless of the damage caused by chemotherapy and radiation therapy. Given the almost 25 year history and intense interest in bone marrow stromal cell cultures, previous documentation of stromal cell abnormalities has been disappointingly low (Martinez & Martinez, Exp. Hematol 11:522-26 (1983); Budak-Alpdogan, et al., Am.J.Hematol, 62:212-20 (1999); Nagao, et al., Blood, 61:589-92

(1983); Peled, et al., Exp.Hematol 24:728-37 (1996); Bhatia, et al., Blood 85:3636-45 (1995); Agarwal, et al., Blood 85:1306-12 (1995); Diana, et al., Blood 96:357a(2000)). By identifying gene sets that are unique to a given state, these differences in the stromal cells can be utilized for diagnostic purposes.

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In one embodiment of the invention, isolated MPCs from a patient are assayed for expression of a large number of genes. The gene expression profile is projected into a profile of gene set expression values according to the definition of gene sets. A reference database containing a number of reference projected profiles is also created from the isolated MPCs of patients with known states, such as normal and various leukemic disease states. The projected profile is then compared with the reference database containing the reference projected profiles. If the projected profile of the patient matches best with the profile of a particular disease state in the database, the patient is diagnosed as having such disease state. Various computer systems and software (see Example 5) can be utilized for implementing the analytical methods of this invention and are apparent to one of skill in the art. Some of these software programs include Cluster & TreeView (Stanford, URLs: rana.lbl.gov or www.microarray.org), GeneCluster (MIT/Whitehead Institute, URL: MPR/GeneCluster/GeneCluster.html), Array Explorer (SpotFire Inc, URL: http://www.spotfire.com/products/scicomp.asp#SAE) and GeneSpring (Silicon Genetics Inc, URL: http://www.sigenetics.com/Products/GeneSpring/index.html) (for computer systems and software, see also U.S. Patent No. 6,203,987).

The methods of the present invention can also be useful for monitoring the progression of diseases and the effectiveness of treatments. For example, by comparing the projected profile prior to treatment with the profile after treatment.

One aspect of the present invention provides methods for therapeutic and drug discovery utilizing bone marrow derived isolated mesenchymal progenitor cells. The present invention can be utilized to identify stromal cell genes that can be therapeutic targets for improvement of normal hematopoietic function, which is constantly compromised, in leukemic patients. In one embodiment, gene sets are defined using cluster analysis. The genes within a gene set are indicated as potentially co-regulated under the conditions of interest. Co-regulated genes are further explored as potentially being involved in a regulatory pathway. Identification

of genes involved in a regulatory pathway provides useful information for designing and screening new drugs.

Some embodiments of the present invention employ gene set definition and projection to identify drug action pathways. In one embodiment, the expression changes of a large number of genes in response to the application of a drug are measured. The expression change profile is projected into a gene set expression change profile. In some cases, each of the gene sets represents one particular pathway with a defined biological purpose. By examining the change of gene sets, the action pathway can be deciphered. In some other cases, the expression change profile is compared with a database of projected profiles obtained by perturbing many different pathways. If the projected profile is similar to a projected profile derived from a known perturbation, the action pathway of the drug is indicated as similar to the known perturbation. Identification of drug action pathways is useful for drug discovery. See, Stoughton and Friend, Methods for Identifying pathways of Drug Action, U.S. patent application Ser. No. 09/074,983.

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The present invention provides a genomics strategy method for identifying genes differentially expressed in MPCs. The method begins with the preparation of total RNA from MPC samples, which leads to the generation of cDNA. From the cDNA, ds DNA can be prepared for *in vitro* transcription into cRNA. The cRNA is then fragmented for the hybridization of target RNA to a microarray of known genes (Affymetrix genechip containing DNA from ~12,000 known human genes, e.g., U95A oligonucleotide microarray). Finally, analysis of differentially expressed genes is accomplished using appropriate software (GeneSpring) to discern the patterns of gene expression or genomic signatures by a given MPC type (e.g., up-regulation or down-regulation).

Up-regulated and down-regulated gene sets for a given disease-associated or cytokine-stimulated MPC are combined. The combination enables those of skill in the art to identify gene sets with minimal number of elements that are unique to a given MPC type with a capability to discriminate one MPC type from another (this can be accomplished by means of a series of Venn diagrams and lists of required genes obtained via GeneSpring). Such gene sets are of immense diagnostic value as they can be routinely used in assays that are simpler than microarray analysis (for example "real-time" quantitative PCR). Such gene sets also

provide insights into pathogenesis and targets for design of new drugs. For example, the method allows one to establish transcriptional profiles of MPC genes that are pathologically altered.

Those of skill in the art can use the data and methods contained herein for the following: a) study select gene or sets of genes that are relevant to hematopoietic disease conditions by using relatively inexpensive but low-throughput technologies such as Northern blotting, RNase protection assays and/or PCR intended for gene expression analysis; b) identify newer drug targets and diagnostic markers relevant to specific diseases, such as MM or CML etc depending on the research interests of the individual investigators.

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The present invention also provides a large-format 2-D gel electrophoretic system for the reproducible separation of MPC proteins and for preparing 2-D PAGE protein maps for normal bone marrow-derived MPCs (untreated and treated with representative cytokines, e.g., TNF- $\alpha$  and/or IL-4) and for MPCs derived from patients with representative pre-leukemic/ premalignant and leukemic/ malignant conditions. The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), acute lyinphocytic leukemia (ALL), and multiple myeloma (MM). The protein samples consist of culture supernatants/secreted proteins, extracellular matrix (ECM) proteins, plasma membrane proteins solubilized using a three-step differential extraction protocol, employing conditions of progressively increasing solubility; and whole cell lysate proteins similarly solubilized using the three-step differential extraction protocol. This subproteome approach not only simplifies the 2-D PAGE electrophoretic protein patterns but also reveals additional proteins, which would otherwise have gone undetected.

The 2-D system described herein utilizes an immobilized pH gradient gel (pH 4-7) in the first dimension and a mini non-denaturing but high-resolution lithium dodecyl sulfate-polyacrylamide gel electrophoresis (LDS-PAGE) in the second dimension. As identified by silver staining, this system has resolved greater than 800 protein spots in a pH interval of 2.5 units (4.25-6.75, the isoelectric pH range for most of plasma membrane proteins to migrate) and a molecular mass range of 10-150 kDa. Equally important, the system is compatible with high sample

loads (up to 1.5 to 2.0 mg of total protein in up to 350 µl sample volume). All the protein species identifiable by a silver stain that is compatible with subsequent mass spectrometric analysis have been analyzed by a 2-D gel software with respect to isoelectric point, molecular weight and mass abundance. The lectin-binding status of these proteins has also been determined by lectin blotting. Lectin blots and Western blots have subsequently been stained by a gold stain for detection of total proteins on the same PVDF membrane. Although gold-staining of the Western blot is not as sensitive as silver-staining of the gel, gold-staining of the Western blot generates the necessary landmarks for alignment with the silver stained gel, facilitating excision of spots of interest from the gel for identification by MALDI-MS. Representative protein spots were excised from gel and subjected to mass spectrometric profiling (MALDI-MS) and/or sequencing (Nano ESI MS/MS) with subsequent database searching, resulting in a productive identification of ten proteins.

The invention is further described in detail by reference to the following experimental examples. These examples are provided for the purpose of illustration only, and are not intended to be limiting unless otherwise specified. Thus, the invention should in no way be construed as being limited to the following examples, but rather, should be construed to encompass any and all variations which become evident as a result of the teaching provided herein.

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#### **EXAMPLES**

The examples presented herein can be summarized as follows. The data disclosed herein demonstrate that Dexter cultures consist of only three cell types macrophages (~35%), hematopoietic cells (~5%), and nonhematopoietic cells (~60%). Using a percoll gradient centrifugation technique, the nonhematopoietic mesenchymal progenitor cells were isolated, free of macrophages and hematopoietic cells. A variety of techniques were used to identify the isolated cells as a multi-differentiated mesenchymal cell lineage co-expressing genes specific for multiple mesenchymal cell lineages including adipocytes, osteoblasts, fibroblasts and muscle cells.

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Evidence that this multi- or pluri-differentiated mesenchymal progenitor cell is capable of supporting hematopoiesis is shown by the expression of a number of hematopoietic growth factors and extracellular matrix receptors. The SCID mouse experimental data provides evidence that since the MPCs can be purified to near

homogeneity (95%) with relative ease, MPCs can be of value for enhancing engraftment of hematopoietic stem cells and bone marrow transplants. Additionally, increased survival rate in the SCID mouse model indicates that isolated MPCs can also be useful for the treatment of GvHD. An example of the administration of bone marrow cells and MPCs to breast cancer patients treated with chemotherapy is also provided.

A stepwise genomics strategy and an example of the genomic changes observed in leukemia associated MPCs is also provided. Cluster analysis was performed to show gene expression patterns in isolated MPCs of a normal individual and individuals with different leukemic conditions. The approach presented provides the basis for a new more objective means to diagnose patients suffering from leukemic conditions.

#### **EXAMPLE 1**

Isolation and Characterization of MPCs from Dexter-Type Bone Marrow Stromal Cell
Culture Systems

Bone marrow culture:

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Bone marrow samples were obtained from posterior superior iliac crest under general anesthesia for standard marrow transplantation. Marrow stromal cell cultures were set up using the residual cells recovered from the filters of Fenwal Bone Marrow Collection System after complete filtration of the marrow samples. The filters were rinsed with phosphate-buffered saline without Ca<sup>2+</sup> and Mg<sup>2+</sup> (PBS-CMF). The cell suspension was subjected to Ficoll gradient isolation of the mononuclear cells (bone marrow MNCs). The bone marrow MNCs were washed (x2) in PBS-CMF and suspended in McCoy's 5A with HEPES medium containing 12.5% fetal bovine serum (FBS), 12.5% horse serum, 1 µM/L hydrocortisone and 1% penicillin/streptomycin (for this study McCoy's complete medium) and cultured under standard stromal-cell culture conditions (Figure 1) (Seshi, *et al. Blood* 83, 2399 (1994) and Gartner, *et al. Proc Natl Acad Sci USA* 77, 4756 (1980). After two weeks, confluent stromal cell cultures were trypsinized (first passage), followed by splitting each T75 flask into two T150 flasks.

Morphologic and phenotypic characteristics of MPCs as uncovered by staining for representative mesenchymal cell lineage markers:

Two weeks after the first passage (above), confluent stromal cells were again trypsinized. Cytospins were prepared using aliquots of unfractionated cells for performance of various cytological, cytochemical and immunocytochemical stains.

Reactivity patterns of the bone marrow culture cells are outlined in Table 1. Figures 4A-E illustrate morphologic and phenotypic characteristics, as uncovered by staining for representative cell lineage markers. As illustrated in Table 1 and Figures 3 and 4A, Wright-Giemsa staining revealed three morphologically identifiable cell populations in Dexter type stromal cell cultures, macrophages, hematopoietic cells, and nonhematopoietic cells (labeled 4, 3, and 5, respectively).

The identity of macrophages was confirmed by immunostain using anti-CD68 antibody (Figure 4B) and cytochemical stains for acid phosphatase and Sudan black. The identity of hematopoietic cells (including macrophages) was confirmed by immunostain using anti-CD45 antibody (Figure 4C).

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The remaining nonhematopoietic cells stained intensely positive for Periodic acid-Schiff, which was diastase sensitive, signifying the presence of large stores of glycogen (Figure 4D). The presence of glycogen (6) was confirmed by electron microscopy (see Figure 5). In this respect, MPCs are reminiscent of the glycogen-laden reticular cells in the developing bone marrow of human fetuses (observed by L-T. Chen, L.Weiss, *Blood* 46, 389 (1975)). Glycogen deposition is viewed to be a developmentally regulated process during morphogenesis (H. Ohshima, J. Wartiovaara, I. Thesleff, *Cell Tissue Res.* 297, 271 (1999)).

In terms of lineage markers, up to 100% of the nonhematopoietic cells expressed two fat cell markers (Nile Red (Figure 4E) and Oil Red O); an osteoblast marker (alkaline phosphatase (Figure 4F)); and two fibroblast markers (fibronectin (Figure 4G) and prolyl-4-hydroxylase). Greater than 85% of the nonhematopoietic cells were also positive for a muscle marker, actin (Figure 4H). There was no evidence of expression of endothelial cell differentiation, as judged by immunohistochemical staining for CD34 and CD31 (data not shown).

The results indicate that the nonhematopoietic cells of the Dexter cultures are in fact a single, pluri-differentiated cell type co-expressing multiple mesenchymal cell lineage markers. The pluri-differentiated mesenchymal progenitor cells reported here are to be distinguished from the pluri-potential, but

undifferentiated, MSCs that are generated in the absence of hematopoietic cells, such as in Friedenstein-type cultures.

Table 1. Reactivity patterns f bon marrow stromal c lls based n cyt | gical, cytochemical and immunocytochemical stains\*,\*\*\*

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Mesenchymai Hematopoietic Test Macrophages Figure progenitor cells Utilized cells Small cells with Large cells with a Wright-Large cells with a 3 and 4A relatively irregular Giemsa small round minimal amount of nucleus & cytoplasm nucleus & foamy cytoplasm: (Harleco) compartmentalized into cytoplasm: 35% 5% of total cells ectoplasm and of total cells endoplasm: 60% of total cells ~100% MPCs: staining 0 Periodic ō 2 4D restricted to ectoplasm acid-Schiff in a ring-like fashion; (PAS) and completely (Sigma) abolished by diastase digestion 3 4C CD45 100% 100% HCs (Dako, macrophages (M PD7/26 & Φ) 2B11) 100% МФ 0 **CD68** 0 4 4B (Immunotec h, clone PG-M1) 0 0 Sudan 5 ~100% MΦ Black (Sigma) 100% MPCs; positive 6 Acid 100% MΦ: 0 granules in moderate phosphatas positive granules amounts; staining e (Sigma Kit packed No. 387) restricted to throughout cytoplasm endoplasm ~100% MPCs: staining Nile Red 0 4E 7 restricted to (Sigma) endoplasm Oil Red O ō ~ 95% MPCs: 0 8 (Sigma) variable number of positive granules; staining preferentially in the endoplasm ~100% MPCs: variable 4F Alkaline 0 0 9 phosphatas number of positive granules; staining e (Sigma Kit restricted to No. 85) endoplasm & plasma membrane\*\* 4G Fibronectin ~100% MPCs: staining restricted to 0 (immunotec endoplasm h. clone 120.5) ~100% MPCs: staining 0 ProlvI-4o 1 preferentially in the hydroxylase 1 ndoplasm (Dako.

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		clone 5B5)			
1 2	4H	Muscle actin (Ventana, clone HUC 1-1)	0	0	> 85% MPCs: variable staining restricted to ectoplasm

\*The lineages of the markers tested above are: 3, hematopoietic cell marker; 4, 5 and 6, monocyte/macrophage markers; 7 and 8, adipocyte markers; 9, osteoblast marker; 10 and 11, fibroblast markers; 12 muscle marker.

\*\*One earlier study (Simmons, et al., Nature 328, 429-432) interpreted the localization of alkaline phosphatase staining as confined to the plasma membrane when in fact it is predominately present within the endoplasm (compare Figure 1C of this reference with Figure 4F).

\*\*\* While well-accepted mesenchymal lineage markers were used, these markers do not necessarily lend themselves to simultaneous assessment of the same cell. For example, muscle-specific actin antibody worked only on formalin-fixed, paraffin embedded material, whereas stains like alkaline phosphatase, Oil Red and Nile Red are not anti-body based and involve varying fixing and staining conditions. Thus, the evidence shows that close to 100% of members of a morphologically distinct population express multiple lineage markers of interest.

Bone marrow mesenchymal progenitor cell (MPC) purification:

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To further investigate the characteristics of the MPCs, the nonhematopoietic stromal cells were then purified from the macrophages (~95% pure), the dominant "contaminating" cell type using the following method. Confluent monolayers of stromal cells resulting from first passage, above, were washed for three minutes in Ca<sup>2+</sup>/Mg<sup>2+</sup> free Hanks' balanced salt solution. Cells were incubated at room temperature for 45 minutes with intermittent mixing in serum-free McCoy's medium containing 10 mM L-leucine methyl ester (LME, Sigma). LME is a lysosomotropic agent that selectively kills and detaches macrophages. The detached macrophages were removed by washing the monolayers twice in McCoy's complete medium, followed by trypsinization of the monolayers. The resulting single cell suspensions were fractionated by discontinuous Percoll gradient (70%, 50%, 30%, 20%, 10%) centrifugation at 800xG for 15 minutes at 4°C in a fixed angle rotor (Avanti-J25 Beckman centrifuge) (Figure 2). Low-density cells representing the

macrophages resistant to detachment by LME separate as a band at the interface of serum and 10% Percoll and were discarded (1). High-density nonhematopoietic cells representing MPCs form a layer in the region of 30-50% Percoll (2). These were collected and washed twice by centrifugation through PBS-CMF. This protocol is conservatively expected to yield, >2.5x10<sup>6</sup> MPCs per T-150 flask (i.e., >50x10<sup>6</sup> MPCs per batch of 20 flasks). The purity of these preparations, typically about 95%, was routinely monitored by Wright-Giemsa staining.

Northern Blotting:

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Additional sets of multiple mesenchymal lineage markers were assessed by Northern blotting to eliminate any observer bias that might be inherent in morphological assessment. Figures 6A-M represent different gene probes used for hybridization. The sources of the gene probes employed and the major transcripts observed are outlined in the brief description of the figures.

Total RNA was prepared by dissolving the high-density cell pellets in Trizol (Life-Technologies). Total RNA samples from unfractionated stromal cells and BM MNCs were similarly prepared. The RNA samples were electrophoresed in a standard 1% agarose gel containing 2% formaldehyde in MOPS/EDTA buffer and blotted onto Immobilon-Ny+ membrane. Probes were labeled using Prime-A-Gene Kit (Promega) and a<sup>32</sup>P dCTP (NEN). Hybridization was performed at 65°C in modified Church's hybridization solution using 3x10<sup>6</sup> counts/ml in 10 ml (Millipore, 1998).

In Figures **6A-M**, Northern blot analysis was performed side-by-side on fractionated stromal cells, non-hematopoietic cells freed of macrophages, and initial bone marrow mononuclear cell samples. Lanes 1 and 2 represent total RNA samples (10µg each) from unfractionated stromal cells (subjects S1 and S2, respectively). Lanes 3 and 4 represent total RNA samples (10µg each) from purified stromal MPCs (subjects S1 and S2, respectively). Lanes 5 and 6 represent total RNA samples (10µg each) from bone marrow mononuclear cells, the starting cells for bone marrow cell cultures (subjects S3 and S4, respectively).

The large transcripts, especially of collagen (lane 1, Figure 6G) and fibronectin (lane 1, Figure 6J), in RNA extracted from unfractionated stromal cells of subject 1 showed difficulty migrating into the gel. This observation correlates with the presence of an artifact of unresolved positive material in lane 1, Figure 6A. Since

the RNA extracted from unfractionated stromal cells of the subject 2 did not present this problem (lane 2, Figure 6G, Figure 6J and Figure 6A), the observation does not impact on the overall interpretation of the results (see text). The lineages of markers tested were: monocyte/macrophage markers, CD68 and cathepsin B; adipocyte marker, adipsin; osteoblast markers, osteoblast-specific cadherin-11, chondroitin sulfate proteoglycan 2, collagen type I alpha 1 and decorin; fibroblast marker, fibronectin; muscle markers, caldesmon and transgelin. Marker signals were normalized to the amount of RNA loaded, which was based on densitometry of the GAPDH signals on the corresponding blot (Bio-Rad Model GS-700 Imaging Densitometer). Attenuation or enhancement of the marker signals in the purified stromal MPCs (i.e., lanes 3 and 4) relative to unfractionated stromal cells (i.e., lanes 1 and 2, respectively) is shown as fold  $\Delta$  (decrease/increase) underneath the lanes 3 and 4; ND, means not determined.

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The purity of the nonhematopoietic cells was demonstrated by a near complete absence of two macrophage markers, CD68 and cathepsin B (as shown by Northern blotting data, Figure 6A and 6B). As a positive control, bone marrow mononuclear cells rich in myelomonocytic cells abundantly expressed CD68 (lanes 5 & 6, Figure 6A). The Northern blot results are consistent with a purity estimate of ~95% (vs. 60% in unfractionated samples) based on morphology and immunocytochemical staining for CD68.

Compared to unfractionated cells, the purified nonhematopoietic cells expressed significantly higher levels of markers representing fat cells (adipsin, Figure 6D); osteoblasts (osteoblast-specific cadherin-11, chondroitin sulfate, collagen type 1 and decorin, Figures 6E-H); fibroblasts (fibronectin, Figure 6J); and smooth muscle cells (caldesmon and transgelin, Figures 6K-L).

No trace of osteoblast, fibroblast, or smooth muscle cell markers were detected in the bone marrow mononuclear cells, suggesting a less than detectable level of stromal cells or their precursors in bone marrow mononuclear cells. However, the fat cell marker, adipsin, was detected in all samples including the bone marrow mononuclear cells.

Taken together, the morphologic, cytochemical and immunocytochemical results (Figure 4A-H and Table 1), and the Northern blotting data (Figure 6A-M) indicate that the nonhematopoietic stromal cells of the Dexter

cultures co-express markers specific for at least four different mesenchymal cell lineages.

This finding is especially intriguing because pluri-differentiation is often a feature of neoplastic cells (Brambilia and Brambilia, *Rev. Mal. Respir.* 3,235 (1986); Pfeifer et al., *Cancer Res.* 51, 3793-3801 (1991); Tolmay *et al.*, *Virchow's Arch* 430, 209-12 (1997). However, a cytogenetic analysis of the Percoll-gradient purified MPCs showed a normal GTW banding pattern.

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RT-PCR Analysis for expression of representative hematopoietic growth factors and extracellular matrix receptors by MPCs

RT-PCR was conducted in a total reaction volume of 100 μl using 2 μg each of total RNA; corresponding primers; and a master mix of the PCR reagents. The RT conditions included sequential incubations at 42°C for 15 minutes, 99°C for five minutes, and 5°C for five minutes. The PCR conditions included: initial melting at 94°C for four minutes; and cyclical melting at 94°C for 45 seconds, annealing at 55°C for 45 seconds and extension at 72°C for 45 seconds with 34 cycles. PCR was terminated after final extension at 72°C for ten minutes. Reaction products (G-CSF, SCF, each 25 μl; VCAM-1, ALCAM, each 50 μl; ICAM-1, 75 μl) were concentrated as necessary; electrophoresed along with a 100-bp DNA ladder (GIBCO-BRL) in a standard agarose (1%) gel in TAE buffer; and stained with ethidium bromide.

PCR products, shown in Figure 7 lanes labeled 1-2, were generated using aliquots of the same RNA samples from purified stromal MPCs, as used for Northern blotting shown under Figure 6 lanes 3 and 4 respectively. The gene transcripts amplified were as follows: G-CSF (granulocyte-colony stimulating factor); (Tachibana et al., Br. J. Cancer, 76, 163-74 (1997); SCF (stem cell factor, i.e., c-Kit ligand); (Saito et al., Biochem, Biophys. Res. Commun., 13, 1762-69 (1994); ICAM-1 (intercellular adhesion molecule-1, CD54) and VCAM-1 (vascular cell adhesion molecule-1, CD106) (primers from R&D); and ALCAM (activated leukocyte cell adhesion molecule, CD166) (Bruder et al., J. Bone Miner. Res., 13, 655-63 (1998)).

The observed PCR products for G-CSF (600 bp, i.e., the top bright band) and ALCAM (175 bp) were significantly different from the expected sizes (278 bp; 372 bp, respectively). However, sequencing of the gel-purified PCR bands and subsequent BLAST search showed a 99-100% identity with respective members. Attempts to detect c-Kit (i.e., SCF receptor) using primers as described (Saito et al.,

Biochem, Biophys. Res. Commun., 13, 1762-69 (1994)) amplified a PCR product of ~300 bp with no homology to c-Kit (data not shown). The observed product sizes for SCF (~730 bp); ICAM-1 (~750 bp); and VCAM-1 (~500 bp) were as expected.

As illustrated in Figure 7, RT-PCR analysis showed that purified, multidifferentiated MPCs express both critical hematopoietic growth factor/cytokines, such as G-CSF and SCF as well as matrix receptors/hematopoietic cell adhesion molecules, i.e. ICAM-1, VCAM-1, and ALCAM.

#### **EXAMPLE 2**

Comparison of the Ability to Support in vitro Hematopoiesis by Purified MPCs vs.

Unfractionated Bone Marrow Stromal Cells

CD34+ positive cells (hematopoietic progenitor cells) were purified (Dynal kit) and cocultured with irradiated stromal monolayers for five weeks, followed by performance of standard colony assays for hematopoietic progenitors using methylcellulose medium supplemented with colony stimulating factors (using MethoCult medium from Stem Cell Technologies, Inc, Canada). Unfractionated bone marrow stromal cells and purified MPCs were prepared in the same manner as in Example 1. Data in Figure 8 represents results from three experiments. Purified MPC provides increased preservation of hematopoietic progenitor cells compared to unfractionated stromal cells.

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#### **EXAMPLE 3**

Animal Model for Enhanced Engraftment Capacity of MPCs

The Severe Combined Immunodeficiency Disease (SCID) mouse model is an ideal system in which to investigate MPC function. Engraftment of human hematopoietic progenitors in SCID mice requires either coadministration of exogenous human cytokines, or cotransplantation of human bone marrow plugs or bone fragments.

There has been discovered a convenient, new source for human bone marrow stromal cells for enhancing transplantation that does not require cytokines, bone fragment, or marrow. Unlike prior methods, the isolated cells of the present invention support human hematopoiesis in the SCID mouse model as effectively as whole marrow stroma. The transplantation of human marrow mononuclear cells combined with purified MPCs results in dramatically vigorous engraftment of human cells in spleen, bone marrow, liver, pancreas, lungs, stomach, and paravertebral

neuronal ganglia of SCID mice. By contrast, mice receiving human bone marrow mononuclear cells alone or MPCs alone expectedly showed no detectable evidence of human hematopoietic cell engraftment. Also notably, the mortality rate was highest in mice that received unfractionated whole marrow stroma whereas purified MPC increased the survival rate which can be due to reduction in GvHD.

Transplantation of human cells in SCID mice:

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Homozygous CB-17 scid/scid mice, six to eight weeks of age, were used. Lyophilized anti-asialo GM1 rabbit antibody (Wako Chemicals) was suspended in 1 ml sterile ddH<sub>2</sub>O, followed by pretreatment of mice with an IP injection of 20 ml (600 mg) ASGM1 antibody (to specifically deplete mouse macrophages and NK cells). Alternatively, one could use NOD/SCID mice lacking NK cell function, however, in light of highly promising preliminary results it was elected to continue use of scid/scid mice. The antibody treatment schedule included four-hour pre-engraftment and every seven days thereafter for the duration of the experiment. On the day of transplantation, the mice were irradiated with 200 or 300 cGy gamma-irradiation from a <sup>137</sup>Cs source. Approximately 2.5 x 10<sup>6</sup> MPCs suspended in 0.5 ml McCoy's medium and/ or 25x10<sup>6</sup> MNCs suspended in 0.2 ml were injected per mouse, intraperitoneally. Hematopoietic cell engraftment was assessed after five weeks by harvesting and analyzing representative hematopoietic and nonhematopoietic organs including blood, spleen, bone marrow (from two femurs and tibia) from euthanized mice.

Flow Cytometric Evidence

Figure **9A** and **9B** are flow cytometric evidence of human hemopoietic cells in a SCID mouse cotransplanted with marrow MPC. Figure **9A** shows the presence of CD45+/CD34+ progenitors in the marrow. Figure **9B** shows CD45/CD34- mature hematopoietic cells circulating in the mouse's blood. *Photomicrographs of Cells* 

Figures 10A-H shows engraftment of human hematopoietic cells in a SCID mouse cotransplanted with the purified marrow MPCs of the present invention. Figure 10A shows a serial section of a mouse spleen stained with H & E. Figure 10B shows a serial section of a mouse spleen stained with immunoperoxidase stain for CD45. Figure 10C shows bone marrow stained for CD45. Figure 10D shows a serial section of the mouse liver stained with H&E depicting involvement of periportal

areas. Figure 10E shows a serial section of the mouse stomach stained with H&E showing transmural infiltration. Figure 10F shows a serial section of the mouse lung stained with H&E showing involvement of peribronchial area. Figure 10G shows a serial section of the mouse pancreas stained with H&E. Figure 10H shows a serial section of the mouse paravertebral ganglia stained with H&E.

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Figure 11A is a photomicrograph of a serial section of the spleen of a normal BALB/C mouse showing white pulp populated by darkly staining lymphocytes (H&E). Figure 11B is a photomicrograph of the spleen of a SCID mouse showing white pulp largely consisting of lightly staining stromal framework (H&E). Figure 11C is a photomicrograph of the spleen of a SCID mouse cotransplanted with human bone marrow MNC and the purified bone marrow MPCs of the present invention showing homing (engraftment) of human B cells to white pulp.

Southern Blotting Data

Hybridization of sample DNA using a DNA probe specific for human chromosome 17 alpha satellite DNA (p17H8) shows linear signal intensity with a 2.7 Kb band (arrow; autoradiogram exposed for only 45 minutes) (Figure 12A). Lanes 1-10 contain human DNA starting 1000 ng to 100 ng admixed with 0 ng 900 ng of mouse DNA, total amount DNA loaded in each lane being 1 ug, allowing construction of a standard curve. The reported limit of detection with this technique is 0.05% human cells, which is more reliable than flow cytometry in detecting very low levels of human cell engraftment.

Figure 12B is a Southern blot of EcoR1 digest of thymic genomic DNA from SCID mice. Lanes 1-5 were loaded with 500 through 100 ng human DNA. Lanes 6, 9-11 were loaded with DNA from mice which received unfractionated bone marrow stroma plus bone marrow mononuclear cells. Lanes 7, 8, 14, 15 were loaded with DNA from mice that received MPCs plus bone marrow mononuclear cells. Lanes 12, 13 were loaded with DNA from mice that received bone marrow mononuclear cells only. There is evidence of human cell engraftment in the mouse thymus in lanes 9 and 11 and lanes 14 and 15 evidenced by the 2.7 Kb band. There was no evidence of engraftment in mice that only received only bone marrow mononuclear cells, lanes 12 and 13.

Figure 12C isEcoR1 digest of Lymph Node genomic DNA from SCID mice. Lanes 1-5 were loaded with 500 through 100 ng human DNA. Lanes 6, 9-11 were loaded with DNA from mice which received unfractionated bone marrow stroma plus bone marrow mononuclear cells. Lanes 7, 8, 14, 15 were loaded with DNA from mice that received MPCs plus bone marrow mononuclear cells. Lanes 12, 13 were loaded with DNA from mice that received bone marrow mononuclear cells only. While there was evidence of engraftment of human cells in the mouse lymph nodes for mice that received unfractioned bone marrow stromal cells and MPCs, there was no evidence of engraftment in mice that only received only bone marrow mononuclear cells, lanes 12 and 13.

Increased Survival and Evidence of MPC Effect on GvHD

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Figure 13A and Figure 13 B show graphs comparing the survival rate and engraftment of human hematopoietic cells in SCID mice cotransplanted with the purified bone marrow MPCs of the present invention versus unpurified bone marrow stromal cells. Mice in Figure 13A received 300 cGy irradiation dose and mice in Figure 13B received 200 cGY of irradiation. Figure 13A and Figure 13B show comparable engraftment of human hematopoietic cells in SCID mice cotransplanted with purified MPCs versus unpurified bone marrow stromal cells and the markedly enhanced survival of mice receiving purified MPCs. Notably, no engraftment was observed in mice receiving bone marrow mononuclear cells alone.

The highest mortality rate, Figure 13B, was observed in mice receiving the unpurified stromal cells and the bone marrow mononuclear cells. The increased mortality observed can be related to the presence of highly immunogenic macrophages and consequent GvHD. The mice with the highest survival rate, as shown in Figure 13A, were the mice receiving purified MPCs and bone marrow mononuclear cells.

Figures 14A-C demonstrate apoptosis by TUNEL assay in organs of SCID mice that died after transplantation with human bone marrow mononuclear cells and unpurified bone marrow stromal cells. Figure 14A shows a serial section of the liver of the mouse that survived. Figure 14B shows a serial section of the liver of the mouse that died. Figure 14C shows a serial section of the spleen of the mouse that survived. Figure 14D shows a serial section of the spleen of the mouse that died. Hematoxylin counterstain was applied to sections in Figure 14A and Figure

14C. Methylgreen counterstain was applied to sections in Figure 14B and Figure 14D.

Notably, there is discrete TUNEL-positive nuclei in the liver of the expired mouse in Figure 14B and complete absence of staining in the liver of the surviving mouse Figure 14A. While some ill-defined globules of staining are observed in the spleen of the mouse that survived, the nuclear integrity of most of the cells is well preserved suggesting minimal or no apoptosis (Figure 14C). By contrast, the dead mouse spleen (Figure 14D) showed extensive TUNEL positivity precluding accurate interpretation. Control mouse liver and spleen showed results similar to those of the mouse that survived.

The size of the spleens from the mice that survived and the mice that died were compared. The dead mice were observed to have small and atrophic spleens correlating with lymphoid cell depletion and apoptosis.

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The above results indicate that purified MPC can support human hematopoiesis in SCID mice as effectively as whole marrow stroma. Equally important is that the purified MPCs increased the survival rate. Evidence suggests that the increased survival can be due to a reduction in GVHD.

#### **EXAMPLE 4**

Administration of Bone Marrow Cells and Mesenchymal Progenitor Cells to Breast Cancer Patients Treated with Chemotherapy

A breast cancer patient undergoes a diagnostic posterior iliac crest bone marrow aspiration and biopsy using a local anesthetic. A small portion (2 to 3 ml) of the aliquot (10 to 20 ml) of marrow is submitted for routine histologic testing and determination of the presence of tumor cells using immunoperoxidase testing. The remainder of the cells are Dexter cultured for MPCs as described above in Example 1.

The patient also undergoes placement of a pheresis central venous catheter, and receives subcutaneous injections of G-CSF (filgrastin) 10µg/kg/day as described in Peters, et al, Blood, Vol. 81, pgs. 1709-1719 (1993); Chao, et al, Blood, Vol. 81, pgs. 2031-2035 (1993); Sheridan, et al, The Lancet, Vol. 2, pgs. 891-895 (1989); and Winter, et al, Blood, Vol. 82, pg. 293a (1993). G-CSF injections begin at least three days before the first pheresis is initiated. G-CSF therapy is withheld if the

white blood cell count rises above  $40,000/\mu L$  and is resumed once the white blood cell count drops to less than  $20,000/\mu L$ .

If the patient is receiving only G-CSF as the vehicle for "mobilization" of peripheral blood progenitor cells, the patient must not have received chemotherapy within four weeks of the planned pheresis. If the patient has received both conventional chemotherapy and G-CSF treatment for mobilization, the patient must not have received chemotherapy within ten days of the planned pheresis, and the white blood cell count must be at least  $800/\mu L$  and the platelet count at least  $30,000/\mu L$ .

Daily pheresis procedures are performed using a Cobe Spectra instrument (Cobe, Lakewood, Col.), and each cellular collection is cryopreserved using a controlled-rate liquid nitrogen freezer, until at least 15x10<sup>8</sup> mononuclear cells/kg are collected (Lazarus, et al., Bone Marrow Transplant, Vol. 7, pgs. 241-246 (1991)). Each peripheral blood progenitor cell is processed and cryopreserved according to previously published techniques. (Lazarus, et al., J. Clin, Oncol., Vol. 10, pgs, 1682-1689) (1992); Lazarus et al., (1991)):

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Eight days before the patient is infused with the autologous peripheral blood progenitor cells, the patient receives chemotherapy over a period of 96 hours (four days), with the following chemotherapy agents: 1) Cyclophosphamide in a total dosage of 6 g/m² (1.5 g/m 2/day for four days) is given via continuous intravenous infusion at 500 mg/m² in 1,000 ml normal saline every eight hours; 2) Thiotepa in a total dosage of 500 mg/ m² /day for four days) is given via continuous intravenous infusion at 125 mg/² in 1,000 ml normal saline every 24 hours; and 3) Carboplatin in a total dosage of 1,800 mg/m² (200 mg/m² /day for four days) is given via continuous intravenous infusion at 200 mg/m² in 1,000 ml of 5% dextrose in water every 24 hours.

The patient also receives 500 mg of Mesna in 50 ml normal saline IV over 15 minutes every four hours for six days (144 hours), beginning with the first dose of cyclophosphamide.

At least 72 hours after the completion of the chemotherapy, the MPCs are harvested from the Dexter culture(s). MPCs are collected and purified as described in Example 1. Cells are resuspended at approximately 10<sup>6</sup> cells/ml, and

injected slowly intravenously over 15 minutes to provide a total dosage of from 10 to about 5x10<sup>6</sup> cells.

MPCs can also be frozen and thawed to use when needed. For example, unfractionated cells from a Dexter culture are frozen. Upon thawing the cells are plated for about two days. The MPCs are then purified as in Example 1 above. The MPCs are then replated with serum or in a serum free media and can remain stable for up to six days.

The day after the patient receives the MPCs, the frozen autologous peripheral blood progenitor cells are removed from the liquid nitrogen refrigerator, transported to the patient in liquid nitrogen, submersed in a 37°C to 40°C sterile water bath, and infused rapidly intravenously without additional filtering or washing steps. GM-CSF in an amount of 250  $\mu g/m^2$  then is given as a daily subcutaneous injection, beginning three hours after completion of the autologous blood progenitor cell infusion. The GM-CSF is given daily until the peripheral blood neutrophil count exceeds 1,000/ $\mu$ L for three consecutive days.

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### **EXAMPLE 5**

## Genomic Changes Observed in Leukemia Associated MPCs

The following is one example of how normal hematopoiesis might be compromised in leukemic conditions. The cellular interactions that underlie leukemic bone marrow involve stromal cells, leukemia/ lymphoma cells, and normal hematopoietic pro`genitors (including those of myelopoiesis, erythropoiesis and megakaryocytopoiesis). In addition to displacing normal hematopoietic cells, the leukemia/ lymphoma cells can potentially cause direct damage to the hematopoietic supportive stromal cells by inducing unwanted gene expression profiles and adversely affecting the normal hematopoiesis. The cellular interactions can be schematized as:

Leukemia/lymphoma cells stromal cells normal hematopoietic progenitors.

The point of this scheme is that regardless of whether stromal cell lesions are primary or secondary to leukemogenesis, the normal hematopoietic function is invariably compromised in leukemic conditions, though different leukemias affect myelopoiesis, erythropoiesis and megakaryocytopoiesis differentially. Contrary to the prevailing notion (see Marini, F et al., Mesenchymal Stem Cells from Patients with Chronic Myelogenous Leukemia Patients can be

Transduced with Common Gene Transfer Vectors at High Efficiency, and are Genotypically Normal, 42<sup>nd</sup> Annual Meeting of the American Society of Hematology, Dec. 1-5, 2000 Poster # 665), there has been observed extensive and striking gene expression changes in leukemia-associated bone marrow MPCs by using high-resolution genomics. Therefore, one embodiment of the present invention is to use transplantation of tissue-culture expanded, purified normal MPCs to improve granulopoiesis, erythropoiesis and thrombopoiesis, in for example MDS (most of MDS patients do not die from blast transformation but from complications related to cytopenias, i.e., hematopoietic failure).

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The studies targeted acute myeloid leukemia (AML), chronic myeloid leukemia (CML) and multiple myeloma (MM), one case of each. The AML patient was a 57 year-old woman with 52% myeloblasts in the bone marrow with immunophenotype confirmed by flow cytometry and a karyotypic abnormality of 45, XX, -7(6)/46, XX [6]. Together with morphology, the diagnosis was AML arising in a background of myelodysplasia. The CML patient was a 35 year-old man with 2% blasts in the bone marrow and karyotypic abnormalities of Philadelphia chromosome and BCR/ABL gene rearrangement. Together with morphology, the diagnosis was CML in chronic phase. The MM patient was a 61 year-old woman with a IgA myeloma. The serum IgA level was 2.4 g/dl and the marrow plasma cell count was 37%. None of the patients was treated prior to obtaining marrow samples used in this study, to avoid any therapy-induced changes complicating the disease-associated changes.

The leukemic samples consisted of marrow aspirates that remained unused after clinical diagnostic studies were preformed. A bone marrow sample obtained from an adult healthy male who had consented to donate bone marrow for standard marrow transplantation was simultaneously studied. The normal bone marrow sample consisted of residual cells recovered from the filters after complete filtration of the marrow sample. Setting up of Dexter-type stromal cell cultures and isolation of MPC were as described in Example 1. The normal stromal cells were studied without and after stimulation with TNF $\alpha$  because TNF $\alpha$  (and IL-4) are regarded as negative regulators of hematopoiesis. Notably these cytokines, especially TNF  $\alpha$ , are elevated in marrow plasma of patients with myelodysplastic syndromes (MDS), the clinical hallmarks of which are anemia, leukopenia and

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thrombocytopenia (i.e., pancytopenia). TNF $\alpha$  and IL-4 are considered possible mediators of hematopoietic dysregulation typical of MDS.

A stepwise genomics strategy encompassed:

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Preparation of total RNA from MPC samples → generation of cDNA → preparation of ds DNA → in vitro transcription into cRNA → fragmentation of cRNA → hybridization of target RNA to a microarray of known genes (Affymetrix genechip containing DNA from ~12,000 known human genes, e.g., U95A oligonucleotide microarray) → analysis of differentially expressed genes using an appropriate software (GeneSpring) to discern the patterns of gene expression or genomic signatures by a given MPC type.

Cluster analysis showing gene expression patterns in bone marrow MPC isolated from a normal individual and patients with different leukemic conditions.

Genes with correlated expression across bone marrow MPC types: GeneSpring was used for cluster analysis. Prior to application of an agglomerative hierarchical clustering algorithm, microarray signals were normalized across experiments (i.e., from one MPC type to another) making the median value of all of measurements unity, so different experiments are comparable to one another. The signals were also normalized across genes in order to remove the differing intensity signals from multiple experimental readings. Genes that are inactive across all samples were eliminated from analysis. Notably, 7398 genes out of 12,626 genes (present on the Affymetrix genechip used) passed the filter of a normalized signal intensity of at least 0.1 across at least one of the five experiments performed. Cluster analysis was performed with standard correlation (same as Pearson correlation around zero) as the distance metric, a separation ratio of 0.5 and a minimum distance of 0.001 as provided by the software application. A closer relationship between CML- and MM-associated MPCs was observed, which in turn are related to AML-associated MPC, thus transforming global patterns of gene expression into potentially meaningful relationships.

Two-dimensional cluster analysis of tissue vs. gene expression vectors: A gene tree was constructed. Genes cluster near each other on the "gene tree" if they exhibit a strong correlation across MPC experiments and MPC tree branches move near each other if they exhibit a similar gene expression profile. The data indicated that the two-way clustering readjusted the location of a number of

genes resulting in accentuation of genomic signatures of each cell type. Investigators can usefully catalog genes composing any unique or signature cluster of interest by creating a gene list and disclosing their identities.

Self-organizing map (SOM) clusters (6x5) show differential gene expression in bone marrow MPC isolated from different hematopoietic conditions.

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Generation of SOM clusters involved prior normalization and filtering of the data. SOM algorithm was applied as provided by GeneSpring. Visualization of SOM clusters in combination with hierarchical clustering (i.e., MPC tree) revealed correlated meaningful patterns of gene expression. Predicated on the basis of SOM operating principle, the related SOM clusters tend to be located physically close to each other. For example, the juxtaposition of the SOM clusters with the common denominator containing genes that are up-regulated in AML/MDS-associated MPC. Whole or part of any SOM cluster can be selected to make a gene list providing the identities of the genes involved.

Genes highly expressed in normal MPC but absent or minimally expressed in leukemia-associated MPC

Lists of genes that are down-regulated in leukemia-associated MPC (AML/MDS, CML and MM) were created in comparison to normal MPC. A Venn diagram was made using these three gene lists. GeneSpring allows creation of sublists of genes corresponding to union, intersection and exclusion. Transcriptional profiles of any of these sublists of genes can be visualized across MPC samples of interest. The following is one such sublist of genes containing genes that are highly expressed in normal MPC and down-regulated in leukemia-associated MPCs revealing the identity of the subset of genes of interest: putative, wg66h09.x1 Soares Homo sapiens cDNA clone, Homo sapiens mRNA for CMP-Nacetylneuraminic acid hydroxylase, Homo sapiens cDNA clone DKFZp586G0421 (symptom: hute1), Human mRNA for histone H1x, Putative monocarboxylate transporterHomo sapiens gene for LD78 alpha precursor, Interacts with SH3 proteins; similar to c-cbl proto-oncogene product, wg82b12.x1 Soares Homo sapiens cDNA clone, Human atrial natriuretic peptide clearance receptor (ANP C-receptor) mRNA, Human 71 kDa 2'5' oligoadenylate synthetase (p69 2-5A synthetase) mRNA, Homo sapiens hMmTRA1b mRNA, Human G0S2 protein gene, Preproenkephalin, Human guanylate binding protein isoform I (GBP-2) mRNA, Human gene for

hepatitis C associated microtubular aggregate protein p44, 17-kDa protein, Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA, GS3686, Human monoamine oxidase B (MAOB) mRNA, Insulin-like growth factor II precursor, Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA, Similar to ribosomal protein L21, X-linked mental retardation candidate gene, and Homo sapiens mRNA; cDNA DKFZp434A202. Genes not expressed in normal MPC but highly expressed in leukemia-associated MPC

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Lists of genes that are upregulated (instead of down-regulated) in leukemia-associated MPCs (AML/MDS, CML and MM) were created in comparison to normal MPC and a Venn diagram was made. The following is one such sublist of genes containing genes that are inactive in normal MPC but up-regulated in leukemia-associated MPCs revealing the identity of the subset of genes of interest: Beta- tropomyosin, Homo sapiens clone 24659 mRNA sequence, Human mRNA for DNA helicase Q1, OSF; contains SH3 domain and ankyrin repeat, ym22b12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone, Human mRNA for pre-mRNA splicing factor SRp20, Human mRNA for golgi alpha-mannosidasell, OSF-2os, Homo sapiens gene for Proline synthetase, hk02952 cDNA clone for KIAA0683, wi24g10.x1 Homo sapiens cDNA clone, Lysosomal enzyme; deficient in Sanfilippo B syndrome, CTP synthetase (AA 1-591), WD repeat protein; similar to petunia AN11, Human mRNA for 5'-terminal region of UMK, complete cds, Homo sapiens chemokine exodus-1 mRNA, complete cds, Human GPI-H mRNA, complete cds, Homo sapiens mRNA encoding RAMP1, Transforming growth factor-beta-2 precursor, and Homo sapiens mRNA for KIAA0763 protein.

Visualizing expression of phenotypically & functionally relevant genes across samples of normal & disease-associated BM MPC.

Although GeneSpring is a highly flexible and user-friendly software application, it lacks the facility to create functionally relevant gene lists containing user-defined key words. This limitation was overcome by devising the following method via Microsoft Excel. A stepwise protocol to create such a gene list using Excel includes: Open the annotated microarray genome file (e.g., Affymetrix U95A) in Excel  $\rightarrow$  select the column with gene names  $\rightarrow$  select Data from pull-down menu  $\rightarrow$  Filter  $\rightarrow$  AutoFilter  $\rightarrow$  Custom  $\rightarrow$  enter key words (e.g., cell adhesion or cell cycle)  $\rightarrow$  OK  $\rightarrow$  generates a new Excel worksheet with the list of genes containing the key

words. Copy and paste the list of genes containing the key words into GeneSpring and save the gene list with a meaningful name. Twenty-two (22) such functionally relevant gene lists (Table 2) were created.

The resulting approach is a simple and powerful way to peer into the expression profiles of focused sets of functionally relevant genes across samples of interest. For example, the human vascular cell adhesion molecule-1 (VCAM-1) gene is completely down-regulated in AML/MDS and the human insulin-like growth factor binding protein (hIGFBP1) gene is up-regulated in AML compared to all other samples. Similarly, *Homo sapiens* gene for LD78 alpha precursor is down-regulated in all of leukemia-associated MPCs. Finally, the lineage markers CD45 and CD68 are essentially absent from the leukemia-associated MPCs attesting to the high degree of purity achieved by the sample preparation technique of the present invention.

### Results

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The genomic changes observed in leukemia-associated MPCs are striking. As shown in Table 2, the changes (up-regulation and/ or down-regulation) involved hundreds of genes. These changes were most dramatic in MPC associated with AML arising in a background of MDS and involved multiple classes of genes (Tables 1-2). Expectedly, the TNFa-induced changes were extensive. Given the high level of purity of MPC preparations, the enormous genomic changes observed are reflective of the underlying pathologic lesions in the MPCs themselves (and not due to the contaminating leukemic cells and/ or macrophages). These studies strongly support the hypothesis that stromal cells in a leukemic patient are functionally defective and therefore purified MPCs are of value in restoring the loss of hematopoietic function in leukemic patients.

Table 2. Magnitude of global gene expression changes in leukemia-associated and TNFa-stimulated MPCs in comparison to normal MPC

	AML/MDS MPC	CML MPC	ММ МРС	TNFa MPC
# of genes up- regulated	234	112	108	279
# of genes down- regulated	379	208	251	164

Table 3. Functional classes of genes analyzed across normal and leukemiaassociated MPCs

Annexins (14) Caspases & apoptosis- related transcripts (33) Cadherins (50) Calmodulins/ calmodulin- dependent kinases (25) Cell adhesion molecules (20) Cathepsins (19) Collagens (71)	Cell division cycle-related transcripts (36) Cytokines (19) Epidermal growth factors and related transcripts (22) Fibroblast growth factors (21) Fibronectins (6) Galectins (6) Growth factors (136)	IGF system (24) Interleukins/ receptors (76) Integrins/ disintegrins (70) Lineage-related markers (19) Laminins (13) Platelet-derived growth factors & receptors (12) TNF alpha-related transcripts (29) TGF beta-related transcripts (25)
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The gene lists in Table 3 were created as described above and analyzed using GeneSpring. The numerical value in parenthesis refers to the number of transcripts in the corresponding class of genes analyzed.

## Example 6

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The present invention provides the following benefits: a) identification and documentation of BM stromal cell gene expression patterns under varied, normal, and leukemic hematopoietic conditions; b) identification of stromal cell genes that can be therapeutic targets for improvement of normal hematopoietic function that is constantly compromised in leukemic patients, and identification of similar targets for arresting the growth and progression of neoplastic clones since stromal cells provide the necessary support for preferential growth of leukemic cells (CLL, MM) within BM and protect the leukemic cells from chemotherapy-induced death (MM); and c) identification of new biological bases and new diagnostic markers for refinement of the classification and diagnosis of leukemia. This present invention can also lead to important insights into the pathogenesis of leukemia. In broad terms, analysis of global gene expression or transcriptome (transcriptional profile composed of all transcribed regions of the genome) is considered a nonbiased discovery-driven (as opposed to hypothesis-driven) approach to the analysis of gene expression. A stepwise genomic strategy encompasses preparation of total RNA from cells of interest, to generation of cDNA, to preparation of ds DNA, to in vitro transcription into cRNA, to fragmentation of cRNA, to hybridization of target RNA, to a microarray of known genes (and/or ESTs), to analysis of

differentially expressed genes using an appropriate software to discern the patterns of gene expression or genomic signatures by a given disease-associated cell type.

Further test utility of sample preparation technology applied to normal EM-derived MPCs (untreated and treated with representative cytokines) and MPCs derived from patients with representative pre-leukemic and leukemic conditions for performance of high-resolution DNA microarray technology (Affymetrix genechip containing DNA from 12,000 known human genes, e.g., U95A oligonucleotide microarray).

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Representative cytokines which are pathologically altered in hematopoietic conditions and that can be used in this study include TNF- $\alpha$ , TGF- $\beta$  and interferon- $\gamma$ . The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), acute lymphocytic leukemia (ALL), and multiple myeloma (MM).

The front-end strategy of microarray analysis involves the use of Percoll-gradient purified MPCs. As a follow-up strategy, to validate the stromal cell origin of the differentially expressed genes, MPCs obtained from cytospins of BM stromal cells by laser-capture microdissection (LCM) selected on the basis of morphology (Figure 3) are used followed by "real-time" quantitative polymerase chain reaction (PCR). This can be performed with an LGM system as well as a "real-time" QPCR system. Validation can be performed on at least one sample from each of 6 normal BM M7NC/ MPC types and on one sample from each of 5 leukemia-associated MPC types. Validation is considered successful if the microarray results and PCR results on a given MPC sample match using a suite of 20 genes selected based on median pattern of microarray results for the given cell type. This approach not only validates the microarray results but also ascertains the stromal cell origin of the expressed genes. The standard published protocols involving LGM and "real-time" quantitative PCR and the instructions accompanying the equipment are used for performing the experiments.

Stepwise LCMJ real-time QPCR protocol entails the following. Cytospins are made from BM stromal cells. The cytospins are stained with hematoxylin and MPC is selected for based on morphology. Microdissect up to 1,000 MPC from each sample. RNA is extracted and reverse transcribed into cDNA.

The cDNA is amplified using gene-specific primers and "real-time" quantitative PCR.

By applying the combined power of different analytical techniques (such as hierarchical clustering and self-organizing maps) together with the recently developed sample preparation technology for stromal cells the present invention provides a molecular biological basis that can allow refinement of the classification and diagnosis of leukemias and lymphomas, uncovering the suspected disease heterogeneity. This enables the deciphering of the genomic expression profiles or signatures of bone marrow stromal cells in about 10 different physiologic states and about 20 different leukemic states. In addition to aiding in refinement of the classification and diagnosis of the hematopoietic malignancies, the data provides clues to potential novel drug targets and insights into pathogenesis.

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The present invention functions by identifying the MPC genes that are differentially expressed after stimulation with different hematopoietic cytokines implicated in the pathogenesis of pre-leukemic conditions (MDS); in actual pre-leukemic disorders (MDS); and in overt leukemias (CML, AML, CLL, ALL, MM) as well as in lymphomas that have a leukemic phase with involvement of BM.

The present invention is accomplished by first determining the median gene expression profiles for MPCs associated with each disease and stimulated by each cytokine of interest (this objective can be achieved by treating the gene expression vectors of individual cases in each MPC category as replicates; this capability is available in GeneSpring software application). Then the gene groups that are up regulated and down regulated and that are common to all the members in a given MPC category are identified (this is accomplished using a series of Venn diagrams and creating required gene lists via GeneSpring). Finally, the up-regulated and down-regulated gene sets for a given disease-associated or cytokine-stimulated MPC are combined. This allows the identification of gene sets with minimal number of elements that are unique to a given MPC type with a capability to discriminate one MPC type from another (this can also be accomplished by means of a series of Venn diagrams and lists of required genes obtained via GeneSpring). Such gene sets can be of immense diagnostic value as they can be routinely used in an assay simpler than microarray analysis (for example "real-time" quantitative PCR). Such gene sets can additionally provide insights into pathogenesis and possible targets for design of new drugs.

Determine expression profiles of MPC genes which are regulated as a result of exposure of normal MPCs to cytokines that are known to have a hematopoietic support role and/or are abnormally elevated in pre-leukemic/leukemic conditions, i.e., TNF  $\alpha$ ; IL-4; TNF  $\alpha$ + IL-4; interferon  $\gamma$ , TGF  $\beta$ ; PDGF; FGF; EGF; and calmodulin.

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TNF  $\alpha$ , IL-4 and IFN  $\gamma$  are potent negative regulators of hematopoiesis. Notably these cytokines, especially TNF a, are elevated in marrow plasma of patients with myelodysplastic syndromes (MDS), the clinical hallmarks of which are anemia, leukopenia and thrombocytopenia (i.e., pancytopenia). TNF  $\alpha$  and IL-4 are thus possible mediators of hematopoietic dysregulation typical of MDS. Studies regarding these regulators can uncover the molecular pathways leading to cytopenias in MDS patients. As indicated earlier, myeloproliferative disorders are another, in some ways similar, group of hematopoietic disorders that are clonal in origin but not overtly malignant clinically. These MPDs include polycythemia vera. essential thrombocythemia, idiopathic myelofibrosis (agnogenic myeloid metaplasia) and chronic myelogenous leukemia. These disorders have the potential to change from one to the other at any time, however the signals that trigger such conversion remain enigmatic. Idiopathic myelofibrosis (IMF), in which stromal cells seem to play a profound pathogenetic role, is characterized by fibrosis of the marrow cavity, extramedullary hematopoiesis, splenomegaly, and anemia and leukoerythroblastic features in the peripheral blood. While myeloproliferation is known to be a clonal process, the accompanying stromal cell proliferation and fibrosis are believed to be a polyclonal reactive process that is likely to be due to increased intramedullary activity of a number of cytokines including TGF B, PDGF, FGF, EGF and calmodulin, as shown by other investigators.

Cancer genomics is a rapidly expanding area of investigation. The focus is unique however in emphasizing not the leukemic cells themselves but rather BM stromal cells that provide a haven to various types of pre-leukemia and leukemia cells, non-Hodgkin's lymphomas (NHLs) and metastatic cancers (METs). Pre-leukemic clonal neoplastic conditions include myelodysplastic syndromes (MDSs) and myeloproliferative disorders (MPD5). Stromal cells are known to produce and/or respond to growth factors such as EGF, PDGF, FGF, VEGF, and cytokines such as IL-I or TNF a, partially explaining the interactive relationship between stromal cells

and cancer cells, especially in MDS and CML.

Table 4, accounting for a total of 310 samples.

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In spite of similarities between BM stroma and non-BM stroma, certain sharp distinctions do stand out. Non-BM stromal cells are terminally differentiated fibroblasts, while BM stromal cells represent a unique pluripotent or pluridifferentiated mesenchymal cell type, thus exhibiting preserved developmental "plasticity". Using 5-10 cc BM aspirate samples from adult leukemic patients and 3-5 cc BM samples from pediatric patients with ALL, the study can analyze the BM stroma. One cc of marrow sample can produce at least 1 T-150 flask of stromal cells. One concern is that it can be hard to obtain marrow samples from cases like CML and myelofibrosis. In such cases stromal cells are grown using peripheral blood samples as described in the prior art. At least one flask of stromal cells (i.e., 1 cc marrow) to yield the RNA required for analysis. About 10 cases of each type of leukemia/lymphoma were studied. The study provided important insights into the functioning of the BM microenvironment in normal and leukemic hematopoiesis.

A database including all of the above information and that can include age, gender and associated major illness in terms of clinical/pathologic diagnosis for each subject/patient can be created. This can also include information on cytogenetic, molecular and flow cytometric studies. Finally, also included can be the information on clinical course in terms of disease progression and response to treatment exercising adequate care to protect the identity of individual patients. The study analyzed genomic expression profiles or signatures of bone marrow stromal cells derived from about 12 different normal bone marrow states and about 19

different leukemia/lymphoma states, approximately 10 cases of each as shown in

Using the information of the present invention, those of skill in the art can: a) study select gene or sets of genes as relevant to hematopoietic disease conditions using relatively inexpensive but low-throughput technologies such as Northern blotting, RNase protection assays and/or PCR intended for gene expression analysis; b) reanalyze the primary data by using newer and more powerful bioinformatic tools as they become available; and/or c) identify newer drug targets and diagnostic markers relevant to specific diseases, such as MM or CML etc.

Table 4 Scope of human BM samples targeted for DNA microarray analysis (approximately 10 cases of each)

Normal BM mononuclear cells (NMNC)

Normal BM stromal cells, unfractionated and unstimulated (NBMS)

Normal purified mesenchymal progenitor cells, unstimulated (NMPC)

NMPC stimulated with 9 different cytokines:

5 NMPC stimulated with TNFα (TNFα MPC)

NMPC stimulated with TGF $\beta$  (TGF $\beta$  MPC)

NMPC stimulated with interferon y (IFNγ MPC)

NMPC stimulated with 1L-4 (IL-4 MPC)

NMPC stimulated with TNF $\alpha$  + IL-4 (TNF $\alpha$  + IL-4 MPC)

10 NMPC stimulated with PDGF (PDGF MPC)

NMPC stimulated with EGF (EGF MPC)

NMPC stimulated with FGF (FGF MPC)

NMPC stimulated with calmodulin (calmodulin MPC)

MDS - Refractory anemia (MDS-RA MPC)

15 MDS - Refractory anemia with ringed sideroblasts (MDS-RARS MPC)

MDS - Refractory anemia with excess blasts (MDS-RAEB MPC)

MDS - Chronic myelomonocytic leukemia (M1)S-CMML MPC)

MPD - Polycytheniia vera (MPD-PV MPC)

MPD - Essential thrombocythemia (MPD-ET MPC)

20 MPD - Myelofibrosis (MPD-LMF MPC)

CML (CML MPC)

AML-MO/M1/M2 (AML-MOJM1JM2 MPC)

AML-M3 (APL) (AML-M3 MPC)

AML-M4/M5 (myelomonocytic) (AML-M4i'M5 MPC)

25 ALL-L1/L2 (lymphoblastic) (ALL-L1/L2 MPC)

ALL-L3 (Burkitt's) (ALL-L3 MPC)

Multiple myeloma (MM MPC)

CLLISLL (CLL/SLL MPC)

Follicle center cell lymphoma (FCL MPC)

30 Mantle cell lymphoma (MCL MPC)

Lymphoplasmacytic lymphoma (LPL MPC)

Marginal zone lymphoma (MZL MPC).

### **Human Subjects**

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This study involves the use of bone marrow (BM) samples from human subjects. BM samples can be obtained from normal subjects (male and female 20-45 years) as well as leukemic patients after informed consent is obtained. Leukemic cells can be obtained from diagnostic samples of BM of adult and pediatric patients (in those cases in which cells remain unused after clinical diagnostic studies are

preformed; i.e., about 90% of cases).

## Example 7

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In broad terms, global gene expression analysis is considered a nonbiased discovery-driven (as opposed to hypothesis-driven) approach to the analysis of protein expression. A stepwise proteomics strategy encompasses: solubilization of proteins from cells of interest; 2-D gel electrophoresis (IPG DALT); staining and image analysis of gels; excision of protein spots of interest; trypsin digestion of proteins; mass spectrometry (MALDI-TOF MS and/or ESI MS/MS) performed on tryptic fragments; identification of proteins by database searching. The present invention provides a method to analyze the population of expressed proteins (i.e., proteome) of BM MPCs in relation to hematopoiesis in collaboration with a state-of-the-art mass spectrometry facility.

The large-format 2-D gel electrophoretic system is used for reproducible separation of MPC proteins and to prepare 2-D PAGE protein maps for normal bone marrow-derived MPCs (untreated and treated with representative cytokines, e.g., TNF α and/or IL-4) and for MPCs derived from patients with representative pre-leukemic/premalignant and leukemic/malignant conditions. The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), acute lymphocytic leukemia (ALL), and multiple myeloma (MM). The protein samples can consist of culture supernatants/secreted proteins; extracellular matrix (ECM) proteins; plasma membrane proteins solubilized using a three-step differential extraction protocol, employing conditions of progressively increasing solubility; and whole cell lysate proteins similarly solubilized using the three-step differential extraction protocol. This subproteome approach not only simplifies the 2-D PAGE electrophoretic protein patterns but also reveals additional proteins, which would otherwise have gone undetected.

The system of the present invention can be used to differentially express MPC proteins (i.e., those that increased or decreased in intensity as compared to 2-D PAGE protein maps of normal, unstimulated MPCs) using mass spectrometry (MALDI-MS and/or nanoelectrospray ionization MS/MS) and/or Western blotting and/or Western-ligand blotting.

Using high-resolution proteomics with the added power of high-

throughput robotics, enables the system to identify on a larger (semi-comprehensive) scale the MPC proteins that are differentially expressed in conditions that simulate pre-leukemic bone marrow (following stimulation with different cytokines); and in actual pre-leukemic disorders (MDS) as well as in overt leukemias (CML, AML, CLL, ALL, MM).

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The system of the present invention enables the identification of MPC proteins whose expression is regulated as a result of exposure of normal MPCs to cytokines that are known to have a hematopoietic support role and/or are abnormally elevated in pre-leukemic/leukemic conditions, i.e., TNF  $\alpha$ ; IL-4; TNF  $\alpha$  + IL-4; interferon  $\gamma$ , TGF  $\beta$ ; PDGF; FGF; EGF; and calmodulin.

The system of the present invention also enables the identification of MPC proteins for which expression is altered as a result of exposure of normal MPCs to agents that are clinically used for mobilization of hematopoietic stem cells from BM into peripheral blood to facilitate easy collection and subsequent transplantation, e.g., G-CSF and G-CSF plus cyclophosphaniide.

Further, the system of the present invention enables the identification of Identify the MPC proteins whose expression is pathologically altered in hematopoietic disease states such as: MDS, CML, AML, CLL, ALL and MM by matching the 2-D PAGE protein maps of disease-associated MPCs with the 2-D PAGE database of normal MPCs. If a protein of interest does not exist in the normal MPC proteome, or if it exists in the normal MPC proteome but has not yet been characterized, then such proteins can be identified by MALDI-MS and/or Nano ESI MS/MS.

The system facilitates understanding of the pathogenetic mechanisms by identifying the phosphoproteins involved in cell signaling pathways. The systems immunoblots the whole cell lysate proteins of normal MPCs, untreated and treated with respective cytokines, using antibodies to phosphotyrosine, phosphoserine, and phosphothreonine. The system then locates the corresponding putative phosphoprotein spots on the gel and identifies the proteins by MALDI-MS and/or Nano ESI MS/MS. Similarly, the system can locate the altered phosphoproteins by immunoblotting the whole cell lysate proteins of untreated MPCs derived from leukemic patients. If a protein of interest does not exist in the normal MPC proteome, or if it exists in the normal MPC proteome but has not yet been identified,

then MALDI-MS and/or Nano ESI MS/MS can identify the protein.

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Bone marrow MPCs derived from a leukemia background express distinctively different patterns of cell adhesion molecules from normal MPCs.

BM stromal cells provide the background required for homing and subsequent proliferation and differentiation of hematopoietic stem cells. BM stromal cells also provide a rich microenvironment for metastases and growth of various leukemias. Based on the hypothesis that homing of normal hematopoietic cells and leukemic cells to marrow utilize the same adhesion mechanisms, it was questioned whether there are fine regulatory distinctions in terms of quantitative differences in the expression of the adhesion molecules in normal vs. leukemic BM microenvironments. In a pilot study 11 cell adhesion molecules (CAMs) and several lineage-associated markers for Northern blot analysis were targeted. Dexter-type cultures were grown under standard stromal cell culture conditions using bone marrow samples from a normal individual and from one patient diagnosed with and treated for acute myelogenous leukemia (AML). Representative cultures were treated with cytokines such as TNF  $\alpha$  alone, IL-4 alone, and TNF  $\alpha$  plus IL-4. MPCs from unstimulated and cytokine-treated cultures were purified using Percoll gradient techniques disclosed above. Total RNAs were extracted by a standard method and analyzed by Northern blotting. This study demonstrated expression by MPCs of several CAMs, heretofore unsuspected of expression by BM stroma. These include an embryonic endothelial cell protein Dell (developmental endothelial locus 1), galectin-I, human milk fat globule protein (RMFG, lactadherin), and epithelial membrane protein I (EMP 1). Secondly, MPCs from the AML patient expressed significantly lower levels of mRNA for three CAMs Del- 1, galectin- 1, and collagen type 1 as well as for the adipocyte marker adipsin, and to a minor degree the muscle-associated protein caldesmon. On the other hand, mRNA for CAMs like TGF beta-inducible BiGH3, HMFG, osteoblast-specific cadherin 11, and VCAM1 were dramatically increased in AML-associated MPCs. CAMs such as integrin beta 5, fibronectin, EMP 1 and the muscle-associated molecule transgelin are variably increased in diseased MPCs and appear to be unaffected by treatment with cytokines tested. ICAM I was undetectable at basal level in either patient or normal samples, but was slightly elevated by TNF  $\alpha$  and markedly elevated by TNF  $\alpha$  plus

IL-4. VCAM1 was mildly up regulated by TNF  $\alpha$  alone or IL-4 alone, but markedly up regulated by TNF  $\alpha$ /IL-4 in combination. Also, the MPCs from the patient were much more sensitive to stimulation by these inflammatory cytokines than were the normal MPCs. These studies establish that stromal cells in a leukemic patient are functionally defective.

Role of leptin receptor in hematopoiesis using human marrow stromal cells as a model.

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The receptor for the product of the obesity gene, leptin, is widely distributed in tissues ranging from central nervous system to reproductive system to hematopoietic system. Within hematopoietic system, OB-R is reportedly expressed on diverse cell types ranging from early CD 34+ hematopoietic stem cells to circulating monocytes. Leptin acts on monocytes to induce production of TNF  $\alpha$  and IL-6, which are powerful regulators of hematopoiesis. However, literature reports on the expression of leptin or its receptor on stromal cells are infrequent. To date, one particular report suggests that leptin acts on the stromal cells to enhance their differentiation into osteoblasts and to inhibit differentiation into adipocytes. Because leptin is an adipocyte-generated hormone and because marrow stromal cells represent a unique pluridifferentiated mesenchymal cell type expressing some adipocytic features, the expression of the leptin receptor by these cells was investigated in the hope of revealing its role in hematopoiesis.

By Northern blotting marrow stromal cells showed abundant expression of OB-R, consistent with their adipocytic nature. In terms of regulation, exposure of the stromal cultures to different cytokines revealed an interesting pattern of OB-R. As shown, G-CSF and TNF  $\alpha$  down-regulated OB-R while IL-4 upregulated OB-R expression by stromal cells. Simultaneous treatment of stromal cultures with TNF  $\alpha$  and IL-4 nearly abolished OB-R expression. The expression of OB-R was also analyzed at the protein level by a high-resolution, high capacity 2-D PAGE system, followed by Western blotting.

More specifically, the method provides the identification of leptin receptor in human BM stromal cell membrane protein extracts using 2-D Western blotting. The expression of OB-R was investigated at protein level using 2-D PAGE, followed by Western blotting. Two isoforms differing in molecular weight of 2.2 kDa (60.2; 62) and an isoelectric point of 0.2 pH unit (5.78; 5.98, respectively) have been

identified (the pH was determined by using the values specified by the IPG strip manufacturer). The ability to subsequently stain the same Western blot with gold stain allowed precise localization of the immunoreactive protein spots of interest on the blot. The gold staining of the blot, by revealing other protein spots in addition to the immunoreactive spots, has provided the necessary landmarks in turn facilitating subsequent alignment with the silver-stained gel using an appropriate 2-D analysis software program (Melanie 3).

This technique has identified two OB-R isoforms that differ in molecular mass by 2.2 kDa (60.2; 62.4) and differ in their isoelectric point by 0.2 pH units (5.78; 5.98). The level of macrophage contamination is determined by two macrophage markers, CD68 and cathepsin B. The studies include the determination of OB-R expression in a) unfractionated stromal cells vs. isolated pluri-differentiated mesenchymal progenitor cells; b) unstimulated cultures vs. cultures stimulated with a variety of cytokine/hormones including leptin itself. The studies also include mass spectrometric characterization of the two OB-R isoforms detected by Western blotting in order to establish their exact structural differences.

Proteome analysis of 2-D PAGE separated human BM stromal cell membrane proteins.

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BM stromal cells support the growth and development of normal blood cells as well as providing a haven for malignant leukemia/lymphoma cells. Focusing on stromal cell-surface proteins as potentially playing a role in cell-to-cell communication in normal as well as in abnormal hematopoiesis, the mixtures of stromal-cell plasma membrane, and plasma membrane-associated proteins were analyzed by a high-resolution, high-capacity 2-D gel electrophoresis. The 2-D system described utilizes an immobilized pH gradient gel (pH 4-7) in the first dimension and a mini nondenaturing but high-resolution lithium dodecyl sulfate-polyacrylamide gel electrophoresis (LDS-PAGE) in the second dimension. As identified by silver staining, this system has resolved greater than 800 protein spots in a pH interval of 2.5 units (4.25-6.75, the isoelectric pH range for most of plasma membrane proteins to migrate) and a molecular mass range of 10-150 kDa. Equally important, the system is compatible with high sample loads (up to 1.5 — 2.0 mg of total protein in up to 350-µl sample volume). All the protein species identifiable by a silver stain that is compatible with subsequent mass spectrometric analysis have

been analyzed by a 2-D gel software with respect to isoelectric point, molecular weight and mass abundance. The lectin-binding status of these proteins has also been determined by lectin blotting. Lectin blots and Western blots have subsequently been stained by a gold stain for detection of total proteins on the same PVDF membrane. Although gold-staining of the Western blot is not as sensitive as silver-staining of the gel, gold-staining of the Western blot generates the necessary landmarks for alignment with the silver stained gel, facilitating excision of spots of interest from the gel for identification by MALDI-MS. Representative protein spots were excised from gel and subjected to mass spectrometric profiling (MALDI-MS) and/or sequencing (Nano ESI MS/MS) with subsequent database searching, resulting in a productive identification of ten proteins. The protein digests are then submitted in a near-ready state for mass spectrometry. Upon receiving the MS data the group performs the database searching. MALDI/MS has been used, which identifies a protein on the basis of its characteristic mass sizes, as well as MS/MS studies that provide amino acid sequences of selected masses to identify proteins with enhanced specificity and confidence level. This work represents the first systematic attempt to analyze BM stromal cell proteins by high-resolution 2-D gel electrophoresis and provides the basis for a full-scale proteome mapping of the marrow stromal cells. The present work can facilitate the long-term goal of deciphering the hematopoietic support functions of BM stromal cells.

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Modulation of stromal cell plasma membrane protein expression by TNF  $\alpha$ /IL-4.

The effects of TNF  $\alpha$ /TM on bone marrow stromal cell plasma membrane protein expression has been tested using the described system. TNF  $\alpha$  and IL-4 are regarded as negative regulators of hematopoiesis. Notably these cytokines, especially TNF  $\alpha$ , are elevated in marrow plasma of patients with myelodysplastic syndromes (MDS), the clinical hallmarks of which are anemia, leukopenia and thrombocytopenia (i.e., pancytopenia). TNF  $\alpha$  and IL-4 are thus possible mediators of hematopoietic dysregulation typical of MDS. TNF  $\alpha$ /IL-4 treatment of the stromal cultures induced dramatic changes in the protein profile. Initial studies using plasma membrane protein samples show reduced expression of at least 7 proteins and enhanced expression of 13 proteins.

Analyzing the insulin-like growth factor system in human marrow stromal cells

## by 2-D PAGE analysis of BM stromal cell culture supernatants.

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Proliferation and development of normal and leukemic hematopoietic cells within bone marrow is regulated by interplay of various classes of molecules. These include cell adhesion molecules (CAMs), colony stimulating factors (CSFs), and cytokines as well as growth factors including insulin-like growth factors 1 and 2 (IGF 1 and IGF 2), which are small peptide homologs of prolinsulin. IGF 1 has known erythropoietic activity, whereas the function of IGF 2 is less clear. IGF 1 and 2 exert their activities through two types of receptors. The type I IGF receptor, a tyrosine kinase receptor highly homologous to the insulin receptor, binds to IGF 1 and IGF 2 with high affinity. The type II IGF receptor, a mannose 6-phosphate receptor that lacks intrinsic kinase activity, binds IGF 2 with high affinity and IGF I with low affinity. The type and number of receptors expressed on a target cell determine the strength of the IGF signal. One important key to understanding the IGFs' role in hematopoiesis is to appreciate how biological effects of receptors are modulated by larger soluble proteins, the IGF binding proteins (IGFBPs), which share no homology with the IGF receptors. Because IGFs and IGFBPs play important roles in cell growth and proliferation in many tissues, and because marrow stromal cells support hematopoietic growth and development, the patterns of expression of the IGF system components by marrow stromal cells cultured under serum-free conditions is necessary. To this end, unfractionated and purified stromal cells were analyzed, side-by-side, by Northern blotting, under varied stimulatory conditions for expression of IGFs and IGFBPs with surprising results. IGF 2 is constitutively expressed at a high level by macrophages in Dexter cultures; it is down regulated markedly by TNF  $\alpha$  alone; moderately by TNF  $\alpha$  plus IL-4; and unaffected by IL-4 alone. On the other hand, IGF 2 is minimally expressed by unstimulated MPCs, but is markedly up regulated by TNF  $\alpha$  alone or IL-4 alone; and moderately up regulated by combined TNF  $\alpha$  and IL-4. IGFBP4 is abundantly expressed both by macrophages and MPCs and is unaffected by cytokine treatment. In contrast, IGFBPs 5, 7, and 10, selectively expressed by MPCs, show no evidence of expression by macrophages and are unaffected by cytokine treatments. IGF 1 and the precursor to IOFBP 3 are not expressed in either macrophages or MPCs, either constitutively or after stimulation with TNF  $\alpha$ , IL-4 or both. In initial studies, bone marrow mononuclear cells expressed none of the IGFs or IGFBPs tested. These

results provide important insights into the operation of the IGF system in stromal cells and it is likely that potentially novel IGFBPs can be uncovered by ligand blotting studies.

The present invention provides a large-format 2-D gel electrophoretic system for reproducible separation of MPC proteins and to prepare 2-D PAGE protein maps for normal bone marrow-derived MPCs (untreated and treated with representative cytokines, e.g. TNF  $\alpha$  or IL-4) and for MPCs derived from patients with representative pre-leukemic and leukemic conditions. The pre-leukemic conditions include myelodysplastic syndromes (MDS) and the leukemic conditions include chronic myeloid leukemia (CML), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), acute lymphocytic leukemia (ALL), and multiple myeloma (MM). The protein samples can consist of culture supernatants/secreted proteins; extracellular matrix (ECM) proteins; plasma membrane proteins solubilized using a three-step differential extraction protocol employing conditions of progressively increasing solubility; and whole cell lysate proteins similarly solubilized using the three-step differential extraction protocol. This subproteome approach not only simplifies the 2-D PAGE electrophoretic protein patterns but also reveals additional proteins, which would otherwise have gone undetected.

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Molecular analysis assay involving the high-resolution 2-D PAGE and mass spectrometric identification of gel-separated proteins.

The completion of human genome project has provided a huge proteome database including the theoretical mass databases generated on the basis of site-specific cleavage employing proteolytic enzymes, such as trypsin and others. The availability of highly sensitive biological mass spectrometers together with the capability of bioinformatics to search extremely large amounts of data and identify the relevant proteins matching the mass spectrometry data provides the basis for the current excitement in proteomics. The focus of the interest is the BM MPC proteome as expressed under varied functional and disease states. The goal of the present invention is to identify BM MPC proteins that have possible functional and/or pathologic significance, that is, those proteins that show altered levels of expression in response to cytokine treatments and various leukemic states.

Until recently, the focus of the laboratory has centered on isolation and characterization of BM stromal cell adhesion molecules using a novel 2-D cell

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blotting technique. For this purpose, applicants have established an analytical 2-D mini gel system that separates stromal cell plasma membrane proteins using 18-cm long 4-7 pH range IPG strips in the 1<sup>St</sup> D (Amersham Pharmacia Biotech). Subsequent to IEF, the IPG strip is cut into appropriately small pieces and subjected to 2 D separation using nondenaturing lithium dodecyl sulfate-polyacrylamide gel electrophoresis (LDSPAGE) and mini gels. The reason for using mini gels in the 2<sup>nd</sup> D is that they are compatible with a downstream functional assay involving cell adhesion. The stromal cell membrane proteins are blotted on to a PVDF membrane and assayed for hematopoietic cell-binding proteins directly on the blotting membrane. The system can be extended using 17-cm long 3-10 pH range IPG strips (Bio-Rad) for separation of stromal cell culture supernatants, ECM proteins, and whole cell lysates. As detected by silver staining of the gels, and analyzed by appropriate software (GelLab II or Melanie 3) this 2-D system has resolved greater than 800 membrane protein spots within a pH interval of 2.5 units (4.25-6.75) and a MW range of 10-150 kDa. Similarly, the ECM samples showed 475 spots; and conditioned media from BM stromal cell cultures grown under serum free conditions showed 524 spots. Not surprisingly, the total cell lysate of BM stromal cultures showed only 553 spots, most likely representing the abundant housekeeping proteins and masking detection of many functionally relevant proteins. These observations provide the rationale for the proposed subproteome approach involving the use of differential solubilization of sample proteins and multiple large gels. Membrane proteins thus far identified by mass spectrometry followed by database searching; proteins are identified by standard Western blotting. Select IGF binding proteins were identified by ligand Western blotting. The blotting shows the identification of IGF-binding proteins (IGFBPs) using 2-D ligand blotting. The conditioned media from BM stromal cultures grown under serum-free conditions were concentrated using Microcon concentrator, and proteins were fractionated using a high-resolution 2-D PAGE. The separated proteins were electroblotted onto PVDF membrane and subjected to Western ligand-blotting assays using 1-125 labeled IGF-2, resulting in the identification of a series of IGFBPs (up to 30 spots). Notably, TNF  $\alpha$  treatment of the cultures down-regulated two LGFBPs and upregulated IGFBP labeled 6.

By necessity the protein work began on BM stromal cells using a

nondenaturing (LDS-PAGE) mini gel system that contained no reducing/alkylating agents. To preserve the function of 2-D gel separated proteins many otherwise powerful sample preparation methodologies designed for proteomic studies (such as multiple surfactant solution, MSS) were avoided. While mini gels are convenient and allow comparison and information transfer to large-format gels, they are less sensitive.

## Subproteomes according to sample prefractionation.

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In order to be able to identify the low-abundance proteins implicated in the regulatory and pathologic processes, a number of approaches to prefractionation of the whole cell lysates have been described. Applicant studied the subproteomes of secreted proteins from BM stromal cell culture supernatants as well as ECM proteins. Notably, the ECM protein samples can be a rich source of functionally relevant cytokines and chemokines since the latter are known to mediate function by binding to ECM. In addition, the plasma membrane and whole cell samples were subjected to the 3-step sequential solubilization protocol shown. The solubilizing solutions can be prepared in-house or purchased commercially (Bio-Rad). The first step involves the use of Tris base, which can solubilize the peripheral membrane proteins and cytosolic proteins. These proteins are lyophilized and subsequently solubilized prior to 2-D PAGE in a standard solubilizing medium (the modified O'Farrell cell lysis solution containing urea, CHAPS, DII, Iris, ampholytes and appropriate protease inhibitors). The resulting pellet can also be solubilized in the standard 2-D solubilizing medium and subjected to 2-D PAGE. Because the standard solution cannot solubulize some proteins, the membrane-rich pellet is finally solubilized in a potent multiple surfactant solution (MSS) consisting of urea, thitheea, CI-LAPS, zwittergent 3-10 and tributyl phosphine (TBP) in addition to Iris base and ampholytes that is compatible with subsequent IEF. The MSS has been shown to solubilize the hydrophobic proteins with as many as 12 transmembrane regions (TMRs), facilitating their 2-D analysis. Another final step incorporating 1% SDS in boiling sample buffer can be used to test by 1-D SDS-PAGE if any proteins remained unsolubilized after these extractions (notably, SDS extract is unsuitable for 2-D PAGE analysis since SDS interferes with IEF). The prefractionation step clearly reduces the complexity of the sample. Thus, the serial extractions not only simplify the gel images and reduce spot overlapping frequently encountered in single-step

extractions but also correlate closely with the cellular location of specific proteins, providing clues to their function. The prefractionation strategy can be extended to enriching low-abundance proteins in culture supernatants by selective removal of contaminating albumin using an Albumin Depletion Kit (containing Cibachron Blue resins) (Genomic Solutions, mc). Similarly membrane glycoproteins can be enriched by a Glycoprotein Enrichment Kit (containing lectins) prior to 2-D PAGE analysis (Genomic Solutions, Inc.).

## Subproteomes according to overlapping pH gradients.

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Using a series of medium-range and partially overlapping pH gradients (3-6, 5-8, 7-10, each 17-cm long) (Bio-Rad) can enhance reproducibility and resolution by creating "virtual" gels with up to 40 cm equivalent of PI separation across a pH 3-10 range. Alternatively, a combination of two pH gradients, pH 4-7 and pH 6-11, each 24 cm-long (Amersham Pharmacia Biotech) can be used, also providing a "virtual" separation distance of 40 cm across a pH range of 4-11. These strips accept micropreparative sample loads (1-2 mg). Notably, a given sample of cells yields a total of 8 protein samples. These samples include one protein sample composed of conditioned medium, one protein sample comprising of ECM proteins, three protein samples derived from plasma membrane lysates and three protein samples derived from total cell lysates, following application of a three-step protein extraction protocol to purified plasma membranes and total cells. Eight protein samples can thus translate into 24 large format (18 cm) gels corresponding to three overlapping 1st D gels; or 16 extra large format gels (24 cm) corresponding to two overlapping 1st D gels. Proteomics is no longer considered a single 2-D gel study. Taking advantage of the common spots in the 2nd D corresponding to overlapping regions, PDQUEST software can allow "stitching together" of the constituent gels, creating the so-called "cyber gel" providing a composite map for each protein sample. The data generated can be stored in an internet-accessible 2-D PAGE database in the form of 8 submaps. Three of these submaps correspond to plasma membrane proteins representing 3-step solubilization; one of them corresponds to secreted proteins; one of them corresponds to ECM proteins; and 3 of them correspond to total cell lysate proteins representing 3-step solubilization. These submaps can be linked to a master synthetic gel, a conglomerate of the submaps, representing the so-called "cyberproteome" of MPCs. Given the ability to run up to

12 IPG strips per 1st D gel (using IPGPhor) and 10 to 12 large or extra large SDS-PAGE gels per 2nd D gel run (using Hoefer DALI and Ettan DALI II, respectively), the resulting number of gels can be well within the manageable workload of one person (36). Although not easily accessible now, some innovative technological developments are on the horizon, e.g., development of fluorescence 2-D difference gel electrophoresis (DIGE), which could minimize the tedium. Unlike the current practice of running different protein samples on separate gels, and then staining and comparing the gels, DIGE technology uses matched, spectrally resolvable dyes (e.g., Cy2, Cy3 and Cy5) to label protein samples prior to 2-D separation. Differentially labeled protein samples are mixed and co-separated by 2-D electrophoresis, allowing analysis of at least three samples on a single gel. Gels are scanned and proteins are subjected to image analysis using appropriate software. Alternatively, one can use a highly sensitive silver stain to visualize the proteins after electrophoretic separation. Notably, the silver stain is compatible with subsequent mass spectrometry analysis.

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# Follow-up strategy for 2-D PAGE using the so-called ultrazoom LPG gels with narrow-range pH gradients.

Commercially available narrow-range IPG strips include pH 3.54.5; 4.0-5.0; 4.5-5.5;5.0-6.0; 5.5-6.7. These are available as 18 cm and 24 cm-long strips, consequently allowing spanning of 1 pH unit over a distance of 18-24 cm and providing extraordinary resolution. By using narrow pH gradients (IpH unit) up to 10mg of protein would be loaded onto a single IPG gel strip, either by repeated sample cup application or by in-gel rehydration without incurring vertical or horizontal streaking. Employing a combination of such narrow-range overlapping IPG strips, one study utilized up to 40 2-D gels for analysis of a single protein sample. The preference is not to follow such extreme approach but rather to use these gradients as a backup in situations where a functionally relevant protein is first detected by the front-end strategy but could not be studied by mass spectrometry for lack of adequate resolution or due to overlapping spots. The 24-cm long narrow IPG strips can be subjected to 2nd D using correspondingly extra large slab gels (the required precast, plastic-backed gels can be purchased from Amersham Pharmacia Biotech). However, the "giant 2-DE" 30 X 40cm size gels are impractical to handle. The situations for the use of narrow range pH gradients include situations like detection

of proteins by Western blotting using anti-phosphotyrosine antibodies or Western ligand blotting using labeled IGF 1 or 2, which are probably more sensitive than silver staining. Consequently, these assays identify the functionally relevant proteins but without providing the actual identity of the individual proteins. Because the frontend strategy can at least provide the range of the phosphoprotein or the IGF-binding protein identified, on the basis of this information samples can be subjected 2-D PAGE using the appropriate ultrazoom IPG strip, which as indicated above can permit loading of several mg of protein sample. Extra large precast slab gels (26x20 cm) with plastic backing suitable for running the 24-cm long ultrazoom IPG strips and the appropriate electrophoretic system (Ettan DALI II 2 dimension electrophoresis system) that runs up to 12 of these gels are commercially available (Amersham Pharmacia Biotech).

## Summary of subproteome strategy.

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The subproteome approach involves: 1) Cellular fractionation involving isolation of purified MPCs. 2) Subcellular fractionation involving preparation of functionally relevant protein sets. These include: 2a) secreted proteins such as colony stimulating factors (CSFs), cytokines, etc in the conditioned media; 2b) ECM proteins such as cell adhesion molecules (CAMs), etc; 2c) plasma membrane proteins such as various receptor molecules, CAMs and components of cell signaling systems, etc; 2d) finally, whole cell lysate proteins that include some of these proteins plus cytosolic and nuclear proteins. The cytosolic and nuclear proteins can be a rich source of target proteins for phosphorylation with a regulatory function.

## 2-D PAGE data capture and analysis

2-D PAGE data capture and analysis can be performed using standard equipment and protocols. Silver-stained gels can be scanned using an imaging densitometer and processed with QuantOne software (Bio-Rad) whereas gels stained with fluorescent Sypro Ruby (with 450 nm in the excitation range) can be scanned using a STORM 860 gel and blot imaging system and processed with ImageQuant Solutions software (Amersham Pharmacia Biotech). A number of factors, including differences in sample preparation and loading, staining and image acquisition can influence the reproducibility of 2-D gel protein separation. Quantitative data are reported as spot volumes (integrated spot densities). In

experiments comparing replicate 2-DE patterns of the same sample or 2-DE patterns of samples from different individuals, the spot volumes in each pattern are scaled to correct for differences in the total amount of protein loaded onto each gel. These variations are compensated by accurately comparing the quantity of any spot across multiple gels. These operations can be performed using a dedicated 2-D gel analysis software, Melanie 3. This program can analyze such variations by scatter analysis and can compensate for varying staining absorption across proteins by normalizing protein expression change. Varying stain intensities and sample sizes can be compensated for by relative spots quantification. The Melanie 3 software also has the capability to merge several gel electrophoretic patterns from the same sample into a composite gel, providing fine control over the included proteins. Finally, the software can compensate for gel distortions caused by variations in protein migration through alignment of the gels.

## Mass spectrometric instrumentation.

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Examples of such mass spectrometers include, but are not limited to, Voyager DE Pro (Applied Biosystems, formerly Perceptive Biosystems, Inc.) and QSTAR (Applied Biosystems). Voyager DE Pro is a matrix-assisted laser desorption time-of-flight mass spectrometer (MALDI-IOF) that can be operated in a linear mode for the analysis of large biomolecules or in a reflector mode for high-resolution analysis of smaller molecules, i.e., peptides. The MALDI-TOF instrument also utilizes delayed extraction technology that results in greatly increased resolution, sensitivity and mass accuracy. This is the instrument of choice for high throughput analysis, with a capacity of up to 100 samples per sample plate. On the other hand, the QSTAR is a hybrid quadrupole-quadrupole-time-of-flight mass• spectrometer. Samples are introduced in solution and are ionized by electrospray. For samples requiring the highest sensitivity, Dr. Jackson utilizes a low flow rate (25 nl miff') electrospray called nanoelectrospray, typically requiring only 1-2 μl of a solution for sample analysis. The QSTAR instrument yields data quite similar to those obtained from the MALDI-TOF instrument, except that the QSTAR data analysis is somewhat more complex due to the multiple charging of peptides by the electrospray process compared to the single charging applied to peptides on the MALDI-TOF instrument. One important additional characteristic of the QSTAR is its ability to determine structural information from sample molecules by tandem MS/MS. This is achieved by

effectively "purifying" selected molecules within the mass spectrometer's first quadrupole section. For analysis of peptides produced by tryptic digestion, a single MS experiment is initially performed to determine the masses of components present in the mixture. Next, MS/MS experiments are carried out to select specific peptides for  $de\ novo$  amino acid sequence determination. Typically 2  $\mu$ l of peptide mixture is sufficient for determining the sequences of ten to twelve peptides.

## Mass spectrometric analysis by MALDI

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The scheme for mass spectrometral analysis of in-gel tryptic digests of proteins for the purpose of protein identification consists of several steps. First, the peptides extracted from the gel must be cleaned and concentrated. The cleanup is necessary to remove residual detergent and other non-peptide materials that can interfere with the analysis of the tryptic peptides. This step involves binding of the peptides to a Microcon-SCX adsorptive microconcentrator. This is a cation exchange membrane held within a microcentrifuge device. At low pH, the peptides bind to the negatively charged membrane, while uncharged or negatively charged molecules pass through. After a brief wash, the peptides are eluted from the membrane in two 25-μl steps of 1.5 N ammonium hydroxide in 1:1 methanol/water. The samples are then speed-vac dried for 10 minutes, and fresh solvent is added for additional treatment to concentrate the sample prior to MS analysis. Initially, all samples can be analyzed by MALDI-TOF MS. For this analysis, the sample from the Microcon-SCX elution can be dissolved in 0.1% trifluoroacetic acid (TFA) in water and loaded on a ZipTipC 18 Pipette tip. The tip is then washed with the same solution and the peptides are then eluted directly onto the MALDI-TOF sample plate with 2 μl matrix solution (cyano-4-hydroxy-cinnamic acid, 10 mg/mi in 0.1% TFA in 1:1 acetonitrile/water). The spotted sample is dried at room temperature for at least five minutes before the sample plate is loaded in the instrument. The instrument calibration is performed externally by the addition of a calibration mixture to the sample plate. Samples are calibrated internally if the known tryptic autodigestion peptides are observed in the sample. This can be used as long as the specific type of trypsin used in the proteolytic digestion step is known. After data collection, the data can be further processed in two ways. First, the data can be treated by noise reduction software and second, it can be deisotoped. Software for both operations of these programs are standard features of the Data Explorer system provided with the

Voyager DE Pro mass spectrometer. The obtained peptide mass data can be subjected to peptide fingerprint analysis utilizing one of the protein database search sites on the Internet, such as Mascot or MS-Fit. While each of these search sites has access to several databases, one can initially select either OWL or NCBInr. One can search the database with a standard set of criteria without using a species filter. The practice is to select three variable modifications to allow for conversion of peptide N-terminal glutamine to pyroglutamate, and oxidation of methionine residues; allowing for up to one missed cleavage. Neither the protein MW nor the PI can be used as a search parameter (these, however, can be used for subsequent validation of the matched protein). Also important is that expected peptide masses of known potential "contaminants" such as keratin and trypsin can be excluded from analysis. Finally, the peptide mass tolerance can be set to +1-0.15 Da relative to the monoisotopic MW of the singly charged peptide ion. Positive database hits are scored with a MOWSE number. The higher the number of hits the greater the confidence level. The database search algorithm relates the significance level for a given search. If a high MOWSE score is obtained indicating an unambiguous match, one can consider the protein positively identified, otherwise the sample can be subjected to analysis by use of the QSTAR mass spectrometer.

## Mass spectrometric analysis by Nano ESI MS/MS.

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Samples that require analysis utilizing the QSTAR, following cleanup by Microcon-SCX adsorptive microconcentrator, can be concentrated by binding the peptide mix to a small amount of POROS R12 reversed-phase C18 chromatographic support packed into a nanopurification capillary. The packed capillary column volume is ~ 10-15 nl. The sample, dissolved in 10-p.l of 5% acetic acid in water, is applied to the capillary by use of a ten-µl gel loading pipette tip. A brief centrifugation forces the liquid down the capillary so that the peptides can bind to the support. The support is then washed with 10-15 p.1 of 0.5% acetic acid in 1:50 methanol/water. The peptides are eluted from the purification capillary into a nanospray capillary by the addition of 2 µ1 of 0.5% act id in 1:1 methanol/water followed by brief centrifugation with the nanospray capillary stacked just below the purification capillary in a micropurification holder (MDS Protana). Initially, data for a single MS run is collected. The peak masses are labeled and peptides are selected for potential MS/MS sequencing by locating those that appear to be doubly charged.

Most peptides resulting from a tryptic digest can have a significant doubly charged form, which is ideal for MS/MS sequencing. The first quadrupole of the QSTAR is tuned to pass a 2 Dalton window for the pre-selected doubly charged peptide ions, one at a time, for fragmentation by collision with low-pressure argon gas in the second quadrupole. Collision energy is adjusted for each peptide to obtain the best possible MS/MS spectra. Data are collected long enough to get good quality spectra. After MS/MS spectra are collected for all selected peptides, the data are manually interpreted. Internet protein database searches are performed similar to that for MALDI-TOF peptide fingerprint, except that the search is a partial amino acid sequence search with mass information (i.e., Mascot, employing Sequence Query format). The search criteria cannot screen for a species or a protein MW or PI (which, however, can be used for subsequent validation of the protein matched). Also important is that expected peptide masses of known potential "contaminants" such as keratin and trypsin can be excluded from MS/MS analysis. One missed cleavage can be allowed and two variable modifications can be selected, carbamidomethylation of cysteine and oxidation of methionine. The tolerance of the peptide monoisotopic mass can be set to +1- 0.3 and the MS/MS tolerance can be set at +1- 0.2. This type of search generally requires only two or three peptide sequences consisting of three of the amino acids per peptide to obtain a statistically significant match (a high MOWSE score). Once a match is identified, a list of the matched peptide's theoretical MS/MS fragments can be generated to compare with the observed fragments to further confirm the correctness of the match.

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Establishment of large-format 2-D PAGE protein maps for MPCs derived from normal BM.

The normal cell samples include, A) Untreated normal MPCs; B) Normal MPCs treated with TNF  $\alpha$ ; C) Normal MPCs treated with TNF- $\alpha$  and IL-4. Each cell sample can generate a total of 8 protein samples, 1) culture supernatants/ secreted proteins (1 protein sample); 2) extracellular matrix (ECM) proteins (1 protein sample); 3) plasma membrane proteins solubilized using a three-step differential extraction protocol employing conditions of progressively increasing solubility (3 protein samples); 4) whole cell lysate proteins similarly solubilized using a 3-step differential extraction protocol (3 protein samples). Each protein sample can generate 3 large format 2 D gels (corresponding to 3 medium-range, overlapping

IPG gradient gels, pH 3-6; 5-8; 7-10). This means each cell sample can generate 24 large format 2 D gels, leading to generation of at least 72 large format gels for analysis of normal MPCs. To account for duplicate or triplicate samples, the gel number falls in the range of 200-300.

Establishment of large-format 2-D PAGE protein maps for MPCs derived from BM involved with representative pre-leukemic and leukemic conditions.

The disease-associated MPCs include those from MDS, CML, AML, CLL, ALL, and MM. As above, each MPC sample can generate 24 large-format 2 D gels. With 6 such diseases being studied, the gel number can reach 144. To account for duplicate or triplicate samples, the gel number falls within the range of 400-500. The use of IPGPhor, together with ready-made IPG strips, permits sample in-gel rehydration and performance of unattended IEF overnight by adding automation to the 2-D procedure.

Using high-resolution proteomics and with the added power of high-throughput robotics, identify on a larger (semi-comprehensive) scale the MPC proteins that are differentially expressed in conditions that simulate pre-leukemic bone marrow (following stimulation with different cytokines); and in actual pre-leukemic disorders (MDS) as well as in overt leukemias (CML, AML, CLL, ALL, MM).

A robotically guided system facilitates excision of protein spots (by a spot cutter or picker) from 2-D PAGE gels, transfer of protein samples to 96-well microplates, and automated protein digestion in the microwells. Such a system reduces the time and labor relative to manual procedures and provides high throughput while minimizing keratin contamination from human skin, a frequent problem in proteomics research. The preferred method is to excise all spots from a gel but to process only the spots of interest, storing the remaining excised proteins frozen at -70°C for a later use. The robotic components can include MALDI slide spotter in addition to an automated protein spot picker and digestion station.

## Example 8

### 30 Methods

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The present study involved microarray analysis of 23 samples and a corresponding number of chips. The samples were obtained from 4 normal healthy adult human subjects, consisting of mixtures of unfractionated stromal cells

(collective USCs or cUSCs, 8 samples), Percoll gradient-purified MPCs (collective MPCs or cMPCs, 5 samples) and single-cell MPCs (sMPCs, 10 samples) obtained by laser-capture microdissection (LCM). The study design allowed for adequate controls and replicates appropriate for a comprehensive gene expression profiling of normal BM stromal cells. The isolated single stromal cells were selected on the basis of morphology. Wright-Giemsa stained cytospin preparation revealed characteristically large cells with a relatively irregular nucleus and cytoplasm compartmentalized into ectoplasm and endoplasm. Subsequently, applicant identified a hematoxylin stain as a substitute for Wright-Giemsa stain. The hematoxylin stain is simpler to use and provides morphologic detail sufficient to allow recognition and isolation of these cells by laser capture microdissection and does not interfere with the downstream microarray testing (see details under Materials & Methods). The photomicrographs of 10 stromal cells that have been subjected to microarray testing are shown in Figure 15. To serve as controls and facilitate comparison, applicant analyzed side-by-side 8 samples of unfractionated stromal cells that are "contaminated" by up to 35% macrophages and 5% hematopoietic cells (referred to collective USC, or cUSC), and 5 samples of Percollgradient purified stromal cells, up to 95% pure (referred to collective MPC, or cMPC to distinguish from sMPC). RNA isolated from sMPC samples was subjected to 2 rounds of amplification using RiboAmp kit (Arcturus, Inc) prior to in vitro transcription (IVT). In contrast, RNA samples isolated from cUSCs and cMPCs were used without amplification for IVT. The subsequent steps of microarray testing were standard for all 3 types of samples and are schematized as follows: Preparation of total RNA ightarrowgeneration of cDNA → preparation of ds cDNA → in vitro transcription into cRNA → fragmentation of cRNA  $\rightarrow$  hybridization of target RNA to a microarray of known genes (Affymetrix U95Av2 oligonucleotide microarray, with 12,625 probe sets) → Signal quantification and first-tier analysis using the microarray quantification software, Microarray Suite (MAS v. 5, Affymetrix, Inc). The presence of a gene within a given a sample was determined at a detection p-value of <0.05, according to the statistical expression analysis algorithm employed by MAS v.5, and was graded absent (A), marginal (M) or present/ positive (P).

## Assessment of RNA amplification method

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Since single-cell microarrays are relatively novel, applicant critically reviewed the

data with respect to two important statistics that would reflect on the reliability of RNA amplification assay procedure employed before analysis involving data-mining techniques. a) 3': 5' ratios of housekeeping control genes: As shown in Table 9, these ratios were close to 1 in the standard unamplified samples, whereas, they were increased in the amplified samples. Although this is to be expected due to preferential amplification toward 3' end, since amplification may not proceed all the way up to 5' end, applicant wanted to exclude possible sample degradation. For reasons unclear, in the case of ACTB (beta actin), the 3': 5' ratios were highly variable across single cell MPC samples. In any event, the 3': 5' ratios in case of GAPD (glyceraldehyde 3-phosphate dehydrogenase) were relatively tight, suggesting no evidence of sample degradation. Furthermore, both GAPD and ACTB gene probes that were employed as part of the standard gene probe set yielded relatively stable signals across replicates in each sample type, which is further evidence of intactness of RNA samples targeted for microarray analysis. b) Number of genes present or detected: As outlined in Table 9, the amplified single cell MPC RNA samples expectedly showed significantly lower number of genes compared to the standard RNA samples (on average 34% vs. 46% of the genes etched on the array). The fact that the number is relatively constant across single cell replicate samples is further indication of the reliability of the data. Notwithstanding the shortcomings of the amplification procedure, it is important to bear in mind that the conclusions are based only on those stromal cell genes that are detected commonly across unamplifed cMPCs and cUSCs as well as in amplified sMPCs (but do not include the genes undetected or the genes selectively detected in sMPCs).

### Data mining and reproducibility of overall procedures

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The thrust of the present invention is to identify genes that are relatively uniformly expressed across normal untreated bone marrow stromal cell samples, regardless whether they are of single cell type or collective cell samples, purified or unpurified. As detailed under Materials & Methods, GeneSpring was used to achieve the following data-analysis objectives: a) Filtering for genes reliably detected in each sample group by eliminating the genes with weak expressions that are statistically close to the background estimate. b) Filtering for genes that are active or "present" across replicates in each sample group. c) Exclusion of genes

with weak expressions from genes "present" in each sample group. d) Preparation of master stromal cell gene list by intersecting gene lists from step (c) (as shown in Figure 16). These steps have led to identification of a list of 2755 genes that are detected in at least 7 of 8 cUSC samples AND 4 of 5 cMPC samples AND 9 of 10 sMPC samples, i.e., in at least 20 of 23 stromal cell samples investigated. The main conclusions of the present report are based on this "stromal cell gene list" that is broadly representative of all 3 types of stromal cell samples investigated, and not on a gene list that is selective to sMPCs. A hallmark of the quality of microarray data can be discerned from hierarchical cluster analysis of replicates, which involves the principles of vector algebra. An array of numbers representing expression levels of a particular gene in terms of normalized signal intensity in a group of samples is considered a gene expression vector. Likewise, an array of numbers showing expression levels of a group of genes by a particular tissue sample is considered a tissue expression vector. In the case, applicants have 2755 gene expression vectors and 23 tissue or sample expression vectors. These vectors are amenable to algebraic treatment, facilitating calculation of similarity between any two gene- or tissue-expression vectors on the basis of a correlative metric or a similarity-measure employed, e.g., Euclidean angle. Grouping together of two samples on the basis of these principles signifies that they are most closely related out of all the samples in terms of their overall pattern of gene expression. Construction of a bone marrow stromal cell hierarchical tree has enabled visualization of global gene expression patterns across replicates and conditions. As shown in Figure 17, stromal cell genes that are expressed at a relatively lower level in amplified samples (sMPCs) are clustered to the left of gene tree, genes that are more strongly expressed in sMPCs are prominently figured in the middle of gene tree, and genes that are expressed approximately at same level as in unamplified samples (cMPCs and cUSCs) are clustered to right of gene tree. Even more important as noticeable on the sample or experiment tree, hierarchical clustering segregated the members of each sample type into a separate group (cMPC, cUSC and sMPC). Note within each sample type, corresponding subject replicates clustered together with minor exceptions. This is a reflection on the reproducibility of the overall assay-procedures employed, which encompass a variety of stages and steps in addition to target RNA amplification prior to in vitro transcription (see Materials & Methods for details).

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Finally, it is important to keep in mind that the measured level of a transcript following amplification does not necessarily provide a quantitative estimate of gene expression, but only provides a qualitative indication that the gene is transcriptionally active, which by itself is sufficient grounds for the conclusions arrived at in the present report. As shown in Figure 18, the expression of genes within the stromal cell gene list ranges from 0.2 to 6 (on the log scale) in unamplified samples (cMPC and cUSC) and from 0.02 to 36 in amplified samples (sMPC), thus showing much greater variability in the amplified samples. For illustration purpose, the coloring of gene expression curves (following the linear color bar shown on the right) was based on the gene expression pattern of a particular single-cell sample, SCA1. Note that the genes that are detected at a low level in this sample (as indicated in blue) are not necessarily expressed at a low level in unamplified samples (as read by the log scale on Y-axis). In fact, a significant number of them are expressed at a high level in the unamplified samples. This finding together with the observation that amplified samples detected about 34% of genes as opposed to unamplified samples detecting about 46% of genes tested (Table 9), strikes a cautious note that some genes do not amplify at all by the method used, and other genes amplify to a sufficient degree to be detectable (shown in blue), while some other genes amplify to a degree equal to (in yellow) or surpassing (in red) the amounts in the collective samples. (The curve shown in white is the housekeeping gene, GAPD.) The statistical algorithm as implemented in the latest version of Microarray Analysis Suite (MAS v.5) determined that a gene within a given sample as positive, regardless of grading. To overcome the limitations of the amplification procedure employed, applicant focused only on genes that were positive in at least 20 of the 23 stromal cell samples investigated.

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A stromal cell gene list is expected to be representative of typical stromal cell gene expression profile. Such master gene list forms the basis for derivation of all other stromal cell gene lists, organized in accordance with lineage or functional categories. As depicted in Figure 19A & 19B, and listed in Tables 10 through Table 17, that were prepared according to lineage/ functional assignment, the findings show that isolated single cells simultaneously express genes associated with diverse mesenchymal cell lineages, namely osteoblasts, muscle cells, fibroblasts, adipocytes, epithelial cells, endothelial cells, nerve cells and glial cells,

providing confirmation of the existence of a pluridifferentiated progenitor cell type. By definition the stromal cell genes are present in at least 4 of 5 collective MPC samples AND 7 of 8 collective USC samples AND 9 of 10 single cell MPC samples; consequently, they are active in at least 20 of 23 samples tested, representing a typical genomic profile of stromal cells. The following gene lists are sub-lists of the master stromal cell gene list consisting of 2,755 genes. The stromal cell gene list contains a number of genes that are capable of causing endothelial differentiation and vasculogenesis within the marrow microenvironment; however, these genes themselves are not necessarily endothelial cell markers. In fact, stromal cells express a gene, EDF1, the expression of which inversely correlates with endothelial cell differentiation within the stromal cells. Of the 67AFFX control genes present on the U95A v2 chip, 22 genes are detected in at least 7 of 8 cUSC samples, 24 genes are detected in 4 of 5 cMPC samples and 19 genes are detected in at least in 9 of 10 sMPC samples. Thirteen of these genes are present in the stromal cell gene list, i.e., in 20 of the 23 samples investigated.

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As evident from these gene lists, note that an isolated single stromal cell simultaneously expresses transcripts for epithelial and neuroectodermal cell types as well. Departing even further from the initial thinking, the findings add to the evidence that the MPCs within the Dexter system might represent a form or stage of the progenitor cell that is common to nonhematopoietic and hematopoietic cells. As depicted in Figure 20, and listed in Table 18 through Table 21, the isolated single stromal cells express transcripts that are typical of hematopoietic cells, in particular precursor B cells. That BM stromal cells express CD10 (CALLA) is not novel since BM stromal cells as well as endometrial stromal cells and normal breast myoepithelial cells are known to express CD10. However, the expression of CD19, CD79A and immunoglobulin enhancer binding factors E12/E47 (proto-oncogene TCF3) by BM stromal cells is unforeseen, and forms the basis for postulating the existence of a common progenitor with B cell lineage. B-cell progenitors typically display the phenotype, (CD45 +/-, CD34 +/-, CD20 +/-), (CD10 +, CD19 +, CD79A +, HLA-Dr +), which as reported here is also displayed by isolated single stromal cells at least at the transcriptome level.

CD45 positivity by cMPC and cUSC samples is attributable to coexisting or contaminating hematopoietic cells in these samples as evidenced by

concurrent positivity for myelomonocytic markers CD13, CD33 and CD14 (Table 21). However, a similar explanation cannot hold true in case of isolated single stromal cells. The protein products or transcripts for CD45 and CD19 are most likely present in stromal cells at a basal level that is beyond the detection limits of conventional techniques, e.g., immunocytochemistry and Northern blotting, respectively. Conceivably, two rounds of amplification prior to IVT sufficiently increased their transcript levels to be detected by microarray analysis. In fact, the CD45 levels were several-fold lower in cMPC and cUSC compared to CD45 levels in sMPC, and CD19 was undetectable in unamplified samples. Finally, note that CD45 and CD19 are not isolated examples in this regard since applicant has identified at least 200 other genes that are uniquely present across sMPC samples but undetectable in cMPC and cUSC (Figure 16).

#### The issue of stromal cell – B cell connection

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Although no anlage of Bursa of Fabricius exists in mammals, bone marrow is generally regarded as the site of B-cell generation. While the Dexter type stromal cell culture system was devised for investigation of hematopoiesis, specifically myelopoiesis (see Introduction), Whitlock and Witte developed another system for the study of B-lymphopoiesis. Whitlock-Witte cultures, like Friedenstein cultures, are grown in the absence of hydrocortisone and horse serum. When stromal cell layers in W-W cultures are seeded with fresh bone marrow as a source of B cell precursors or with purified B cell precursors, the latter then differentiate into mature B cells. On the other hand, although Dexter cultures do not promote B cell maturation, Dexter cultures do contain B cell precursors, which upon switching of culture conditions from those of Dexter to Whitlock-Witte, differentiate into mature B cells. While BM stromal cells in one form or another are definitely known to support B-lymphopoiesis, it has not been so clear as to whether stromal cells actually give rise to B-cell precursors. Evidence for a progenitor cell common to stromal cells and hematopoietic cells has been coming to light piecemeal in the form of isolated reports. 1) Singer JW et al in 1984 in the course of investigating bone marrow cultures from human patients with clonal myeloproliferative disorders showed that the nonhematopoietic stromal cells were derived from the same clonal progenitors that were involved by the hematopoietic neoplasm, as revealed by G6PD marker analysis. 2) Huss R et al in 1995 in the course of investigating a canine BM stromal

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cell line showed that the adherent stromal cells had "turned" into nonadherent hematopoietic cells, especially when the latter were cultured in presence of stem cell factor. 3) Pessina et al in 1997 showed that a particular murine stromal cell line upon stimulation with bFGF, expressed a B-cell phenotype, including CD45R and surface 5 immunoglobulin. Although not by design, applicant shows for the first time that isolated single stromal cells express transcripts that are typically associated with hematopoietic lineage, namely, CD45 and CD19, as well as relevant protooncogenes and transcription factors. These results are strongly supportive of the existence of a progenitor cell common to bone marrow stromal cells and hematopoietic cells, particularly the bone marrow-derived (B) lymphocytes. Note that the study involves no feeder cells, no embryonic stem cells, no cell lines and no colonies of cells. Contrasting with the existing literature, the present study embarks on a new path of investigation entailing gene expression analysis of single, primary, normal human stromal cells that suggest a broad capacity for multilineage differentiation. On this model, progenitor cells express genes that are characteristic of any of the lineage fates that these cells are capable of adopting.

# Perspective on pluripotentiality vs. pluridifferentiation

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The present investigation involves isolated single stromal cells, consisting of 10 cells from 4 different individuals (Figure 15). The cell culture system has been earlier characterized at light microscopic level, ultrastructural level and by karyotypic analysis, showing no evidence to suggest the artifacts discussed. Spontaneous cell fusion most likely involves monocytes/macrophages, forming multinucleated giant cells; however applicant observed no expression of myelomonocytic marker genes by isolated single stromal cells (Table 12). Keep in mind that the readout of in vivo transdifferentiation studies involves localization of different lineage cells in different tissues or organs; such a situation only requires fusion between two cell types (one donor cell and one recipient cell) for the investigators to believe the artifact as transdifferentiation. In contrast, applicant shows here presence of genes for a variety of cell-lineages simultaneously within the same cell. The probability of an array of different cell types fusing into one cell which then masquerading as a pluridifferentiated cell, and that too happening with 10 of 10 cells investigated, is in the opinion close to zero. There has never before been an opportunity to assess the extent of differentiation within these multipotential

progenitor cells in molecular terms at the single-cell level. Theoretically, a) A stem cell can directly become a terminally differentiated cell, or b) A stem cell can enter a phase of multilineage differentiation prior to becoming a single-lineage, mature cell. To the knowledge, this study is the first systematic attempt to answer these questions at the single cell level by using the marrow stromal cells as a model. Although numerous forward-looking reviews exist on the topic of single-cell genomics, only a rare report is available on the actual application of this technology. Applicant has applied this frontier technology to show that a phase of multilineage differentiation indeed exists at least in Dexter-type stromal cells. Pluripotentiality of the bone marrow mesenchymal stromal cells in terms of their ability to become muscle cells, bone cells, fat cells and fibroblasts under select culture conditions has been described by other investigators. Instead of documenting another example of the phenomenon per se, the results provide an independent validation of the studies on transdifferentiation by casting light at the molecular basis of cellular plasticity. Finally, to borrow a concept from the clinical practice setting, a morphologically "poorly" differentiated neoplasm expressing hematopoletic markers is classified as a leukemia/ lymphoma and treated as such. Similarly, a morphologically "undifferentiated" neoplasm marking for epithelial gene expression is diagnosed as a carcinoma and treated according to the protocols designed for a carcinoma. It is in this sense that applicant uses the term "pluridifferentiated" as opposed to "pluripotential" to characterize the BM stromal cells. Notwithstanding the semantics, applicant shows that the pluripotent stromal cells are pluridifferentiated, at least at the molecular level.

### **Conclusions**

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The findings of the present study clarify the on-going controversy as to the co-existence of multiple stromal cell types vs. one stromal cell type with co-expression of multiple phenotypes within the Dexter system of BM stromal cell cultures. An isolated single stromal cell from these cultures simultaneously expresses an array of phenotypes, i.e., osteoblasts, fibroblasts, muscle cells, adipocytes, epithelial cells, endothelial cells, neural cells/glial cells and even hematopoietic cells, in particular, B-lymphoid progenitors, thus documenting its wide differentiation repertoire. The significance of the findings is three-fold, 1<sup>st</sup>) They validate the hypothesis that the BM stromal cells express a pluridifferentiated

progenitor cell phenotype, providing insight into the molecular basis of cellular plasticity as well as establishing the utility of single-cell genomics, 2<sup>nd</sup>) They provide evidence for a common progenitor for mesenchymal progenitors and BM-derived (B) lymphoid progenitors, 3<sup>rd</sup>) By establishing a comprehensive phenotype of cultured bone marrow stromal cells at single cell level for the first time, the findings pave the road for ultimate identification and investigation of these cells in fresh samples of marrow, normal as well as diseased, in which they occur at a low frequency.

## Materials & Methods

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# Second-tier data-analysis/ data mining

The microarray data outputted by MAS v.5 (in the form of tab delimited text files) were imported into GeneSpring<sup>™</sup> software version 4.2.1 (Silicon Genetics, Redwood City, CA). Following instructions accompanying GeneSpring, each gene was normalized to itself (per-gene normalization) by using the median of the gene's expression values over all the samples of an experimental group (or groups) and dividing each measurement for that gene by the corresponding median value, assuming that it was at least 0.01. The ratios were then log transformed to base e. No per-sample normalization was performed in GeneSpring since it was already accomplished as part of MAS v.5 analysis. The purpose of the above data transformations, including scaling and normalization, was to remove systematic error within and across conditions or experimental groups prior to further analysis. GeneSpring was used to achieve the following data-analysis objectives. a) Filtering for reliably present genes by eliminating the genes with weak expressions that are statistically close to the background estimate. As per the instructions accompanying GeneSpring, random error was estimated from control strength or median measurement level using the two-component global error model of Rocke-Lorenzato that assumes variability between replicates as being similar for all genes showing similar measurement level. The formula for the error model of normalized expression levels can be written as follows:

$$S (norm)^2 = a^2/C^2 + b^2$$

Where, S = standard error of normalized expression data, a & b are the two error components, a = an absolute or fixed error component impacting at lower measurement values, b = a relative or proportional error component impacting at higher measurement levels, and C = control strength. According to the

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manufacturer, a curve is fitted for each group of replicates, with standard error of normalized data on Y-axis vs. control strength on X-axis. At lower end of control strength, the normalized standard error would be high and as the control strength increases, the standard error would decrease reaching a point where the curve flattens and data become more reliable. Control strength for each condition or sample group at which the above-referred two error components contribute equally, was calculated as follows, for collective MPCs, C = 128.68; collective USCs, C = 253.52; single-cell MPCs, C = 348.32. Each condition was filtered for genes expressing signals greater than the respective control strength, thus eliminating the genes with weak expressions from each group. Note 7,196 genes (out of 12,625 gene probes tested) passed the restriction in case of cMPCs, 7,287 genes in case of cUSCs and 5,937 in case of sMPCs. Corresponding gene lists were created. b) Filtering for genes "present" across replicates in each sample group. GeneSpring's "Add data file restriction" feature was used to prepare the respective lists of genes that were present (or expressed or active) in a least 7 of 8 cUSC samples, 4 of 5 cMPC samples, and 9 of 10 sMPC samples. Note 5,204 genes (out of 12,625 gene probes tested) passed the restriction in case of cMPCs, 4,763 genes in case of cUSCs, and 3,124 genes in case of sMPCs. Corresponding gene lists were created. c) Exclusion of genes with weak expressions from genes "present" in each sample group. Respective gene-lists for each sample group from steps (a) and (b), were intersected via Venn diagrams. Note 5,204 genes passed the restriction in case of cMPCs, 4,761 genes in case of cUSCs, and 3,124 genes in case of sMPCs, which are almost identical to the numbers obtained as under step (b), except for a difference of 2 genes in case of cUSCs, thus providing no significant improvement in restricting the data beyond under step (b). This is a reflection of the high stringency of the criterion employed under step (b). The 2 genes in case of cUSCs that passed the restriction under step (b) but failed the combined restriction under step (c) did show weak expressions (raw signals ranging, 142-331). Corresponding gene lists were created. d) Preparation of master stromal cell gene list. Respective gene lists for the three sample groups from step (c) were intersected via Venn diagrams, resulting in identification of a list of 2,755 genes that are uniformly present or expressed in at least 20 of 23 stromal cell samples investigated. The stromal cell gene list thus arrived at contained genes that

are representative of diverse mesenchymal lineages. Parenthetically, intersecting of gene lists corresponding to the three sample groups from step (b) resulted in a stromal cell gene list consisting of 2,756 genes, thus differing by 1 gene from the "official" master stromal cell gene list. e) Two-way hierarchical clustering of 2755 stromal cell genes based on expression profiles in 23 stromal cell samples. Only the data that were "cleaned up" of genes with weak expressions as outlined under step (a) were used for hierarchical clustering. This necessitated further processing of data in Microsoft Access prior to analysis by GeneSpring. Note that the data for each individual sample as outputted by MAS v.5 contained probe IDs, quantitative and qualitative data, as well as other information such as annotations and are readily recognizable by GeneSpring. In contrast, the gene list, resulting from step (a), contained only probe IDs and could not contain the data associated with each individual sample and was not recognizable by GeneSpring for inputting as part of an Experiment. Therefore, the microarray data for each group of individual samples (in Excel format) as well as the corresponding gene list for that group from step (a) (also in Excel format) were imported into an Access database. The genes that did not pass the test under step (a) were deleted from the microarray data for each individual sample by querying and intersecting with the appropriate post-cleanup gene list. The resulting data files were saved first as Excel files, then re-saved as tab delimited text files and then imported into GeneSpring. Per-gene normalization and log transformation were applied as described above. "Gene Tree" and "Experiment Tree" were constructed by applying a method similar to that of Eisen et al as implemented in GeneSpring and by using the stromal cell gene list and the following parameters: standard correlation as similarity measure; a minimum distance of 0.001; and a separation ratio of 0.5 in case of Gene Tree and 1.0 in case of Experiment Tree. f) Preparation of stromal cell gene lists as relevant to different cellular phenotypes and/ or functions. The gene lists associated with distinct mesenchymal cell lineages or phenotypes, i.e., osteoblasts, fibroblasts, muscle cells and adipocytes, etc, were prepared using a combination of methods. These include 1) Visually inspecting the entire stromal-cell gene list for relevant key words. 2) Directly searching the stromal cell gene list by using key words of interest via "Advanced Find Genes" feature under Edit menu in GeneSpring and by selecting "Search Only Current Gene List". 3) Intersecting the stromal cell gene list with gene

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lists of interest from Gene Ontology lists, e.g., list of oncogenes, via Venn diagrams. g) Visualization of gene-expression plots. The expression pattern of a gene across a given group (or groups) of samples of interest was pictured via Gene Inspector window, utilizing desired display options.

Throughout this application, various publications, are referenced by author and year. Full citations for the publications are listed below. The disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

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The invention has been described in an illustrative manner, and it is to be understood that the terminology which has been used is intended to be in the nature of words of description rather than of limitation.

The preceding descriptions of the invention are merely illustrative and should not be considered as limiting the scope of the invention in any way. From the foregoing description, one of ordinary skill in the art can easily ascertain the essential characteristics of the instant invention, and without departing from the spirit and scope thereof, can make various changes and/or modifications of the inventions to adapt it to various usages and conditions. As such, these changes and/or modifications are properly, equitably, and intended to be, within the full range of equivalence of the following claims.

**Tables** 

Table 5.

Summary of bone marrow stromal cell samples targeted for microarray analysis with an outline of the corresponding indicators of assay quality performance

	Unfractionated stromal cells (Collective USC, 8 replicates)	Percoll gradient- purified stromal cells (Collective MPC, 5 replicates)	LCM-dissected single cell samples (Single Cell MPC, 10 replicates)
Subject A	UNFR A	MPC A	SCA1, SCA2, SCA3
Subject B	UNFR B, UNFR B RI, UNFR B R2	MPC B R2	SCB1, SCB3
Subject C	UNFR C R1, UNFR C R2	MPC C R2	SCC1, SCC3
Subject D	UNFR D RI, UNFR D R2	MPC D R1, MPC D R2	SCD1, SCD2, SCD3
Amplification of RNA before IVT	No	No	Two rounds
Number of genes present (% of 12,625)	Mean: 46.63 SD: 5.95	Mean: 46.54 SD:3.66	Mean: 33.93 SD: 3.94
3':5' ratio, GAPD M33197 (Probe used as part of housekeeping control gene probe set)	Mean: 0.89 SD: 0.33	Mean: 1.23 SD:0.53	Mean: 6.76 SD: 2.97
GAPD signal 35905_s_at (Probe used as part of standard gene probe set)	Mean: 130,723 SD: 36,990	Mean: 164,593 SD: 40,204 (See Figure 5B.)	Mean: 43,235 SD: 14,413 (See Figure 5B.)
3':5' ratio, ACTB X00351 (Probe used as part of housekeeping control gene probe set)	Mean: 1.44 SD: 0.60	Mean: 2.29 SD: 1.57	Mean: 57.92 SD: 67.82
ACTB signal 32318_s_at (Probe used as part of standard gene probe set)	Mean: 86,104 SD: 18,458	Mean: 100,383 SD: 28,427 (See Figure 5B.)	◆Mean: 4,445 ◆SD: 884 (See Figure 5B.)

Footnote to Table 5

Replicate samples shown under each sample type as indicated correspond to each subject. The replicates of collective USC and collective MPC represent cell-culture or biological replicates of stromal cells grown in parallel flasks (instead of technical replicates). We started with 27 samples of which 2 collective MPC samples and 2 single cell MPC samples failed either at the test chip stage or produced unusual results in terms of the number of genes present and/ or 3':5' ratios and were therefore excluded as outliers. Only those samples that were targeted for the data mining analysis are represented in this table. The statistics shown (means and SDs) were based on the number of sample replicates indicated in the top row of the table except for ACTB-signal for single cell MPCs (noted in the table by  $\spadesuit$ ), which were based on 9 replicates instead of 10.

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Table 6:.. Osteoblast/ bon cell/ bone dis rders (S shi, B)

Systematic	Common	Genbank	Descripti n	Phenotype/ Function
38112_g_at	CSPG2	X15998	chondroitin sulfate proteoglycan 2 (versican)	
38111_at	CSPG2	X15998	chondroitin sulfate proteoglycan 2 (versican)	•
38126_at	BGN	J04599	biglycan	
36976_at	CDH11	D21255	cadherin 11, type 2, OB-cadherin (osteoblast)	
37315_f_at	BM036	AI057607	uncharacterized bone marrow protein BM036	
36996_at	OS-9	U41635	amplified in osteosarcoma	
41202_s_at	OS4	AF000152	conserved gene amplified in osteosarcoma	
671_at	SPARC	J03040	secreted protein, acidic, cysteine-rich (osteonectin)	
2087_s_at	CDH11	D21254	cadherin 11, type 2, OB-cadherin (osteoblast)	
1916_s_at	c-fos	V01512	Human cellular oncogene c-fos (complete sequence).	OMIM Notes: c-fos restricted to perichondrial growth regions of the cartilaginous skeleton.
1915_s_at	c-fos	V01512	Human cellular oncogene c-fos	• .
1388_g_at	VDR .	J03258	(complete sequence). vitamin D (1,25- dihydroxyvitamin D3) receptor	?Osteoporosis, involutional; Rickets, vitamin D-resistant
1451_s_at	OSF-2	D13666	osteoblast specific factor 2 (fasciclin I-like)	
32094_at	CHST3	AB017915	carbohydrate (chondroitin 6) sulfotransferase 3	
32307_s_at	COL1A2	V00503	collagen, type I, alpha 2	Ehlers-Danlos syndrome, type VIIA2; Marfan syndrome, atypical; Osteogenesis imperfecta, 3 clinical forms, 166200, 166210; Osteoporosis, idiopathic
32306_g_at	COL1A2	J03464	collagen, type I, alpha 2	Ehlers-Danlos syndrome, type VIIA2; Marfan syndrome, atypical; Osteogenesis imperfecta, 3 clinical forms, 166200, 166210; Osteoporosis, idiopathic

32305_at	COL1A2	J03464	collagen, type I, alpha 2	Ehlers-Danlos syndrome, type VIIA2; Marfan syndrome, atypical; Osteogenesis imperfecta, 3 clinical forms, 166200, 166210; Osteoporosis, idiopathic
34321_i_at	GS3786	D87120	predicted osteoblast protein	
34342_s_at	SPP1	AF052124	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	
34763_at	CSPG6	AF020043	chondroitin sulfate proteoglycan 6 (barnacan)	
222_at	EXT1	S79639	exostoses (multiple) 1	Chondrosarcoma; Exostoses, multiple, type 1
36822_at	WAC	U51334	WW domain-containing adapter with a coiled-coil region	Chondrosarcoma, extraskeletal myxoid
41202_s_at	OS4	AF000152	conserved gene amplified in osteosarcoma	
40790_at	BHLHB2	AB004066	basic helix-loop-helix domain containing, class B, 2; OMIM Notes: Alternative title, DEC1, expressed primarily in differentiated chondrocytes.	/ transcription factor

Table 7: Muscl / muscle disorders (Seshi, B)

O		Caabank	Description .	Phenotype/ Function
Syst matic	Common '	Genbank	Description .	, menetype i andien
38251_at	MLC1SA	Al127424	myosin light chain 1 slow a	•
38923_at	FRG1	L76159	FSHD (Facioscapulohumoral	·
			muscular dystrophy) region gene 1	
37012_at	CAPZB	U03271	capping protein (actin filament)	
<b>–</b> .			muscle Z-line, beta	
37279_at	GEM	U10550	GTP binding protein overexpressed in skeletal muscle	/ GTPase
36791_g_at	TPM1	M19267	tropomyosin 1 (alpha)	Cardiomyopathy, familial hypertrophic, 3
36790_at	TPM1	M19267	tropomyosin 1 (alpha)	Cardiomyopathy, familial hypertrophic, 3
36792_at	TPM1	Z24727	tropomyosin 1 (alpha)	••
36678_at	TAGLN2	D21261	transgelin 2	
36641_at	CAPZA2	U03851	capping protein (actin filament) muscle Z-line, alpha 2	·
36931_at	TAGLN	M95787	transgelin	•
37631_at	MYO1E	U14391	myosin IE	
41439_at	MYO1B	AJ001381	myosin IB	
40910_at	CAPZA1	U56637	capping protein (actin filament) muscle Z-line, alpha 1 -	/ binds barbed ends of actin filaments
41187_at	MLC-B	U26162	myosin regulatory light chain	
41747_s_at	MEF2A	U49020	Human myocyte-specific enhancer	•
			factor 2A (MEF2A) gene, last coding	}
			exon, and complete cds.	
41738_at	CALD1	M64110	caldesmon 1	
41739_s_at	CALD1	M83216	caldesmon 1	
39791_at	ATP2A2	M23114	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	
39790_at	ATP2A2	M23115	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	Darier disease
39378_at	BECN1	U17999	beclin 1 (coiled-coil, myosin-like BCL2 interacting protein)	
40488_at	DMD .	M18533	dystrophin (muscular dystrophy,	Becker muscular
<b>=</b>			Duchenne and Becker types)	dystrophy;
	•			Cardiomyopathy, dilated,
				X-linked; Duchenne muscular dystrophy
40438_at	PPP1R12A	D87930	protein (myosin) phosphatase 1,	OMIM Notes: Regulates
			regulatory (inhibitor) subunit 12A	the interaction of actin
				and myosin downstream
				of the guanosine
	:			triphosphatase Rho.

				• .	
	32838_at	smooth muscle myosin heavy chain isoform SMemb	S67247	Homo sapiens cDNA: FLJ23324 fis, clone HEP12482, highly similar to HUMMYOHCB Human nonmuscle myosin heavy chain-B (MYH10) mRNA	
	32755_at	ACTA2	X13839	actin, alpha 2, smooth muscle, aorta	•
	33994_g_at	MLC	M22919	Human nonmuscle/smooth muscle alkali myosin light chain gene, complete cds.	
	33447_at	MLCB	X54304	myosin, light polypeptide, regulatory, non-sarcomeric (20kD)	
	32313_at	TPM2	M12125	tropomyosin 2 (beta)	OMIM Notes: Fibroblast and muscle isoforms result from alternative splicing on exons 6 and
					.9.
	35362_at	MYO10	AB018342	myosin X	
	34306_at	MBNL	AB007888	muscleblind-like (Drosophila)	
•	36989_at	DAG1	L19711	dystroglycan 1 (dystrophin-	
				associated glycoprotein 1)	
	40022_at	FCMD	AB008226	Fukuyama type congenital muscular dystrophy (fukutin)	?Walker-Warburg syndrome; Muscular dystrophy, Fukuyama congenital
	39031_at	COX7A1	AA152406	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	congerma
	35729_at	MYO1D	AB018270	myosin ID	,
	32378_at	PKM2	M26252	pyruvate kinase, muscle	
	40375_at	EGR3	X63741	early growth response 3; OMIM	
	40070_at	·	X03741	Notes: Expressed in developing muscle spindles.	
	1637_at	МАРКАРКЗ	U09578	mitogen-activated protein kinase- activated protein kinase 3; OMIM Notes: Expressed especially high in heart and skeletal muscle.	
	40399_r_at	MEOX2	A1743406	mesenchyme homeobox 2 (growth arrest-specific homeobox).OMIM Notes: Important regulator of myogenesis.	
	39565_at	BMPR1A.	Z22535	bone morphogenetic protein receptor, type IA. OMIM Notes: Alternative title, activin receptor-like kinase 3; ALK3. Expressed almost exclusively in skeletal muscle with weak expression in heart and placenta.	Polyposis, juvenile intestinal
	41449_at	SGCE	AJ000534	sarcoglycan, epsilon	Dystonia, myoclonic
	at		74000004	daicogiyean, eponon	Dysionia, myocionic

Table 8: Fibroblast (Seshi, B)

Systematic	Common	Genbank	Description	Phenotype/ Function
39333_at	COL4A1	M26576	Human alpha-1 collagen type IV gene, exon 52.	
37037_at	P4HA1	M24486	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase),	•
. 36666_at	P4HB	M22806	alpha polypeptide I precursor; Human prolyl 4- hydroxylase beta-subunit and disulfide isomerase (P4HB) gene, exon 11, clones 6B-(1,3,5,6).	
41504_s_at	MAF	AF055376	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	
39757_at	SDC2	J04621	syndecan 2 (heparan sulfate proteoglycan 1, cell surface- associated, fibroglycan)	
39945_at	FAP	U09278	fibroblast activation protein, alpha	OMIM Notes: Expressed in fetal normal mesenchymal tissues and stromal fibroblasts within common types of epithelial tumors.
32835_at	MAFF	AA725102	v-maf musculoaponeurotic - fibrosarcoma oncogene homolog F (avian)	
32535_at	FBN1	X63556	fibrillin 1 (Marfan syndrome)	Ectopia lentis, familial; Marfan syndrome; MASS syndrome; Shprintzen- Goldberg syndrome
2057_g_at	FGFR1	M34641	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	Jackson-Weiss sydnrome; Pteiffer syndrome
1380_at	FGF7	M60828	fibroblast growth factor 7 (keratinocyte growth factor)	OMIM Notes: May play a role in mesenchymal stimulation of epithelial cell proliferation.
32313_at	TPM2	M12125	tropomyosin 2 (beta)	OMIM Notes: Fibroblast and muscle isoforms result from alternative splicing on exons 6 and 9.
31720_s_at	FN1	M10905	fibronectin 1	·
31719_at	FN1	X02761	fibronectin 1	•
35835_at	PDL-108	AB019409	periodontal ligament fibroblast protein	
34390_at	P4HA2	U90441	procollagen-proline, 2-oxoglutarate 4 dioxygenase (proline 4-hydroxylase) alpha polypeptide II	

Table 9: Adipocyte (Seshi, B, et al)

Prob ID	Gene Name	Genbank ID	Description	OMIM Notes
343,78_at	ADRP	X97324	adipose differentiation-related protein (adipophilin) / lipid-droplet binding/ adipocyte-specific	mRNA levels are induced rapidly and maximally after triggering adipocyte differentiation.
40282_s_at	DF	M84526	D component of complement (adipsin)	High level of expression in fat.
33337_at	DEGS	AF002668	degenerative spermatocyte homolog, lipid desaturase (Drosophila)	
39673_i_at	ECM2	AB011792	extracellular matrix protein 2, female organ and adipocyte specific	• • • • • • • • • • • • • • • • • • • •
39674_r_at	ECM2	AB011792	extracellular matrix protein 2, female organ and adipocyte specific	
31504_at	HDLBP	M64098	high density lipoprotein binding protein (vigilin)	•
37542_at	LHFPL2	D86961	lipoma HMGIC fusion partner-like	
36073_at	NDN	U35139	necdin homolog (mouse)/ Prader- Willi syndrome	
37122_at	PLIN	AB005293	Perilipin (Did not meet the criteria to be included in stromal cell gene list because it was positive in 5 of 5 cMPC and 9 of 10 sMPCs, but only 6 of 8 cUSc instead of 7 of 8 cUSC samples).	Plays an important role in adipocyte metaboloism. Has significant sequence relationship with ADRP.

Table 10::Epithelial cell/ carcin ma (S shi, B)

Systematic	Common	G nbank	Description	Phenotype/ Function
38590_r_at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	
38589_i_at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	
38610_s_at	KRT10; KPP	X14487	unnamed protein product; Human gene for acidic (type I) cytokeratin 10.	Epidermolytic hyperkeratosis
37326_at	A4	U93305	integral membrane protein; swiss-prot accession: O04901; may play role in cell differentiation in intestinal epithelium	·
36812_at	BCAR3	U92715	breast cancer anti-estrogen resistance	
36953_at	MADH4	U44378	MAD, mothers against decapentaplegic homolog 4 (Drosophila)	Pancreatic cancer; Polyposis, juvenile intestinal
36852_at	N33	U42349	Putative prostate cancer tumor suppressor	•
36851_g_at	N33	U42360	39 kDa protein; Human N33 protein form 2 (N33) gene, exon 11 and complete cds.	?Prostate cancer, susceptibility to
37762_at	EMP1	Y07909	epithelial membrane protein 1	/ receptor
37731_at	EPS15	Z29064	epidermal growth factor receptor pathway substrate 15	·
40856_at	SERPINF1; PEDF; EPC		PEDF; Human pigment epithelium- derived factor gene, complete cds.	
41431_at	ICK	AB023153	intestinal cell kinase	
39363_at	BC-2	AF042384	putative breast adenocarcinoma marker (32kD)	
39631_at	EMP2	U52100	epithelial membrane protein 2	
39542_at	ENC1	AF059611	ectodermal-neural cortex (with BTB-like domain)	e / associates with p110(RB)
40454_at	FAT	X87241	FAT tumor suppressor homolog 1 (Drosophila)	
32781_f_at	BPAG1	AA058762	bullous pemphigoid antigen 1 (230/240kD)	-
32780_at	BPAG1	AB018271	bullous pemphigoid antigen 1 (230/240kD)	
32329_at 34005_at	KRTHB6 PIGR	X99142 X73079	keratin, hair, basic, 6 (monilethrix) polymeric immunoglobulin receptor, expressed in glomerular epithelial cells	Monilethrix / Binds and transports . polymeric immunoglobulin
1846_at	LGALS8	L78132	lectin, galactoside-binding, soluble, 8 (galectin 8); OMIM Notes: Expressed in prostate carcinoma cells but only rarely in prostatic hypertrophy.	- 1

Table 11: Endoth lial cell (Seshi, B)

Systematic	Common	Genbank	Description	Phenotype/ Function
32755_at	ACTA2	X13839	actin, alpha 2, smooth muscle, aorta	
39315_at 1929_at	ANGPT1 ANGPT1	D13628 U83508	angiopoietin 1 angiopoietin 1	/ ligand for the TIE2 receptor
40387_at	EDG2	U80811	endothelial differentiation, lysophosphatidic acid (LPA) G- protein-coupled receptor, 2	
40874_at	EDF1	• •	endothelial differentiation-related factor 1; OMIM Notes: EDF1 level inversely correlates with the level of endothelial differentiation. Inhibition of EDF1 expression promotes endothelial cell differentiation. It is postulated that EDF1 may function as a bridging molecule that interconnects regulatory proteins and the basal transcriptional machinery, thus modulating the transcription of the genes involved in endothelial differentiation.	
37907_at	F8A; DXS522E	M34677	Factor VIII-associated gene 1; CpG island protein; Human nested gene protein gene, complete cds.	
41433_at	VCAM1	M73255	Human vascular cell adhesion molecule-1 (VCAM1) gene, complete CDS.	
36988_at	TNFAIP1	M80783	tumor necrosis factor, alpha-induced protein 1 (endothelial); OMIM Notes: Involved in the promary response of the endothelium to TNF.	
583_s_at 1953_at 36100_at 37268_at	VCAM1 VEGF VEGF VEGFB	M30257 AF024710 AF022375 U43368	vascular cell adhesion molecule 1 vascular endothelial growth factor vascular endothelial growth factor vascular endothelial growth factor B	
159_at	VEGFC ·	U43142 .	vascular endothelial growth factor C	/ ligand and activator of the receptor tyrosine kinase Flt4

Table 12: Nerve cell/ neuro indocrine/ neurologic disorders (Seshi, B)

			, , ,	
Systematic	Common	G nbank	Description	Phenotype/ Function
37298_at	GABARAP	AF044671	GABA(A) receptor-associated protein diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme	
37692_at	DBI GABARAPL	Al557240	A binding protein) GABA(A) receptor-associated	
35767_at	2 GABARAPL	AI565760	protein-like 2 GABA(A) receptor-associated	
35785_at	1	W28281	protein like 1	
38406_f_at	PTGDS	Al207842	prostaglandin D2 synthase (21kD, brain)	
38657_s_at	CLTA	M20471	clathrin, light polypeptide (Lca), brain specific insertion sequences	
38653_at	PMP22	D11428	peripheral myelin protein 22	Charcot-Marie-Tooth disease with deafness; Charcot-Marie-Tooth neuropathy-1A; Dejerine- Sottas disease; Neuropathy, recurrent, with pressure palsies
38291_at	PENK	J00123	preproenkephalin (; Human enkephalin gene: exon 3 and 3 flank.	
39072_at	MXI1	L07648	MAX interacting protein 1	Neurofibrosarcoma; Prostate cancer, susceptibility to/ transcription factor; forms heterodimers with Max protein
38841_at	GDBR1	AF068195	putative glialblastoma cell differentiation-related	
38818_at	SPTLC1	Y08685	serine palmitoyltransferase, long chain base subunit 1	Neuropathy, hereditary sensory and autonomic, type 1
36990_at	UCHL1	X04741	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase), neuron- specific. OMIM Notes: Highly specific to neurons and to cells of the diffuse neuroendocrine system and their tumors.	Parkinson disease, familial
37005_at	NBL1	D28124	neuroblastoma, suppression of tumorigenicity 1	
37286_at	NRCAM	AB002341	neuronal cell adhesion molecule	
36667_at	PYGB	U47025	phosphorylase, glycogen; brain	
36965_at	- ANK3	U13616	ankyrin 3, node of Ranvier (ankyrin G)	/ peripheral proteins believed to act as membrane-cytoskeleton linker molecules
	•			WW. 11101002100

				•
38040_at	SPF30	AF107463	splicing factor 30, survival of motor neuron-related	
37958_at	BCMP1	AL049257	brain cell membrane protein 1	
41221_at	PGAM1	J04173	phosphoglycerate mutase 1 (brain)	
40936_at 41091_at	CRIM1 FALZ	Al651806 U05237	cysteine-rich motor neuron 1 fetal Alzheimer antigen. OMIM Notes: Abnormally expressed in feta brain. The corresponding antibody ALZ50 recognizes neurofibrillary pathology associated with Alzheimer's disease.	I ·
41136_s_at	APP	Y00264	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	Alzheimer disease-1, APP- related; Amyloidosis, cerebroarterial, Dutch type; Schizophrenia, chronic
763_at 641_at	GMFB PSEN1	AB001106 L76517	glia maturation factor, beta presenilin 1 (Alzheimer disease 3)	Alzheimer disease, familial, with spastic paraparesis and unusual plaques;
				Alzheimer disease-3
39793_at 40023_at 39687_at 39686_g_at 39542_at	GBAS BDNF E46L E46L ENC1	AF029786 X60201 AI524873 AL050282 AF059611	glioblastoma amplified sequence brain-derived neurotrophic factor like mouse brain protein E46 like mouse brain protein E46 ectodermal-neural cortex (with BTB- like domain)	/ associates with p110(RB). OMIM Notes: Expressed highest in brain.
40193_at	ENO2	X51956	Human ENO2 gene for neuron specific (gamma) enolase.	
40121_at	HIP2	U58522	huntingtin interacting protein 2	
40467_at	SDHD	AB006202	succinate dehydrogenase complex, subunit D, integral membrane protein	Paragangliomas, familial central nervous system; Paragangliomas, familial nonchromaffin, 1, with and without deafness; Pheochromocytoma
40281_at	NEDD5	D63878	neural precursor cell expressed, developmentally down-regulated 5	·
32824_at	CLN2	AF039704	deficient in late-infantile neuronal ceroid lipofuscinosis; Homo sapiens lysosomal pepstatin insensitive protease (CLN2) gene, complete cds.	Ceroid-lipofuscinosis, neuronal 2, classic late infantile
32607_at	BASP1	AF039656	brain abundant, membrane attached signal protein 1	

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33817_at	D10S102	S63912	FBRNP; heterogeneous ribonucleoprotein homolog; This sequence comes from Fig. 3; D10S102=FBRNP [human, fetal brain, mRNA, 3043 nt].	·
- 33942_s_at	STXBP1	AF004563		/ implicated in vesicle trafficking and neurotransmitter release
1659_s_at 1695_at	RHEB2 NEDD8	D78132 D23662	Ras homolog enriched in brain 2 neural precursor cell expressed, developmentally down-regulated 8	
2053_at	CDH2	M34064	cadherin 2, type 1, N-cadherin (neuronal)	
216_at	PTGDS	M98539	Human prostaglandin D2 synthase gene, exon 7, brain	
32102_at	SACS	AB018273	spastic ataxia of Charlevoix- Saguenay (sacsin)	Spastic ataxia, Charlevoix- Saguenay type
31896_at 35681_r_at	NAG ZFHX1B	AL050281 AB011141	neuroblastoma-amplified protein zinc finger homeobox 1b. OMIM Notes: SMAD-interacting protein 1 (SMADIP1) appears to be essential to embryonic neural and neural crest development.	syndrome without
er.			<u>-</u>	Hirschsprung disease
35268_at 36190_at	AXOT CDR2	AL050171 M63256	axotrophin cerebellar degeneration-related protein (62kD)	
36609_at	SLC1A3	D26443	solute carrier family 1 (glial high affinity glutamate transporter), member 3	
35973_at 36142_at	HYPH SCA1	AB023163 X79204	Huntingtin interacting protein H spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1)	Spinocerebellar ataxia-1
34817_s_at	A2LP	U70671	ataxin 2 related protein	•
34777_at 34394_at	ADM ADNP	D14874 AB018327	adrenomedullin activity-dependent neuroprotector	
32606_at	BASP1	AA135683	brain abundant, membrane attached signal protein 1	
38233_at	HOMER-3	AF093265	Homer, neuronal immediate early gene, 3	
36998_s_at	SCA2	Y08262	spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2)	Spinocerebellar ataxia-2
35150_at	TNFRSF5	X60592	tumor necrosis factor receptor superfamily, member 5	Immunodeficiency with hyper-IgM, type 3
34166_at	SLC6A7	S80071	solute carrier family 6 (neurotransmitter transporter, L- proline), member 7	

34265_at	SGNE1	Y00757	secretory granule, neuroendocrine protein 1 (782 protein)	
654_at	MXI1	L07648	MAX interacting prot in 1	Neurofibrosarcoma; Prostate cancer, susceptibility to/ transcription factor; forms heterodimers with Max protein
37945_at 39685_at 33769_at 39356_at	BACH E46L MPZL1 NEDD4L	U91316 AL050282 AF087020 AB007899	brain acyl-CoA hydrolase like mouse brain protein E46 myelin protein zero-like 1 neural precursor cell expressed, developmentally down-regulated 4- like	
38800_at	STMN2	D45352	stathmin-like 2; OMIM Notes: Neuronal growth-associated protein SCG10.	
36933_at	NDRG1	D87953	N-myc downstream regulated gene	Neuropathy, hereditary motor and sensory, Lom type
40140_at	ZFP103	D76444	zinc finger protein 103 homolog (mouse); OMIM Notes: Alternative title, KF1, expressed in normal cerebellum and Alzheimer disease cerebral cortex, but not in normal cerebral cortex.	
1452_at	LMO4	U24576	LIM domain only 4	OMIM Notes: is highly expressed in the cranial neural crest cells, somite, dorsal limb bud mesenchyme, motor neurons, Schwann cell progenitors, and T-
1058_at	WASF3	S69790	WAS protein family, member 3	lymphocyte lineage.

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Table 13: Drosophila and/ or homeotic genes (S shi, B)

Systematic	Common	Genbank	D scription	Ph notype/ Function
38288_at	SNAI2	U69196	snail homolog 2 (Drosophila). OMIM Notes: Neural crest transcription factor SLUG. A zinc fanger protein that plays an important role in the transition of epithelial to mesenchymal characteristics within the neural crest.	
39037_at	MLLT2	L13773	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2	
39070_at	SNL	U03057	singed-like (fascin homolog, sea urchin) (Drosophila). OMIM Notes: Positive in dendritic cells of lymph nodes and Reed-Sternberg cells.	
39164_at	ARIH2	AF099149	ariadne homolog 2 (Drosophila). OMIM Notes: Upregulated during retinoic acid-induced granulocytic differentiation of APL cells.	
38750_at	<b>NOTCH3</b>	U97669	Notch homolog 3 (Drosophila).  OMIM Notes: Promotes the differentiation of astroglia from multipotent progenitors.	Cerebral (autosomal dominant) arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL)
38944_at	марнз	U68019	MAD, mothers against decapentaplegic homolog 3 (Drosophila)	OMIM Notes: SMAD3 signal transduction important in the regulation of muscle-specific genes.
37693_at	NUMB	L40393	numb homolog (Drosophila)	OMIM Notes: Numb directs neuronal cell fate decisions.
40004_at	SIX1	X91868	sine oculis homeobox homolog 1 (Drosophila)	OMIM Notes: Expressed in adult skeletal muscle, and in multiple tumors including mammary carcinoma.
39610_at	HOXB2	X16665	homeo box 82	OMIM Notes: Essential for motor neuron development. Within the hematopoietic compartment, expressed specifically in erythromegakaryocytic cell lines.

				•
40575_at	DLG5	AB011155	discs, large (Drosophila) homolog 5	OMIM Notes: Expressed in prostate gland epithelial cells.
40570_at	FOXO1A	AF032885	forkhead box O1A (rhabdomyosarcoma)	Rhabdomyosarcoma, alveolar. OMIM Notes: Activates myogenic transcription program.
40127_at	PMX1	M95929	paired mesoderm homeo box 1	OMIM Notes: Expressed in cardiac, skeletal and smooth muscle tissues.
40454_at	FAT .	X87241	FAT tumor suppressor homolog 1 (Drosophila)	OMIM Notes: Expressed in many epithelial, some endothelial and smooth muscle cells.
40328_at	TWIST	X99268 .	twist homolog (acrocephalosyndactyly 3; Saethre- Chotzen syndrome) (Drosophila)	Saethre-Chotzen syndrome. OMIM Notes: Required for cranial neural tube morphogenesis.
33222_at	FZD7	AB017365	frizzled homolog 7 (Drosophila)	OMIM Notes: Highest expression adult skeletal muscle and fetal kidney. FZD7 dependent PKC signaling controls cell sorting behaviour in the mesoderm.
32696_at	PBX3	X59841	pre-B-cell leukemia transcription factor 3	
33337_at	DEGS	AF002668	degenerative spermatocyte homolog, lipid desaturase (Drosophila); adipocyte associated.	
_1857_at	MADH7	AF010193	MAD, mothers against decapentaplegic homolog 7 (Drosophila)	OMIM Notes: MAD proteins were originally defined in Drosophila as essential components of the signaling pathways of the TGF-beta receptor family (e.g., TGFBR1). MADH7 and MADH6 as shown by IHC and ISH are predominantly expressed in vascular endothelium.
1955_s_at	MADH6	AF035528	MAD, mothers against decapentaplegic homolog 6 (Drosophila)	/ inhibitor of BMP signaling

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1013_at	MADH5	U59913	MAD, mothers against decapentaplegic homolog 5 (Drosophila)	OMIM Notes: SMAD5 plays a critical role in the signaling pathway by which TGF-beta inhibits the proliferation of human hematopoietic progenitor cells.
1453_at	MADH2	U68018	MAD, mothers against decapentaplegic homolog 2 (Drosophila)	
1433 <u>g</u> _at	MADH3	U68019	MAD, mothers against decapentaplegic homolog 3 (Drosophila)	OMIM Notes: SMAD2/ SMAD3 signal transduction appears to be important in the regulation of muscle-specific genes.
35681_r_at	ZFHX1B	AB011141	zinc finger homeobox 1b. OMIM Notes: SMAD-interacting protein 1 (SMADIP1) appears to be essential to embryonic neural and neural crest development.	Hirschsprung disease- mental retardation syndrome; Hirschsprung disease-mental retardation syndrome without Hirschsprung disease
35226_at	EYA2	U71207	eyes absent homolog 2 (Drosophila)	OMIM Notes: Expressed in extensor tendons, and in lens fibers and participates inconnective tissue patterning.
36308_at	ZIC1	D76435	Zic family member 1 (odd-paired homolog, Drosophila)	OMIM Notes: Specifically expressed in nervous tissue and in particular cerebellar granule cells,
				potential biomarker for cerebellar granule cell lineage and medulloblastoma.
34306_at	MBNL	AB007888	muscleblind-like (Drosophila)	OMIM Notes: Expressed in skeletal muscle myoblasts, also in lymphoblastoid cell lines.
33710_at	C3F	U72515	putative protein similar to nessy (Drosophila)	OMIM Notes: Expressed in fibroblasts and hepatocytes.

Table 14:	B-cell/ B-c II n oplasms (Seshi, B)				
Systematic	Common	Genbank	Description	Phenotype/ Function	
41562_at	BMI1	L13689	B lymphoma Mo-MLV insertion region (mouse)	/ proto-oncogene	
37294_at	BTG1	X61123	B-cell translocation gene 1, anti-proliferative		
38418_at	CCND1	X59798	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	Centrocytic lymphoma; Leukemia/lymphoma, B- cell, 1; Multiple myeloma; Parathyroid adenomatosis 1	
37730_at	p100	U22055	EBNA-2 co-activator (100kD); OMIM Notes: EBNA-2 activates transcription of specific genes and is essential for EBV-mediated Blymphocyte transformation.	nuclear protein 2 acidic	
466_at	GTF2I	U77948	general transcription factor II, I; OMIM Notes: Alternative title, BTK-associated protein, 135kD (BAP135). Bruton's tyrosine kinase (BTK) is essential for B-cell		
	. •		activation and phosphorylates BAP135 in B cells.		
36875_at 38438_at	IBTK NFKB1	AL050018 M58603	inhibitor of Bruton's tyrsoine kinase nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)		
39730_at	ABL1	X16416	v-abl Abelson murine leukemia viral oncogene homolog 1	Leukemia, chronic . myeloid	
38743_f_at	RAF1	X06409	v-raf-1 murine leukemia viral oncogene homolog 1		
36645_at	RELA	L19067	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)		
41436_at	ZNF198	AJ224901	zinc finger protein 198; OMIM Notes: ZNF198 involves T- or B-cell lymphoblastic lymphoma, myeloid hyperplasia, and eosinophilia and evolves toward AML. This multilineage involvement suggests the malignant transformation of primitive hematopoietic stem cell.	Stem-cell leukemia/lymphoma syndrome	
40091_at	BCL6	U00115	B-cell CLL/lymphoma 6 (zinc finger protein 51); OMIM Notes: BCL6 is predominantly expressed in the B-cell lineage, especially mature B cells (centrocytes and centroblasts).	Lymphoma, B-cell, Diffuse Large	
32776_at	RALB	M35416	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	÷ :	
32696_at 33791_at	PBX3 DLEU1	X59841 Y15227	pre-B-cell leukemia transcription factor 3 deleted in lymphocytic leukemia, 1	. •	

34005_at	PIGR	X73079	polymeric immunoglobulin receptor	/ Binds and transports polymeric immunoglobulin
1636_g_at	ABL	U07563	ABL is the cellular homolog proto-oncogene of Abelson's murine leukemia virus and is associated with the t9:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia.	Leukemia, chronic myeloid
1728_at	BMI1	L13689	B lymphoma Mo-MLV insertion region (mouse)	/ proto-oncogene
2020_at	CCND1	M73554	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	Centrocytic lymphoma; Leukemia/lymphoma, B- cell, 1; Multiple myeloma; Parathyroid adenomatosis
1295_at	RELA	L19067	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	
1377_at	NFKB1	M58603	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	
1461_at	NFKBIA	M69043	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	/ IkB-like activity
1389_at	MME	J03779	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	
35350_at	GALNAC4 S-6ST	AB011170	B cell RAG associated protein	
35992_at	MSC	AF087036	musculin (activated B-cell factor-1, ABF1); OMIM Notes: Downstream target of B-cell receptor signal transduction pathway. Also expressed in proliferating undifferentiated myeloblasts.	/ basic helix-loop-helix transcription factor
34344_at	IKBKAP	AF044195	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex- associated protein	Dysautonomia, familial
34350_at	RSN .	X64838	restin (Reed-Sternberg cell-expressed intermediate filament-associated protein); Note R-S cell is a form of B-cell.	. •
36204_at	PTPRF	Y00815	protein tyrosine phosphatase, receptor type F; OMIM Notes: Alternative title, Leukocyte antigen-related tyrosine phosphatase (LAR) Both LAR and LCA (CD45) map to chromosome 1. LCA is protein-tyrosine phosphatase, receptor-type C, PTPRC, whereas LAR is PTPRF.	•
34391_at	IGBP1	Y08915	immunoglobulin (CD79A) binding protein 1.	IGBP1, a marker for early B-cells

1373_at	TCF3	M31523	proto-oncogene or transcription factor 3 TCF3 (E2A immunoglobulin enhancer binding factors E12/E47); OMIM Notes: E2A mutant mice will have selective failure to develop B cells, all other hematopoietic c_ll lineages being intact. The block to B cell development occurs before immunoglobulin D(H)-J(H) rearrangement.	contributing the DNA binding domain of the t(1:19) translocation
35150_at	TNFRSF5	X60592	tumor necrosis factor receptor superfamily, member 5; OMIM notes: Alternative title, B-cell associated molecule CD40; expressed on the surface of all mature B cels, most mature B-cell malignancies and some early B-cell ALL.	Immunodeficiency with hyper-IgM, type 3
38740_at	ZFP36L1	X79067	zinc finger protein 36, C3H type-like 1; OMIM Notes: Alternative title, BERG36 (B-cell early response gene encoding a 36 kD protein).	
37026_at	COPEB .	AF001461	· ·	/ transcription factor involved in hepatic wound healing
38050_at	BTF	D79986	Bcl-2-associated transcription factor	
32696_at	PBX3	X59841	pre-B-cell leukemia transcription factor 3	

Table 15: Myel id cell/ myeloid leukemia (Seshi, B) Phenotype/ Function Description **Systematic** Common Genbank 39037\_at MLLT2 myeloid/lymphoid or mixed-lineage L13773 leukemia (trithorax homolog, Drosophila); translocated to, 2 Meis1, myeloid ecotropic viral 37486\_f\_at MEIS3 U68385 integration site 1 homolog 3 (mouse) Leukemia, acute 37685\_at **PICALM** U45976 phosphatidylinositol binding clathrin myeloid; Leukemia, assembly protein acute T-cell lymphoblastic MLL septin-like fusion; a fusion partner Leukemia, acute MSF AB023208 41220\_at myeloid, therapygene of MLL related; Ovarian carcinoma Myeloid leukemia, core-binding factor, beta subunit 41175\_at **CBFB** L20298 acute, M4Eo subtype Leukemia, acute 943\_at **RUNX1** D43968 runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 myeloid; Platelet disorder, familial, with oncogene) associated myeloid malignancy Leukernia, chronic v-abl Abelson murine leukemia viral 39730\_at ABL1 X16416 myeloid oncogene homolog 1 myeloid cell leukemia sequence 1 33146\_at MCL1 L08246 (BCL2-related) Leukemia, chronic ABL is the cellular homolog proto-ABL U07563 1636\_q\_at myeloid oncogene of Abelson's murine leukemia virus and is associated with the t9:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia. myeloid cell leukemia sequence 1 . 277\_at MCL<sub>1</sub> L08246 (BCL2-related) 41388\_at MEIS2 AF017418 Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) SET translocation (myeloid leukemia-40189\_at SET M93651 associated, M2/M4 AML); SET stands for suppressor of variegation, enhancer of zeste and trithorax. Leukemia, acute 38992\_at DEK X64229 DEK oncogene (DNA binding) nonlymphocytic Leukemia, acute 36941\_at AF1Q U16954 ALL1-fused gene from chromosome myelomonocytic 1q

Table 16:	T cell/ NK cell (Seshi, B)						
Systematic	Common	Genbank	D scripti n	Phenotype/ Function			
37685_at	PICALM	U45976	phosphatidylinositol binding clathrin assembly protein	Leukemia, acute myeloid; Leukemia, acute T-cell lymphoblastic			
498_at	TAX1BP1	U33821	Tax1 (human T-cell leukemia virus type I) binding protein 1				
40822_at	NFATC3	L41067	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3				
34003_at	·CD4	U47924	major receptor for HIV-1; member of immunoglobulin supergene family; T cell surface glycoprotein T4	/ T-cell coreceptor; involved in antigen recognition; participant in signal transduction pathway			
32602_at	RAP1GDS1	X63465	RAP1, GTP-GDP dissociation stimulator 1	Lymphocytic leukemia, acute T-cell (T-ALL)			
35279_at	TAX1BP1	U33821	Tax1 (human T-cell leukemia virus type I) binding protein 1				
34234_f_at	NKTR	A1688640	natural killer-tumor recognition sequence; OMIM Notes: The protein product of the NKTR gene is present on the surface of LGLs and facilitates their binding to tumor targets.				
39426_at	TCERG1	AF017789	transcription elongation regulator 1 (CA150)	/ HIV-1 Tat transcriptional coactivator			
32602_at	RAP1GDS1	X63465	RAP1, GTP-GDP dissociation stimulator 1	Lymphocytic leukemia, acute T-cell			

Table 17
Stromal cells showing expression of genes that are typically affiliated with B-cell progenitors

Gene	Probe ID	GenBank ID	cMPC	cUSC	sMPC
CD45	40518_at		Positive in	Positive in	Positive in
		,	4/5 samples	8/8 samples	6/10 samples
CD34	538_at		4/5	5/8	4/10
CD19	1116_at		0/5	0/8	10/10
CD20	619_at		1/5	0/8	3/10
CD22	38521_at		0/5	2/8	1/10
*CD10 (CALLA)	1389_at		5/5	8/8	10/10
Common acute					
lymphoblastic				٠.	
leukemia antigen.		,			
*Transcription	1373_at		5/5	8/8	9/10
factor 3 (E2A)					
Immunoglobulin					
enhancer binding					
factors E12/E47		·		•	
*CD79A (IGBP1)	34391_at		5/5	8/8	9/10
Immunoglobulin			·		
binding protein 1, a					
marker for early B-					
cells				*.	
*HLA class II,	37039_at		5/5	8/8	9/10 .
Dr alpha				·	

*HLA class II,	33261_at	5/5	8/8	10/10
Dr beta 1				:
*B2M	34644_at	5/5	8/8	10/10
Beta-2				
microglobulin				
.CD2	40738_at	1/5	2/8	2/10
CD5	32953_at	0/5	0/8	0/10
CD7	771_s_at	0/5	0/8	0/10
CD13	39385_at	5/5	8/8	0/10
CD33	36802_at	2/5	4/8	0/10
CD14	36661_at	3/5	8/8	0/10

Footnote to Table 17

Genes marked with asterisk (\*) have met the criteria for inclusion in stromal cell gene list.

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## **CLAIMS**

What is claimed is:

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1. Isolated mesenchymal progenitor cells that are pluri-differentiated.

- 2. A therapeutic composition comprising an isolated pluri-differentiated mesenchymal progenitor cells and a pharmaceutically acceptable carrier, wherein said isolated pluri-differentiated mesenchymal progenitor cells are present in an amount effective for treating a disease state in a mammal in need thereof.
- 3. A therapeutic composition comprising isolated pluri-differentiated mesenchymal progenitor cells and a pharmaceutically acceptable carrier, wherein said isolated pluri-differentiated mesenchymal progenitor cells are present in an amount effective to enhance hematopoietic progenitor cell engraftment in a mammal in need thereof.
- 4. A therapeutic composition comprising isolated pluri-differentiated mesenchymal progenitor cells and a pharmaceutically acceptable carrier, wherein said pluri-differentiated mesenchymal progenitor cells are present in an amount effective to treat GvHD in a mammal about to undergo bone marrow or organ transplantation or suffering from GvHD caused by bone marrow or organ transplantation.
- 5. A method for purifying pluri-differentiated mesenchymal progenitor cells comprising the steps of:
  - a) providing a cell culture preparation by the Dexter method;
  - b) treating the cells to obtain a cell suspension;
  - c) removing macrophages;
  - d) fractionating the cells; and
  - e) collecting the fraction of pluri-differentiated mesenchymal progenitor cells.
- 6. A method for enhancing bone marrow engraftment in a mammal in need thereof which comprises administering to the mammal (i) isolated pluri-differentiated mesenchymal progenitor cells and (ii) a bone marrow graft, wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered in an amount effective to promote engraftment of the bone marrow in the mammal.

7. The method according to claim 6, wherein said administrating step includes intravenously injecting or directly injecting the isolated pluri-differentiated mesenchymal progenitor cells to the site of intended activity.

- 8. A gene in an MPC for detecting the presence of cancer or pre-cancer in a cell population.
  - 9. A pharmaceutical for modulating the gene of claim 10.

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- 10. A method for enhancing engraftment of cells in a mammal in need thereof which comprises administering to the mammal isolated pluri-differentiated mesenchymal progenitor cells wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered in an amount effective to promote engraftment of the cells in the mammal.
- 11. The method of claim 10, wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered by intravenous injection or by injecting directly to the site of intended activity.
- 12. The method of claim 10, wherein the isolated pluri-differentiated mesenchymal progenitor cells are administered prior to administration of the hematopoietic progenitor cells.
- 13. The method of claim 10, wherein the isolated pluri-differentiated mesenchymal progenitor cells are introduced in a cell suspension also containing hematopoietic progenitor cells.
  - A SCID mouse model for investigating MPC function.
- 15. Phenotypic cultured bone marrow stromal cells capable of being analyzed at single cell level.
- 16. A diagnostic test for screening for abnormalities of bone marrow stromal cells.
  - 17. The diagnostic test according to claim 16, wherein said test can be used for screening for various hematologic diseases and other diseases effecting stromal cells
- 18. The diagnostic test according to claim 16, wherein said abnormalities are phenotypic abnormalities that can be discerned at a single cell level.
  - 19. Stromal cells for use in combination with engraftment or other similar procedures for enhancing the effectiveness of the treatment.

20. A method for treating graft-versus-host disease (GvHD) in a mammal about to undergo bone marrow or organ transplantation or suffering from GvHD caused by bone marrow or organ transplantation, by administering to the mammal an effective amount of isolated pluri-differentiated mesenchymal progenitor cells.

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- 21. A method for diagnosing a disease state comprising the steps of:
  - a) establishing gene expression patterns of normal state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells;
  - b) establishing gene expression patterns of various leukemic state bone marrow derived isolated pluri-differentiated mesenchymal progenitor cells;
- c) identifying gene sets that are unique to a given state; and
  - d) comparing a profile of bone marrow derived isolated mesenchymal progenitor cell of unknown state to said gene sets.
- 22. A method for identifying therapeutic targets for treatment of hematopoietic function comprising the steps of:
  - a) determining the median gene expression profile of bone marrow isolated pluri-differentiated mesenchymal progenitor cells associated with each disease state of interest;
  - b) identifying gene groups that are up-regulated, down regulated, and common to each disease state; and
  - c) identifying gene sets that are unique to a given state.

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Figure - 1

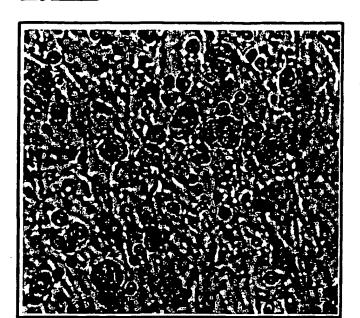
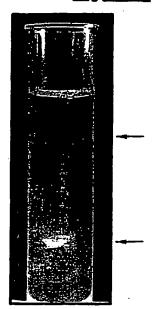


Figure - 2



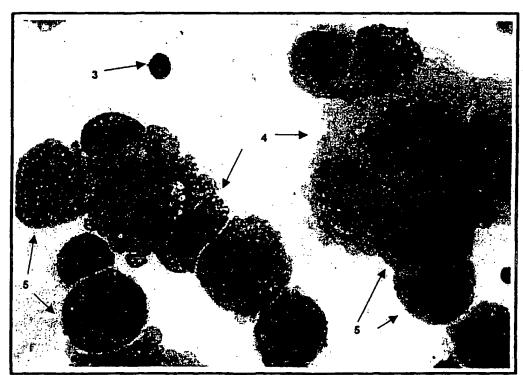
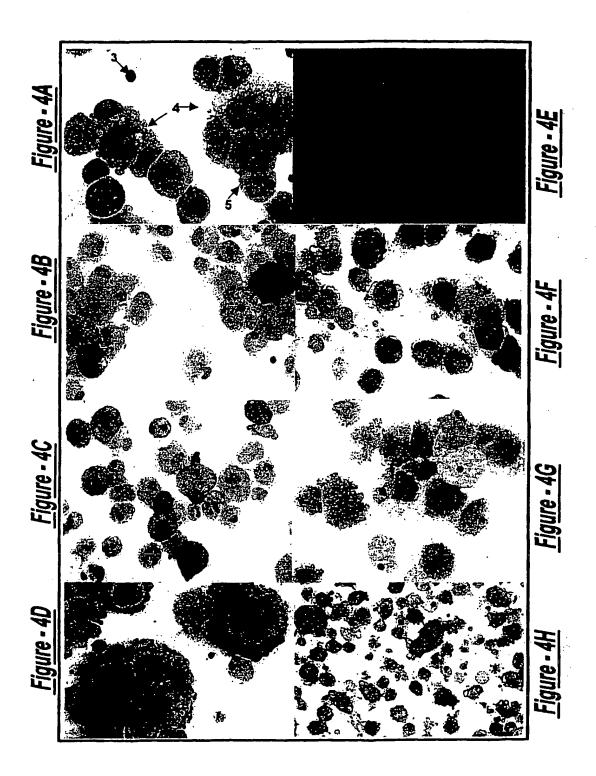


Figure - 3



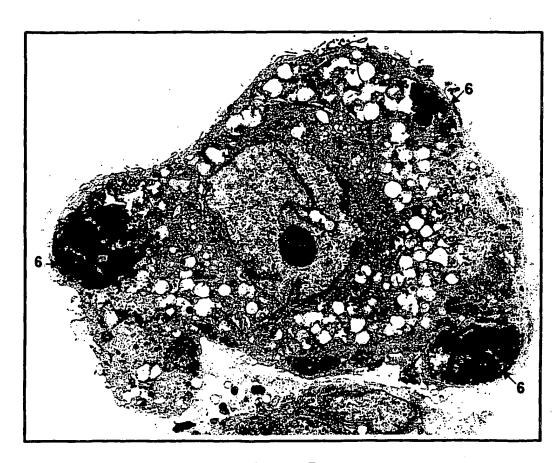
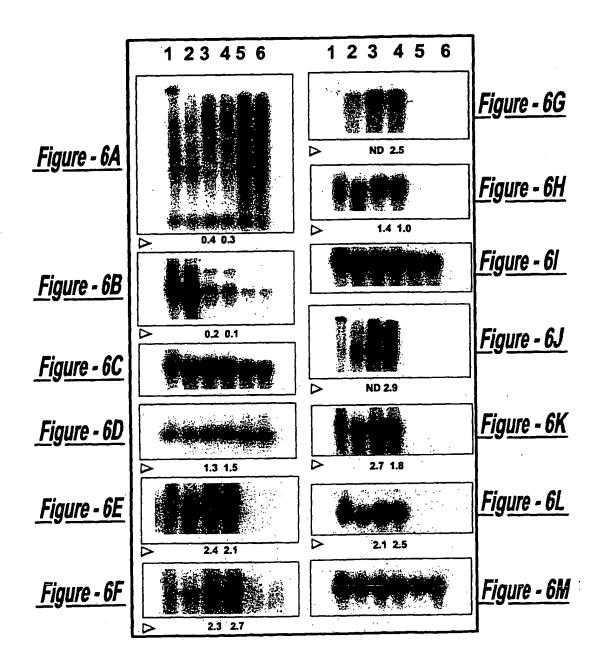


Figure - 5



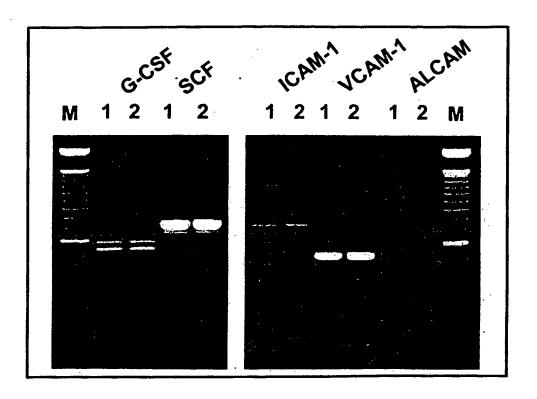


Figure - 7

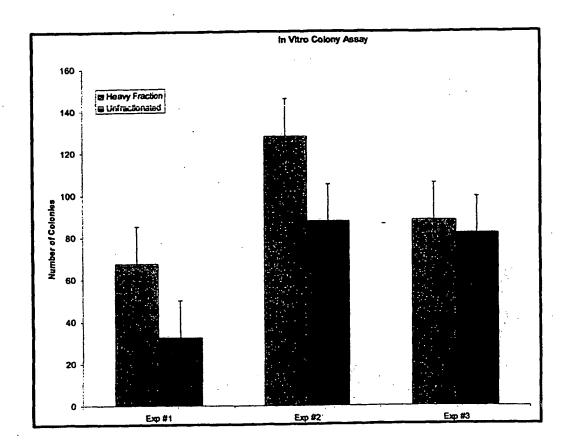


Figure - 8

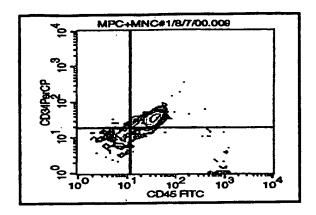


Figure - 9A

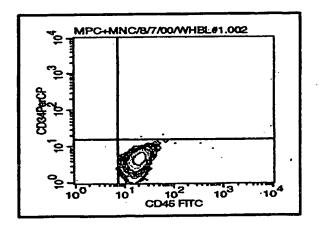


Figure - 9B

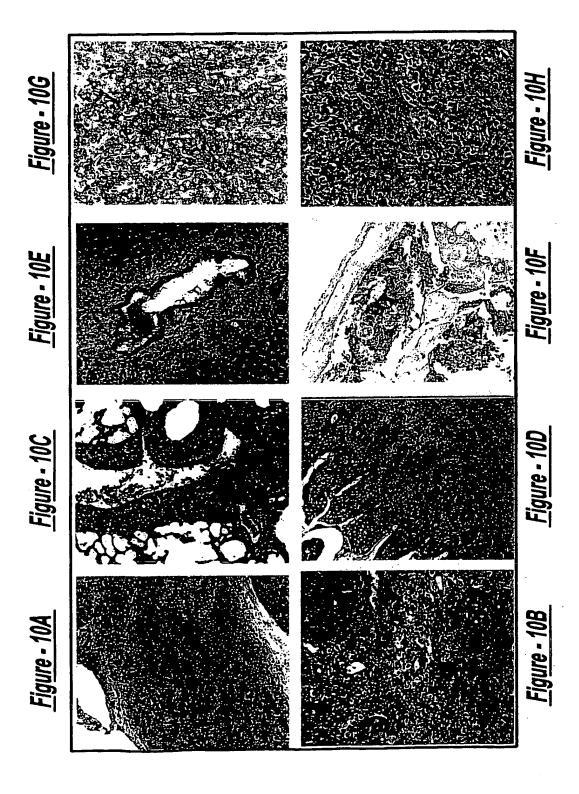


Figure - 11A

Figure - 11B

Figure - 11C

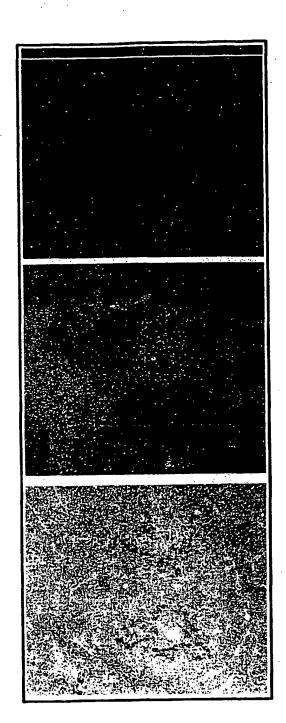


Figure - 12A

Figure - 12B

Figure - 12C

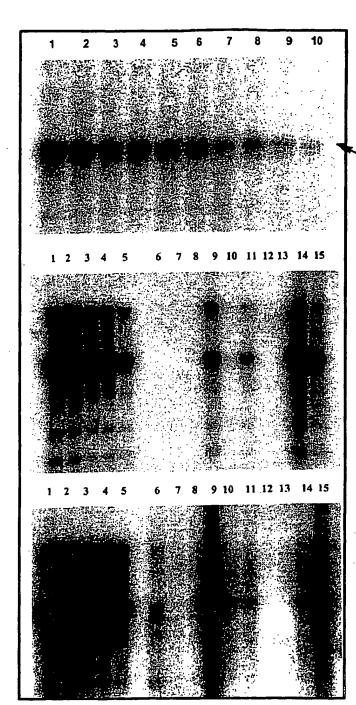


Figure - 13A

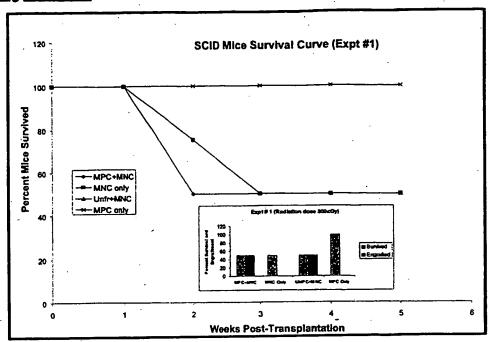
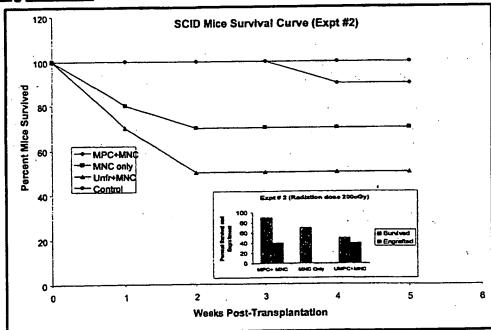
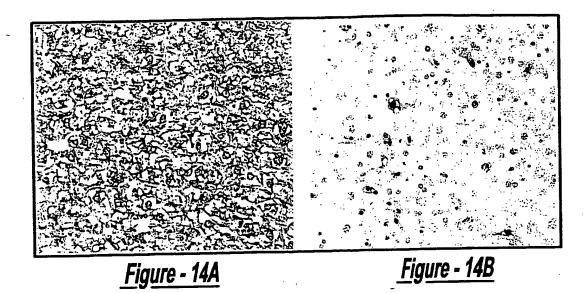


Figure - 13B





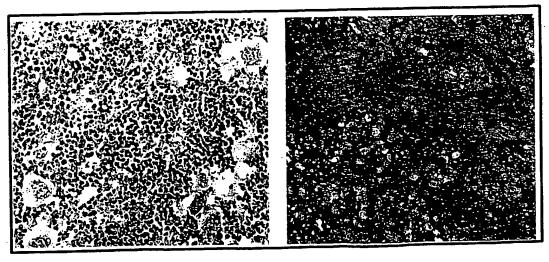
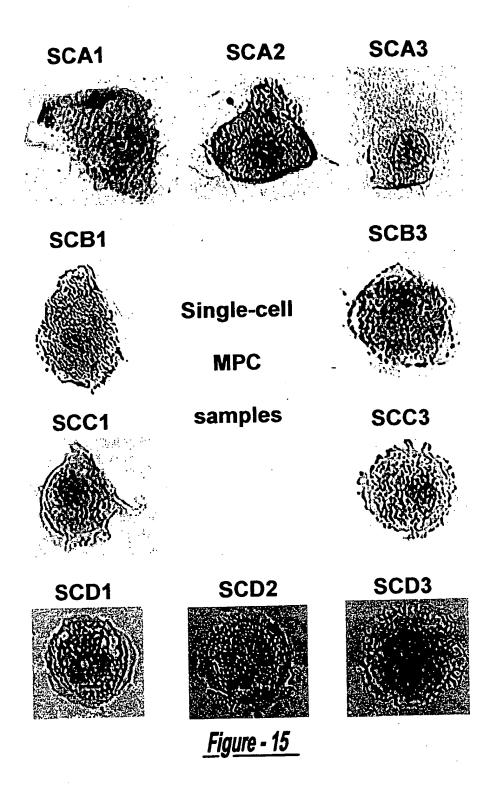


Figure - 14C

Figure - 14D



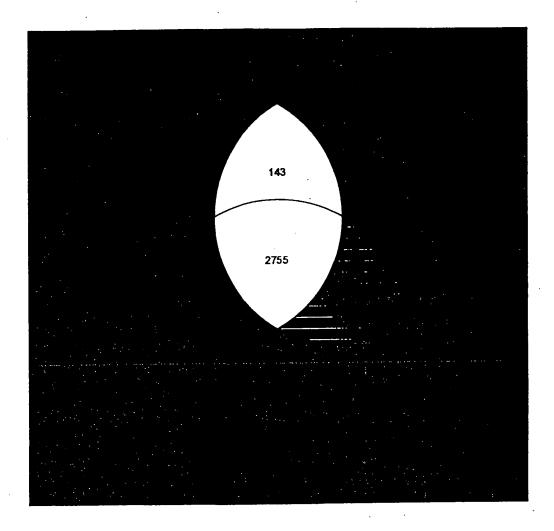


Figure - 16

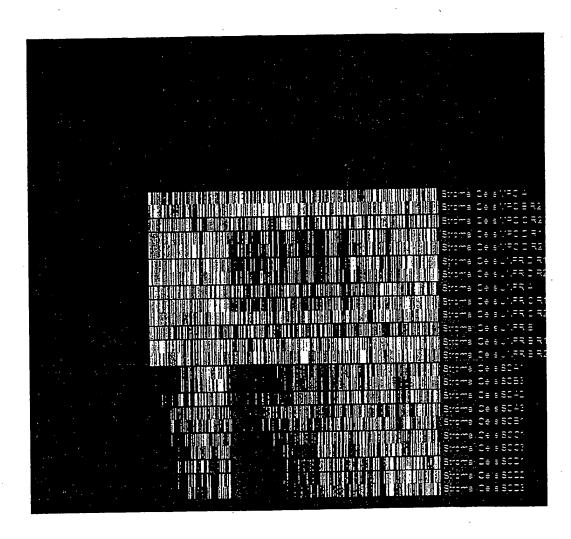


Figure - 17

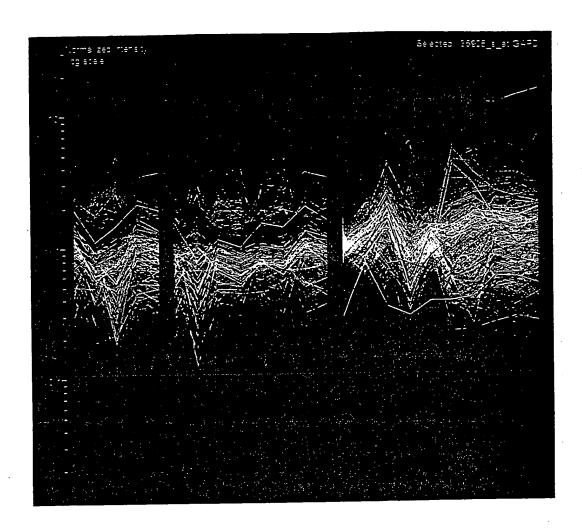
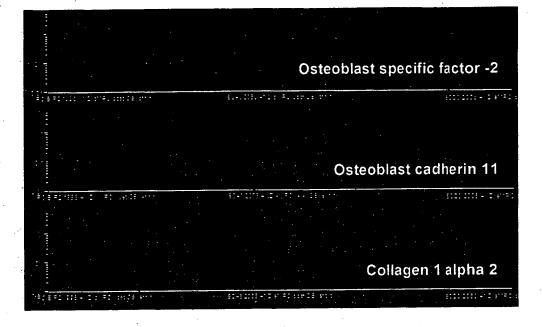


Figure - 18

Collective MPCs (Samples 1-5)

Single cell MPCs (Samples 6-15)

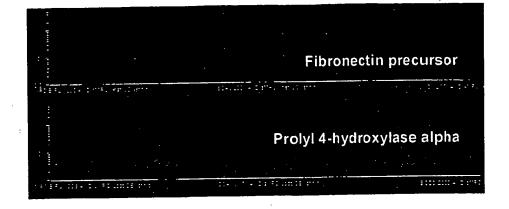


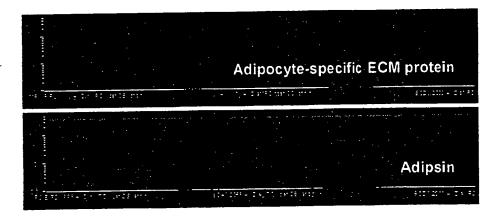
\$41.v	Smooth muscle myos	sin heavy chain
	The Communication of the Commu	<u> </u>
		Caldesmon
	# \$2.000 + 10 + 2.000 + 000 + 000 + 000 + 000 + 100 +	Transgelin 2

Figure - 19

C llective MPCs (Samples 1-5)

Single c II MPCs (Samples 6-15)





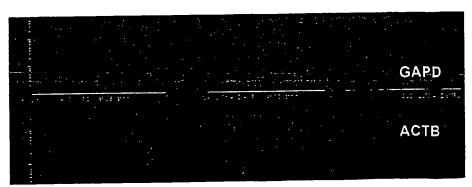


Figure - 20

Collective MPCs (Samples 1-5)

Single cell MPC (Samples 6-15)

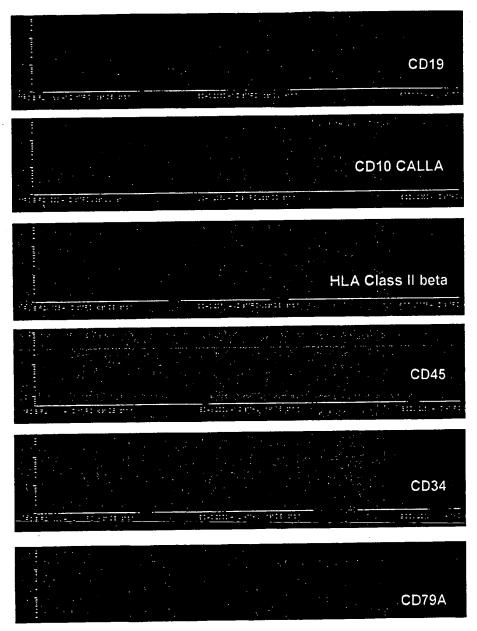


Figure - 21

	٧	8	ပ	Q	ш
1	Systematic	Common	Genbank	Description	Product
				***ALU WARNING: Human Alu-Sq	
2	AFFX-hum_alu_at	at	U14573	subfamily consensus sequence.	
3	38820_at	15-Sep	Sep AF051894	15 kDa selenoprotein	15 kDa selenoprotein
				26S proteasome-associated pad1	
4	33247_at	POH1	U86782	homolog	26S proteasome-associated pad1 homolog
				35 kDa protein; Homo sapiens splicing	
				factor, arginine/serine-rich 7 (SFRS7)	
5	32165_at	SFRS7	L41887	gene, complete cds.	splicing factor, arginine/serine-rich 7
				39 kDa protein: Human N33 protein form	
6	36851_g_at	N33	U42360	2 (N33) gene, exon 11 and complete cds. N33 protein form 2	N33 protein form 2
				3-hydroxy-3-methylglutaryl-Coenzyme A	3-hydroxy-3-methylglutaryl-Coenzyme A
7	39328_at	HMGCR	M11058	reductase	reductase
					succinyl CoA:3-oxoacid CoA transferase
8	41142_at	охст	U62961	3-oxoacid CoA transferase	precursor
				3'-phosphoadenosine 5'-phosphosulfate	
6	34411_at	PAPSS1	Y10387	synthase 1	PAPS sunthetase
10	738_at	NT5C2	D38524	5'-nucleotidase, cytosolic II	5'-nucleotidase
11	31794_at	NT5C2	D38524	5'-nucleotidase, cytosolic II	5'-nucleotidase
				5-aminoimidazole-4-carboxamide	
				ribonucleotide formyttransferase/IMP	5-aminoimidazole-4-carboxamide-1-beta-D-
12	38811_at	ATIC	D82348	cyclohydrolase	ribonucl eotide transformylase/inosinicase
				5-methyltetrahydrofolate-homocysteine	
13	38383_at	MTR	U73338	methyltransferase.	methionine synthase
14	39025_at	LOC54543	AI557912	6.2 kd protein	

ш	divalent cation tolerant protein CUTA	delta7-sterol reductase	ADAM10		metalloprotease/disintegrin/cysteine-rich protein precursor	gravin	KIAA0699 profein	KIAA0920 protein
Q	60S Ribosomal Protein L35A LIKE pseudogene match: proteins P04646 P02434 P18077 P05744 P41056 CE04362 match: cDNAs Y16430 X52966 X03475 V01440 X55030 J00995 match: ESTs AA55469 AA747384 AA572868 AA329139 AA745138 AA330809 AA483371 AA507788 AA483213 D55111 N90267 N91909 AA662153 AA720551 AA836920 AA501529 AA526745 AA608598 AA649846 AA654164 match: genomic DNAs Z32550 X05705 X05706 X05704 I23465 I45758	7-dehydrocholesterol reductase	a disintegrin and metalloproteinase domain 10	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)	a disintegrin and metalloproteinase domain 9 (mettrin gamma)	A kinase (PRKA) anchor protein (gravin) 12	A kinase (PRKA) anchor protein 10	A kinase (PRKA) anchor protein 2
0	AL021366	AF034544	AF009615	AA142964	U41766	U81607	AA114830	AB023137
8	clCK07210.1	DHCR7	ADAM10	ADAM17	ADAM9	AKAP12	AKAP10	AKAP2
A	40446			41601 at			36633_at	35985_at
	Ť.	9	4	8	19	8	2	23

		_		_						$\neg$	$\neg$	
ш	proto-oncogene tyrosine-protein kinase	accessory proteins BAP31/BAP29	mitochondrial 3-oxoacyl-CoA thiolase	acetyl-coenzyme A transporter		acidic nuclear phosphoprotein pp32	APRIL	okadaic acid-inducible phosphoprotein	KIAA0785 protein	iron regulatory factor	actin filament associated protein	actin related protein 2/3 complex, subunit 2 (34 kD)
Q	emia 22 22 9 BCR acute 1b; 1b; 1b; 1cenia 22 acute 9 4co- 4co-	accessory proteins BAP31/BAP29	82 16 A	acetyl-Coenzyme A transporter	acetylserotonin O-methyltransferase-like	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	acid-inducible phosphoprotein	Ac-like transposable element	aconitase 1, soluble	actin filament associated protein	actin related protein 2/3 complex, subunit 2 (34 kD)
O		X81817	D16294	D88152	AA669799	U73477	Y07969	AF069250	AB018328	Z11559	D25248	U50523
В	ABL	DXS1357E	ACAA2	ACATN	ASMTL	ANP32A	ANP32B	OA48-18	ALTE	ACO1	AFAP	ARPC2
¥	1636 g at	41724 at	41530 at	34668 at	_	7			39168_at	40077_at	37578_at	
r	24	25	26	27	78	29	8	3	32	33	ह	ဗွ

F1321

ARPC4   AF006087   4 (20 kD)   AF006087   4 (20 kD)   AF006088   5 (16 kD)   AF006088   5 (16 kD)   ACTA2   X00351   actin alpha 2, smooth muscle, aorta   ACTA2   X00351   actin, abta   ACTA1   X15804   actinin, alpha 1   ACTA1   X15804   actinin, alpha 1   ACTA1   ACTA1   X15804   actinin, alpha 1   ACTA1   ACTA1   X15804   actinin, alpha 1   ACTA1   AC	T		-	C		u
ARPC4   AF066087   actin related protein 2/3 complex, subunit pages2_at ARPC5   AF066088   5 (16 kD)     22755_at ACTA2   X13839   actin, beta actin, apha 1   23218_a actin, beta actin, beta actin, beta actin, apha 1   34160_at ACTR1   X04098   actin, apha 1   33522_at   ACTR1   X04098   actinin, apha 1   33522_at   ACVR1   Z22534   activin A receptor, type   1   34162_a at   ACVR1   Z22534   activin A receptor, type   1   34162_a at   ACVR1   Z22534   activin A receptor, type   1   34163_a at   ACVR1   Z22534   activin A receptor, type   1   34163_a at   ACVR1   Z22534   activin A receptor, type   1   34163_a at   ACVR1   Z22534   activin A receptor, type   1   34163_a at   ACVR1   Z22534   activin A receptor, type   1   34163_a at   ACVR1   Z22534   activin A receptor, type   1   34163_a at   ACVR1   Z62534   activin A receptor, type   1   24163_a at   ACVR1   Z62534   activin A receptor, type   1   ACVR1   ACV		A	8	3		Î
AF622_F at ARPC5   AF00608   5 (16 kD)     38392_at				100000		
APPC5   AF006088   5 (16 kD)   Equin related protein 2/3 complex, subunit 23755_at   ACTA2   X13839   actin, alpha 2, smooth muscle, aorta   Equin per a	_	34692_r_at	ARPC4	AF00608/	7	217.02
38392_at   ARPC5   AF00608B   5 (16 kD)     22755_at   ACTA2   X13839   actin, alpha 2, smooth muscle, aorda   22755_at     24767_4FX-FSACO7/ACTB   X00351   actin, beta   actin, beta   actin, beta   actin, beta   actin, alpha 1   actin, alpha 4   actin, alpha 1   actin, alpha 4   actin, alpha					led protein 2/3 complex, subunit	
32755_at         ACTA2         X13839         actin, elpha 2, smooth muscle, aorta         actin, elpha 2           AFFX-HSAC07/ACTB         X00351         actin, beta         LACTA           AS2318_s_at         ACTG1         X00351         actin, beta         LACTA           32218_s_at         ACTN1         X15804         actin, beta         L           33522_at         ACTN1         X15804         actin, japha 1         f           41753_at         ACTN1         X15804         actinin, alpha 1         f           33622_at         ACTN1         X15804         actinin, alpha 1         f           41753_at         ACTN4         U48734         actinin, alpha 1         f           33642_at         ACTN4         U48734         actinin, alpha 4         f           35172_s_at         ACVR2         activated RNA polymerase II transcription         activated RNA polymerase II transcription           35162_s_at         ACVR1         AZ22534         activiny dependent neuroprotector         f           40459_at         ACADSB         U12778         short/branched chain         f           40459_at         ACADXI         AE018327         activiny dependent neuroprotector           40459_at         ACADXI         AE018		38392_at	ARPC5	AF006088		o16-Arc
AFFX-HSAC07/ACTB         X00351         actin, beta         beta           AFFX-HSAC07/ACTB         X00351         actin, beta         beta           23318 s, at         ACTB         X04322         actin, beta         l           334160_at         ACTG1         X04098         actinin, alpha 1         g           334160_at         ACTN4         U48734         actinin, alpha 4         g           33622_at         ACTN4         U48734         activin A receptor, parallal transcription         activitated leucocyte cell adhesion molecule of activity alpha 4         g           33642_at         ACTN4         U18734         activity dependent neuroprocion         g           33764_at         ACVR1         Z22534         activin A receptor, type I         g           33764_at         ACVR2         D31770         activin A receptor, type II         g           34394_at         ACADSB         U12778         short/branched chain         g           40459_at         ACADSB         U12778         short/branched chain         g           40459_at         ACOX1         S69189         acyl-Coenzyme A oxidase I, palmitoyl         g           40459_at         AP1B1         L13939         subunit         adaptor-related protein complex 2, sigma	1	32755 at	2	X13839		alpha 2 actin
AFFX-HSAC07/A ACTB         X00351         actin, beta           22318 s_at         ACTB         X63432         actin, beta           34160_at         ACTB         X63432         actin, beta           34160_at         ACTB         X63938         actin, beta           34160_at         ACTN1         X15804         actin, alpha 1           41753_at         ACTN4         U48734         actinin, alpha 4           38642_at         ACTN4         U48734         actinin, alpha 4           38642_at         ACTN4         U48734         actinin, alpha 4           38642_at         ACTNA         Y10183         actinin, alpha 4           38676_at         ACNA         X10183         actinin, alpha 4           38677_at         ACVR         AI521453         actinin, alpha 4           38764_at         ACVR         ASE334         actinin A receptor, type I           38764_at         ACVR         ASE3770         activin'A receptor, type II           38374_at         ACVR         ASE3189         activin'A receptor, type II           40659_at         ACADSB         U12778         activin'Arepealeden, then the activin'Arepealed and the activity and activity and activity activity activity and activity activity activity activity activity activity activity activity activ	Т	AFFX-HSAC07/		X00351		oeta actin
32318_s_at         ACTB         X63432         actin, beta           34160_at         ACTG1         X04098         actinin, alpha 1         8           34160_at         ACTN1         X15804         actinin, alpha 1         8           41753_at         ACTN4         U48734         actinin, alpha 1         8           41753_at         ACCNA         U48734         actinin, alpha 1         8           38642_at         ACCMA         V10183         activin A receptor, bype II transcription activin A receptor, bype II         1           39762_at         ACVR1         Z22534         activin A receptor, bype II         1           34394_at         ACNR2         D801837         activin'A receptor, bype II         1           34394_at         ACNP2         AB01837         activin'A receptor, bype II         1           34045_at         ACVR2         D81837         activin'A receptor, bype II         1           40673_at         ACNP2         AB01837         activin'A receptor, bype II         1           40459_at         ACNP2         AB01837         activin'A receptor, bype II         1           40745_at         ACNY2         ACNY2         ACNY2         ACNY2           38275_at         AP181         <	Т	AFFX-HSAC07/)		X00351		oeta actin
34160_at         ACTG1         X04098         actini, gamma 1         gamma 1           39329_at         ACTN1         X15804         actinin, alpha 1         6           41753_at         ACTN4         U48734         actinin, alpha 4         6           41753_at         ACTN4         V10183         actinin, alpha 4         6           38642_at         ALCAM         Y10183         activiny A Polymerase II transcription activated RNA acceptor, type II           38764_at         ACVR1         222534         activiny A receptor, type II         1           34394_at         ACDNP         AB018327         activiny A receptor, type II         1           34394_at         ACDNP         AB018327         activiny A receptor, type II         1           340459_at         ACDNP         AB018327         activiny A receptor, type II         1           40745_at         ACOX1         S69189         activity A receptor, type II         1           40745_at         ACOX1         S69189         activity A receptor, type II         1           40745_at         AP1B1         L13939         activity A receptor, type II         1      <	<del>†                                     </del>	32318 s_at	ACTB	X63432		mutant beta-actin (beta'-actin)
39329_at         ACTN1         X15804         actinin, alpha 1         6           41753_at         ACTN4         U48734         actinin, alpha 4         6           41753_at         ACTN4         U48734         activated BNA polymerase II transcription activated BNA polymera	Т	34160 at	ACTG1	X04098		gamma-actin
41753_at         ACTN4         U48734         activated leucocyte cell adhesion molecule activated RNA polymerase II transcription 222534         activated RNA polymerase II transcription colactor 4           36171_at         ACVR1         222534         activin A receptor, type II           39764_at         ACVR2         D31770         activin A receptor, type II           34394_at         ADNP         AB018327         activin A receptor, type II           40673_at         ACADSB         U12778         activin-dependent neuroprotector           40673_at         ACADSB         U12778         activity-dependent neuroprotector           40673_at         ACOX1         S69189         activity-dependent neuroprotector           40459_at         ACOX1         S69189         activity-dependent neuroprotector           40745_at         AP1B1         L13939         subunit           35275_at         AP1B1         AL050025         gamma 1 subunit           32039_at         AP2M1         D63475         subunit           32039_at         AP2B1         AF002163         subunit           32039_at         AP3B1         AF002163         subunit           32034_at         AP3B1	1	39329_at	ACTN1	X15804	1	actinin, alpha 1
38642_at         ALCAM         Y10183         activated leucocyte cell adhesion molecule activated RNA polymerase II transcription activated RNA polymerase II transcription 222534         activated RNA polymerase II transcription activated RNA polymerase II transcription 222534         activated RNA polymerase II transcription activated RNA polymerase II transcription 222534         AI521453         activated RNA polymerase II transcription activated Robert II	_	41753_at	ACTN4	U48734		alpha actinin
36171_at         PC4         Al521453         activated RNA polymerase II transcription           39764_at         ACVR1         Z22534         activin A receptor, type I           34394_at         ACVR2         D31770         activin A receptor, type II           34394_at         ACVR2         D31770         activity-dependent neuroprotector           40673_at         ACNSB         U12778         activity-dependent neuroprotector           40673_at         ACADSB         U12778         activity-dependent neuroprotector           40459_at         ACADSB         U12778         activity-dependent neuroprotector           40459_at         ACADSB         U12778         activity-dependent neuroprotector           40745_at         ACADSB         U12778         activity-dependent neuroprotector           40745_at         AP181         L13939         activity-dependent neuroprotector           39795_at         AP161         AL050025         gamma 1 subunit           32039_at         AP281         D63475         adaptor-related protein complex 2, sigma           38072_at         AP3B1         AF002163         abunit           38074_at         AP3B1         AF002163         abunit           33102_at         AP3B1         U91932         1 subuni	45	38642 at	ALCAM	Y10183	activated leucocyte cell adhesion molecule	MEMD protein
36171_at         PC4         Al521453         cofactor 4           39764_at         ACVR1         Z22534         activin A receptor, type I           39764_at         ACVR2         D31770         activin A receptor, type II           34394_at         ACVR2         D31770         activity-dependent neuroprotector           34394_at         ADNP         AB018327         activity-dependent neuroprotector           34394_at         ADNP         AB018327         activity-dependent neuroprotector           40673_at         ACADSB         U12778         activity-dependent neuroprotector           40459_at         ACOX1         S69189         activity-dependent neuroprotector           40745_at         ACOX1         S69189         activity-dependent neuroprotector           40745_at         AP1B1         L13939         activity-dependent neuroprotector           35275_at         AP1G1         AL050025         gamma 1 subunit           39347_at         AP2M1         D63475         subunit           32039_at         AP3B1         U81504         subunit           36172_sat         AP3B1         AF002163         subunit           34074_at         AP3B1         U91932         1 subunit           33102_at					activated RNA polymerase II transcription	
39764_at         ACVR1         Z22534         activin A receptor, type I           35162_s_at         ACVR2         D31770         activin A receptor, type II           34394_at         ADNP         AB018327         activity-dependent neuroprotector           40673_at         ACADSB         U12778         shortbranched chain           40459_at         ACADSB         U12778         shortbranched chain           40745_at         APCOX1         S69189         acyl-Coenzyme A dehydrogenase, shortbranched chain           40745_at         APCOX1         S69189         acyl-Coenzyme A dehydrogenase, shortbranched chain           40745_at         APTB1         L13939         acyl-Coenzyme A dehydrogenase, shortbranched chain           35275_at         AP1B1         L13939         acyl-Coenzyme A oxidase 1, palmitoyl           39795_at         AP2M1         AL050025         gamma 1 subunit           32039_at         AP2M1         D63475         subunit           32039_at         AP2S1         X97074         1 subunit           36172_s_at         AP3B1         U81504         subunit           38074_at         AP3B1         AF002163         subunit           33102_at         AP3B1         U91932         1 subunit	46		PC4	AI521453		
35162_s_at         ACVR2         D31770         activin A receptor, type II           34394_at         ADNP         AB018327         activity-dependent neuroprotector           34394_at         ADNP         AB018327         activity-dependent neuroprotector           40673_at         ACADSB         U12778         short/branched chain           40459_at         ACOX1         S69189         acyl-Coenzyme A dehydrogenase,           40745_at         AP1B1         L13939         subunit           39775_at         AP1G1         AL050025         gamma 1 subunit           39347_at         AP2S1         X97074         1 subunit           32039_at         AP3B1         U81504         subunit           36172_s_at         AP3B1         AF002163         subunit           38074_at         AP3B1         AF002163         subunit           33102_at         AP3B1         U91932         1 subunit           33102_at         ADD3         D67031	Г	39764_at	ACVR1	Z22534		ALK-2
34394_at         ADNP         AB018327         activity-dependent neuroprotector           40673_at         ACADSB         U12778         short/branched chain           40459_at         ACOX1         \$69189         acyl-Coenzyme A dehydrogenase, short/branched chain           40745_at         AP1B1         L13939         acyl-Coenzyme A oxidase 1, palmitoyl adaptor-related protein complex 1, beta 1 subunit           35275_at         AP1G1         AL050025         gamma 1 subunit           39795_at         AP2M1         D63475         subunit           39347_at         AP2S1         X97074         1 subunit           32039_at         AP2S1         X97074         1 subunit           36172_s_at         AP3B1         U81504         subunit           36172_s_at         AP3B1         AF002163         subunit           36172_s_at         AP3B1         AF002163         subunit           38074_at         AP3B1         AF002163         subunit           38074_at         AP3B1         AF002163         subunit           33102_at         AP3B1         AF002163         subunit           38074_at         AP3B1         U91932         1 subunit           33102_at         ADD3         D67031	48		ACVR2	D31770		activin typell A receptor precursor
40673_at         ACADSB         U12778         acyl-Coenzyme A dehydrogenase, short/branched chain           40459_at         ACOX1         S69189         acyl-Coenzyme A oxidase 1, palmitoyl adaptor-related protein complex 1, beta 1 subunit           40745_at         AP1B1         L13939         adaptor-related protein complex 1, beta 1 subunit           35275_at         AP2B1         AL050025         gamma 1 subunit           39795_at         AP2M1         D63475         subunit           32039_at         AP2S1         X97074         1 subunit           32039_at         AP3B1         U81504         subunit           36172_s_at         AP3B1         AF002163         subunit           364ptor-related protein complex 3, delta 1 subunit         adaptor-related protein complex 3, delta 1 subunit           36172_s_at         AP3B1         AF002163         subunit           38074_at         AP3S1         U91932         1 subunit           33102_at         AP3S1         U91932         1 subunit           33102_at         ADD3         D67031         adaptor-related protein complex 3, sigma	49	34394_at	ADNP	AB018327		KIAA0784 protein
40673_at         ACADSB         U12778         short/branched chain           40459_at         ACOX1         S69189         acyl-Coenzyme A oxidase 1, palmitoyl           40745_at         AP1B1         L13939         adaptor-related protein complex 1, beta 1           35275_at         AP1G1         AL050025         gamma 1 subunit           39795_at         AP2M1         D63475         subunit           39347_at         AP2S1         X97074         1 subunit           32039_at         AP3B1         U81504         subunit           36172_s_at         AP3B1         U81504         subunit           38074_at         AP3B1         AF002163         subunit           38074_at         AP3B1         AF002163         subunit           38074_at         AP3B1         AF002163         subunit           33102_at         AP3B1         Badaptor-related protein complex 3, sigma           33102_at         AP3B1         Badaptor-related protein complex 3, sigma           33102_at         AP3B1         Badaptor-related protein complex 3, sigma						
40459 at         ACOX1         S69189         acyl-Coenzyme A oxidase 1, palmitoyl           40745_at         AP1B1         L13939         adaptor-related protein complex 1, beta 1           35275_at         AP1G1         AL050025         gamma 1 subunit           39795_at         AP2M1         D63475         adaptor-related protein complex 2, mu 1           39347_at         AP2S1         X97074         1 subunit           32039_at         AP3B1         U81504         subunit           36172_s_at         AP3D1         AF002163         subunit           38074_at         AP3D1         AF002163         subunit           38074_at         AP3S1         U91932         1 subunit           33102_at         AP3S1         U91932         1 subunit           33102_at         AP3S1         U91932         1 subunit           33102_at         AD3         D67031         adaptor-related protein complex 3, sigma	သ	40673_at	ACADSB	U12778		acyl-CoA dehydrogenase
40745_at         AP1B1         L13939         subunit adaptor-related protein complex 1, beta 1           35275_at         AP1G1         AL050025         gamma 1 subunit adaptor-related protein complex 2, mu 1           39795_at         AP2M1         D63475         subunit adaptor-related protein complex 2, sigma adaptor-related protein complex 2, sigma adaptor-related protein complex 3, beta 1           32039_at         AP3B1         U81504         subunit adaptor-related protein complex 3, delta 1           36172_s_at         AP3D1         AF002163         subunit adaptor-related protein complex 3, sigma adaptor-related protein complex 4, sigma adaptor-related protein complex 4, sigma adaptor-related protei	21	40459_at	ACOX1	S69189	acyl-Coenzyme A oxidase 1, palmitoyl	peroxisomal acyl-coenzyme A oxidase
40745_at         AP1B1         L13939         subunit adaptor-related protein complex 1, adaptor-related protein complex 2, mu 1           35275_at         AP1G1         AL050025         gamma 1 subunit adaptor-related protein complex 2, mu 1           39795_at         AP2M1         D63475         subunit adaptor-related protein complex 2, sigma adaptor-related protein complex 3, beta 1           39347_at         AP2S1         X97074         1 subunit adaptor-related protein complex 3, beta 1           32039_at         AP3B1         U81504         subunit adaptor-related protein complex 3, delta 1           36172_s_at         AP3D1         AF002163         subunit adaptor-related protein complex 3, sigma adaptor-related protein complex 3					adaptor-related protein complex 1, beta 1	•
35275_at         AP1G1         AL050025         gamma 1 subunit adaptor-related protein complex 2, sigma adaptor-related protein complex 2, sigma adaptor-related protein complex 2, sigma adaptor-related protein complex 3, beta 1 subunit adaptor-related protein complex 3, delta 1 subunit adaptor-related protein complex 3, delta 1 subunit adaptor-related protein complex 3, sigma adaptor-related protein complex 4, sigma adaptor-related protein complex 4, sigma adaptor-related protein complex 4, sigma adaptor-rel	25	40745_at	AP1B1	L13939	subunit	beta-prime-adaptin
35275_at         AP1G1         AL050025         gamma 1 subunit           39795_at         AP2M1         D63475         subunit           39347_at         AP2S1         X97074         1 subunit           32039_at         AP3B1         U81504         subunit           36172_s_at         AP3D1         AF002163         subunit           38074_at         AP3S1         U91932         1 subunit           33102_at         AP3D3         D67031         adaptor-related protein complex 3, sigma           33102_at         AP3D3         D67031         adducin 3 (gamma)					adaptor-related protein complex 1,	
39795_at         AP2M1         D63475         subunit adaptor-related protein complex 2, mu 1           39347_at         AP2S1         X97074         1 subunit adaptor-related protein complex 2, sigma adaptor-related protein complex 3, beta 1           32039_at         AP3B1         U81504         subunit adaptor-related protein complex 3, delta 1           36172_s_at         AP3D1         AF002163         subunit adaptor-related protein complex 3, sigma adaptor-related protein adaptor-related protein complex 3, sigma adaptor-related protein adaptor-related protein complex 3, sigma adaptor-related protein ada	23	35275_at	AP1G1	AL050025	gamma 1 subunit	hypothetical protein
39795_at         AP2M1         D63475         subunit           39347_at         AP2S1         X97074         1 subunit           32039_at         AP3B1         U81504         subunit           36172_s_at         AP3D1         AF002163         subunit           38074_at         AP3S1         U91932         1 subunit           33102_at         ADD3         D67031         adducin 3 (gamma)					<del></del>	adaptor-related protein complex 2, mu 1
39347_at         AP2S1         X97074         1 subunit           32039_at         AP3B1         U81504         subunit           36172_s_at         AP3D1         AF002163         subunit           38074_at         AP3S1         U91932         1 subunit           33102_at         AD3         D67031         adaptor-related protein complex 3, sigma           33102_at         AD3         D67031         adducin 3 (gamma)	24		AP2M1	D63475		subunit
39347_at         AP2S1         X97074         1 subunit           32039_at         AP3B1         U81504         subunit           36172_s_at         AP3D1         AF002163         subunit           38074_at         AP3S1         U91932         1 subunit           33102_at         AD03         D67031         adducin 3 (gamma)					adaptor-related protein complex 2, sigma	
32039_at         AP3B1         U81504         subunit subunit           36172_s_at         AP3D1         AF002163         subunit adaptor-related protein complex 3, delta 1 subunit           38074_at         AP3S1         U91932         1 subunit adducin 3 (gamma)           33102_at         ADD3         D67031         adducin 3 (gamma)	. 55	39347_at	AP2S1	X97074	1 subunit	clathrin-associated protein
32039_at         AP3B1         U81504         subunit           36172_s_at         AP3D1         AF002163         subunit           38074_at         AP3S1         U91932         1 subunit           33102_at         ADD3         D67031         adducin 3 (gamma)	L				adaptor-related protein complex 3, beta 1	
36172_s_at         AP3D1         AF002163         subunit adaptor-related protein complex 3, delta 1           38074_at         AP3S1         U91932         1 subunit adducin 3 (gamma)           33102_at         ADD3         D67031         adducin 3 (gamma)	56	32039_at	AP3B1	U81504	subunit	beta-3A-adaptin subunit of the AP-3 complex
36172_s_at         AP3D1         AF002163         subunit           38074_at         AP3S1         U91932         1 subunit           33102_at         ADD3         D67031         adducin 3 (gamma)					adaptor-related protein complex 3, delta 1	
38074_at         AP3S1         U91932         1 subunit           33102_at         ADD3         D67031         adducin 3 (gamma)	57	36172_s_at	AP3D1	AF002163	subunit	delta-adaptin
38074_at AP3S1 U91932 1 subunit 33102_at ADD3 D67031 adducin 3 (gamma)					adaptor-related protein complex 3, sigma	
33102_at ADD3 D67031 adducin 3 (gamma)	28		AP3S1	U91932	1 subunit	AP-3 complex sigma3A subunit
	29		ADD3	D67031	adducin 3 (gamma)	adducin-like protein

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	V	8	0	1	U	Ľ.
						adenosine deaminase, RNA-specific, isoform ADAR-a; adenosine deaminase,
38014 at		ADAR	X79448	aden	adenosine deaminase, RNA-specific	RNA-specific, isoform ADAR-b; adenosine deaminase, RNA-specific, isoform ADAR-c
				aden	180	
38748_at		ADARB1	U76421	(RED		dsRNA adenosine deaminase DRADA2b
68_at		ADK	U50196	aden	aderosine kinase	adenosine kinase
33865_at		BS69	AA127624	aden	adenovirus 5 E1A binding protein	
33134 at			AB011083	aden	adenylate cyclase 3	KIAA0511 protein
40585_at			D25538	aden		adenylate cyclase 7
33800_at			AF036927	aden		adenylyl cyclase type IX
40788_at		AK2	U84371	aden	adenylate kinase 2	adenylate kinase 2A
36639_at	at	ADSL	AF067853	aden	adertylosuccinate lyase	adenylosuccinate lyase
935_at			L12168	aden	aderlylyl cyclase-associated protein	adenylyl cyclase-associated protein
33405	at		N90755	ader	adenylyl cyclase-associated protein 2	
34378_at			X97324	adip	adipose differentiation-related protein	adipophilin
36861_at	at	DKFZp56411922	AL049946	adlican	ue	hypothetical protein
33987_at	at	Γ	M36340	ADP	ADP-ribosylation factor 1	ADP-ribosylation factor 1
39336_at	at	ARF3	M74491	ADP	ADP ribosylation factor 3	ADP-ribosylation factor 3
36585_at	at	ARF4	M36341	ADP	ADP-ribosylation factor 4	ADP-ribosylation factor 4
				ADP	ADP-ribosylation factor domain protein 1,	
37537_	jaj	ARFD1	L04510	8 K		nucleotide binding protein
				ADP	ADP-ribosylation factor GTPase activating	
39905_i_at	i_at	ARFGAP1	AA402332	protein 1	in 1	
37296	at	ARL1	L28997	ADP	ADP-ribosylation factor-like 1	ADP-ribosylation factor-like 1
				ADP	ADP-ribosylation factor-like 6 interacting	
36572	r_at	ARLGIP	D31885	prot	oin	
				ADF	ADR-ribosyltransferase (NAD+; poly (ADP-	_
41146	at	ADPRT	J03473	ribo	ribose) polymerase)	poly(ADP-ribosyl)transferase
				ADP	ADP-ribosyltransferase (NAD+; poly (ADP-	-
1287_at	¥	ADPRT	J03473	ri Š	ribose) polymerase)	poly(ADP-ribosyl)transferase
34777	at	ADM	D14874	adre	adrenomedullin	adrenomedullin precursor
				AFO	AF084176 Human mRNA (Tripodis and	
٠				Rag	Ragoussis) Homo sapiens cDNA clone	
32218 at	at		AF034176	ntco	ntcoh5 contig.	

17.55

AFG312		A	8	ပ	O	ш
33454_at         AGRN         AFO16903         agnin           37027_at         AHNAK         M80899         AHNAK nucleoprotein (desmoyokin)           36186_at         AARS         D32050         alanykrhikuk synthetase           36186_at         ALDH1A3         U07919         member A3           32747_at         ALDH3A2         U46689         aldehyde dehydrogenase 1 family.           37331_g_at         ALDH3A2         U46689         member A3           36132_at         ALDH3A2         U46689         member A1           36132_at         ALDH3A1         S74728         member A1           36132_at         ALDH3A1         S74728         member A1           36132_at         ALDH9A1         U34252         member A1           38780_at         AKR1A1         J04794         (aldehyde dehydrogenase 3 family.           38780_at         AKR1B1         X15414         (aldehyde dehydrogenase 3 family.           38780_at         AKR1B1         X15414         (aldehyde dehydrogenase 3 family.           38780_at         AKR1B1         X15414         (aldebyde feductase family 1, member A1           38589_at         AKR1B1         X15414         (aldebyde reductase family 1, member C3           35510_at         AKR		34315 at	AFG3L2	Y18314	AFG3 ATPase family gene 3-like 2 (yeast)	paraplegin-like protein
37027_at         AHNAK         M80899         AHNAK nucleoprotein (desmoyckin)           36185_at         AARS         D32050         alanyl-tRN4 synthetase           36686_at         ALDH1A3         U07919         member A2           aldehyde dehydrogenase 2 family         aldehyde dehydrogenase 2 family         family           40409_at         ALDH3A2         U46689         member A2           37331_g_at         ALDH3A1         U24266         member A1           38899_at         ALDH3A1         U34252         member A1           38780_at         AKR1A1         J04794         (aldehyde dehydrogenase 3 family, member A1           38589_at         ALDH9A1         U34252         nachekato reductase family 1, member A1           38589_at         AKR1A1         J04794         (aldehyde reductase family 1, member C3           38589_at         AKR1A1         J04794         (aldehyde reductase family 1, member C3           38589_at         AKR1B1         X15414         (aldehyde reductase family 1, member C3           38589_at         AKR1C3         D17793         bype II)           38581_at         AKR1C3         D17793         bype II)           38510_at         AKR1A2         AF026947         (aldehyde reductase family 1, member C3		33454 at	AGRN	AF016903	agnin	agrin precursor
36185_at   AARS   D32050   alanyl-tRNA synthetase   sidehyde dehydrogenase 1 family, a latehyde dehydrogenase 2 family, a latehyde dehydrogenase 3 family, a latehyde dehydrogenase 4 family, a latehyde dehydrogenase 5 family, a latehyde dehydrogenase 7 family, a latehyde dehydrogenase 9 family, a latehyde reductase family 1, member A1 latehyde reductase 9 family, a latehyde reductase 6 family, a latehyde reductase 9 family, a latehyde reductas		37027_at	AHNAK	M80899	AK nucleoprotein (desmoyokin)	
ALDH1A3         U07919         member A3           ALDH2         X05409         (mitochondrial)         idehyde dehydrogenase 2 family         idehyde dehydrogenase 2 family         idehyde dehydrogenase 3 family         idehyde dehydrogenase 3 family         idehyde dehydrogenase 4 family         idehyde dehydrogenase 3 family         idehyde dehydrogenase 4 family         idehyde dehydrogenase 4 family         idehyde dehydrogenase 7 family         idehyde dehydrogenase 7 family         idehyde dehydrogenase 7 family         idehyde dehydrogenase 9	7	36185_at	AARS	D32050		alanyi-tRNA synthetase
ALDH1A3         U07919         member A3         4           ALDH2         X05409         (mitochondrial)         idehyde dehydrogenase 2 family.         idehyde dehydrogenase 3 family.           ALDH3A2         U46689         member A2         idehyde dehydrogenase 4 family.         idehyde dehydrogenase 4 family.           ALDH3A1         U24266         member A1         aldehyde dehydrogenase 7 family.         idehyde dehydrogenase 9 family.           ALDH3A1         S74728         member A1         aldehyde dehydrogenase 9 family.         idehyde dehydrogenase 9 family.           AKR1B1         U34252         member A1         alde-keto reductase family 1, member B1           AKR1B1         X15414         (aldehyde reductase family 1, member C3           AKR1B1         X15414         (aldose reductase family 1, member C3           AKR1C3         D17793         iddo-keto reductase family 1, member C3           (3-alpha hydroxysteroid dehydrogenase,         ARR1C3         D17793           AKR1C3         D17793         iddo-keto reductase family 7, member C3           (3-alpha hydroxysteroid dehydrogenase,         ARC26947         (alfatoxin aldehyde reductase)           AFIQ         U16954         ALL1-fused gene from choroses           ARA         ARA         ALL1-fused gene from choroses						,
ALDH2         X05409         (mitochondrial)         (mitochondrial)           ALDH3A2         U46689         member A2         aldehyde dehydrogenase 3 family, member A1         incheber A2           ALDH3A2         U24266         member A1         aldehyde dehydrogenase 4 family, member A1         incheber A1           ALDH3A1         U24266         member A1         aldehyde dehydrogenase 7 family, member A1         incheber A1           ALDH9A1         U34252         member A1         aldehyde dehydrogenase 9 family, member A1           AKR1A1         J04794         (aldehyde reductase family 1, member B1           AKR1B1         X15414         (alde-keto reductase family 1, member C3           AKR1B1         X15414         (aldo-keto reductase family 1, member C3           AKR1C3         D17793         type II)           AKR1C3         D17793         type II)           AKR7A2         AF026947         (alfatoxin aldehyde reductase family 7, member A2           AF1Q         U16954         ALL1-fused gene from chromosome 1q           GZAN         U16954         ALL1-fused gene from chromosome 1q           GZAN         D42041         alpha glucosidase II alpha submit RA4           KIAA1017         AB023234         alpha finassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisis		36686_at	ALDH1A3	U07919		aldehyde dehydrogenase 6
ALDH2         X05409         (mitochondrial)           ALDH3A2         U46689         member A2           aldehyde dehydrogenase 4 family,         aldehyde dehydrogenase 4 family,           ALDH4A1         U24266         member A1           ALDH9A1         U34252         member A1           AKR1A1         U34252         aldehyde dehydrogenase 9 family.           AKR1A1         J04794         (aldehyde reductase family 1, member R1           AKR1B1         X15414         (aldehyde reductase)           AKR1C3         D17793         aldo-keto reductase family 1, member C3           G-alpha hydroxysteroid dehydrogenase,         (aldo-keto reductase)           AKR7A2         AF026947         (aldatoxin aldehyde reductase)           AF1Q         AF026947         (aldo-keto reductase family 1, member C3           G2AN         AF026947         (alfatoxin aldehyde reductase)           AF1Q         U16954         ALL1-fused gene from chromosome 1q           G2AN         AB023234         alpha glucosidase II alpha subunit           KIAA1017         AB023234         alpha integin binding protein 63           ATRX         U72936         cerevisiae)						aldehyde dehydrogenase 2 family
ALDH3A2         U46689         member A2           ALDH3A2         U46689         aldehyde dehydrogenase 4 family, aldehyde dehydrogenase 7 family, member A1           ALDH4A1         U24266         member A1           ALDH3A1         S74728         member A1           ALDH9A1         U34252         member A1           AKR1A1         J04794         (aldehyde reductase)           AKR1B1         X15414         (aldose reductase)           AKR1B1         X15414         (aldose reductase)           AKR1C3         D17793         aldo-keto reductase family 1, member C3           AKR1C3         D17793         aldo-keto reductase family 1, member C3           AKR1C3         D17793         aldo-keto reductase family 1, member C3           AKR1C3         D17793         type II)           AKR1C3         D17793         type II)           AKR7A2         AF026947         (aflatoxin aldehyde reductase)           AF1Q         U16954         ALL1-tused gene from chromosome 1q           G2AN         D42041         alpha glucosidase II alpha subunit           KIAA1017         AB0233234         alpha integrin binding protein 63           ATRX         U72936         cerevisiae)		32747_at	ALDH2	X05409	(mitochondrial)	(mitochondrial)
ALDH3A2         U46689         member A2         aldehyde dehydrogenase 4 family, member A1         aldehyde dehydrogenase 7 family, member A1         aldehyde dehydrogenase 7 family, member A1           ALDH3A1         S74728         member A1         aldehyde dehydrogenase 9 family, member A1         aldehyde dehydrogenase 9 family, member A1           AKR1A1         J04794         (aldehyde reductase family 1, member B1 aldo-keto reductase family 1, member C3 aldo-keto reductase family 1, member C3         aldo-keto reductase family 1, member C3           AKR1B1         X15414         (aldose reductase family 1, member C3         (aldose reductase family 1, member C3           AKR1C3         D17793         lype II)         aldo-keto reductase family 1, member C3           AKR7A2         AF026947         (aflatoxin aldehyde reductase)           AF1Q         U16954         aldo-keto reductase family 1, member A2           AKR7A2         AF026947         (aflatoxin aldehyde reductase)           AF1Q         U16954         ALL1-fused gene from chromosome 1q           G2AN         D42041         alpha glucosidase II alpha subunit           KIAA1017         AB023234         alpha alleassemia/mental retardation syndrome X-linked (RAD54 homolog, S.           ATRX         U72936         cerevisiae)					aldehyde dehydrogenase 3 family,	-
ALDH4A1         U24266         member A1           ALDH7A1         S74728         aldehyde dehydrogenase 7 family, member A1           ALDH7A1         S74728         member A1           ALDH9A1         U34252         member A1           AKR1A1         J04794         aldehyde dehydrogenase 9 family, member A1           AKR1B1         X15414         (aldehyde reductase family 1, member B1 aldo-keto reductase)           AKR1B1         X15414         (aldeoxe reductase family 1, member C3 aldo-keto reductase)           AKR1B1         X15414         (aldose reductase family 1, member C3 aldo-keto reductase family 1, member C3 aldo-keto reductase family 1, member C3 aldo-keto reductase family 7, member A2 aldo-keto reductase family 1, member A2 aldo-keto reductase family 1		40409_at	ALDH3A2	U46689	member A2	aldehyde dehydrogenase
ALDH4A1         U24266         member A1           ALDH7A1         \$74728         member A1           ALDH7A1         \$74728         member A1           ALDH9A1         U34252         member A1           AKR1A1         J04794         aldehyde dehydrogenase 9 family, member A1           AKR1B1         X15414         (aldehyde reductase family 1, member B1           AKR1B1         X15414         (aldebyde reductase)           AKR1B1         X15414         (aldose reductase)           AKR1C3         D17793         1ype II)           AKR7A2         AF026947         (aflatoxin aldehyde reductase)           AF1Q         AF026947         (aflatoxin aldehyde reductase)           AF1Q         AF026947         (aflatoxin aldehyde reductase)           AF1Q         AF026947         (alfatoxin aldehyde reductase)           AF1Q         D42041         alkydglycerone phosphate synthase           AF1Q         D42041         alpha glucosidase II alpha subunit           KIAA1017         AB023234         alpha integrin binding protein 63           ATRX         U72936         cerevisiae)					aldehyde dehydrogenase 4 family,	
ALDH7A1         S74728         aldehyde dehydrogenase 7 family, member A1           ALDH9A1         U34252         aldehyde dehydrogenase 9 family, member A1           AKR1A1         J04794         (aldehyde reductase family 1, member B1 aldo-keto reductase)           AKR1B1         X15414         (aldehyde reductase family 1, member B1 aldo-keto reductase family 1, member C3 (aldose reductase family 1, member C3 (aldose reductase family 1, member C3 (aldose reductase family 7, member A2 (aldose reductase family 7, member B1)           AKR1C3         D17793         type II)         aldo-keto reductase family 7, member A2 (alfatoxin aldehyde reductase)           AKR7A2         AF026947         (alfatoxin aldehyde reductase)           AGPS         Y09443         alkydglycerone phosphate synthase           AF1Q         U16954         ALL1-fused gene from chromosome 1q           G2AN         D42041         alpha glucosidase II alpha subunit           KIAA1017         AB023234         alpha inlegrin binding protein 63           ATRX         U72936         cerevisiae)		37331_g_at	ALDH4A1	U24266	member A1	pyrroline-5-carboxylate dehydrogenase
ALDH7A1         S74728         member A1           ALDH9A1         U34252         member A1           AKR1A1         J04794         (aldehyde reductase) aldo-keto reductase)           AKR1B1         X15414         (aldehyde reductase) aldo-keto reductase family 1, member B1 aldo-keto reductase family 1, member C3 (aldose reductase)           AKR1B1         X15414         (aldose reductase family 1, member C3 (aldo-keto reductase)           AKR1C3         D17793         type II)           AKR7A2         AF026947         (aflatoxin aldehyde reductase)           AF1Q         U16954         ALL1-fused gene from chromosome 1q           G2AN         D42041         alpha glucosidase II alpha subunit           KIAA1017         AB023234         alpha inlegrin binding protein 63           ATRX         U72936         cerevisiae)					aldehyde dehydrogenase 7 family,	
ALDH9A1         U34252         member A1           AKR1A1         J04794         (aldehyde reductase)           AKR1B1         X15414         (aldehyde reductase)           AKR1B1         X15414         (aldo-keto reductase)           AKR1B1         X15414         (aldo-keto reductase)           aldo-keto reductase family 1, member B1         (aldo-keto reductase)           AKR1C3         D17793         type II)           AKR7A2         AF026947         (aflatoxin aldehyde reductase)           AGPS         Y09443         alkydglycerone phosphate synthase           AF1Q         U16954         ALL1-fused gene from chromosome 1q           G2AN         D42041         alpha glucosidase II alpha subunit           KIAA1017         AB023234         alpha inlegrin binding protein 63           ATRX         U72936         cerevisiae)		36132_at	ALDH7A1	S74728	member A1	antiquitin
ALDH9A1         U34252         member A1           AKR1A1         J04794         (aldehyde reductase)           AKR1B1         X15414         (aldo-keto reductase)           AKR1B1         X15414         (aldo-keto reductase)           AKR1B1         X15414         (aldo-keto reductase)           AKR1C3         D17793         pype il)           AKR7A2         AF026947         (aflatoxin aldehyde reductase)           AGPS         Y09443         alkydglycerone phosphate synthase           AGPS         Y09443         alkydglycerone phosphate synthase           AF1Q         U16954         ALL1-fused gene from chromosome 1q           G2AN         D42041         alpha glucosidase il alpha subunit           KIAA1017         AB023234         alpha inlegrin binding protein 63           ATRX         U72936         cerevisiae)					aldehyde dehydrogenase 9 family,	
AKR1A1         J04794         aldo-keto reductase family 1, member A1 aldo-keto reductase)           AKR1B1         X15414         (aldo-keto reductase)           AKR1B1         X15414         (aldose reductase)           AKR1C3         D17793         aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)           AKR7A2         AF026947         (aflatoxin aldehyde reductase)           AGPS         Y09443         alkydglycerone phosphate synthase           AF1Q         U16954         ALL1-fused gene from chromosome 1q           G2AN         D42041         alpha glucosidase II alpha subunit           KIAA1017         AB023234         alpha inlegrin binding protein 63           ATRX         U72936         cerevisiae)		33899_at	ALDH9A1	U34252	member A1	gamma-aminobutyraldehyde dehydrogenase
AKR1A1         J04794         (aldehyde reductase)           AKR1B1         X15414         (aldose reductase)           AKR1B1         X15414         (aldose reductase)           aldo-keto reductase family 1, member C3         (3-alpha hydroxysteroid dehydrogenase, type II)           AKR1C3         D17793         type II)           AKR7A2         AF026947         (aflatoxin aldehyde reductase)           AGPS         Y09443         alkydglycerone phosphate synthase           AF1Q         U16954         ALL1-fused gene from chromosome 1q           G2AN         D42041         alpha glucosidase II alpha subunit           KIAA1017         AB023234         alpha integrin binding protein 63           alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S.         cerevisiae)					aldo-keto reductase family 1, member A1	aldo-keto reductase family 1; member A1
AKR1B1         X15414         aldo-keto reductase family 1, member B1           AKR1B1         X15414         (aldose reductase)           AKR1C3         D17793         aldo-keto reductase family 1, member C3           (3-alpha hydroxysteroid dehydrogenase, type II)         aldo-keto reductase family 7, member A2           AKR7A2         AF026947         (aflatoxin aldehyde reductase)           AGPS         Y09443         alkydglycerone phosphate synthase           AF1Q         U16954         ALL1-fused gene from chromosome 1q           G2AN         D42041         alpha glucosidase II alpha subunit           KIAA1017         AB023234         alpha integrin binding protein 63           alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S.         syndrome X-linked (RAD54 homolog, S.	94	38780_at	AKR1A1	J04794	(aldehyde reductase)	(aldehyde reductase)
AKR1B1         X15414         (aldose reductase)           AKR1B1         AIdo-keto reductase family 1, member C3           (3-alpha hydroxysteroid dehydrogenase, ype II)         (3-alpha hydroxysteroid dehydrogenase, ype II)           AKR7A2         AF026947         (aflatoxin aldehyde reductase)           AGPS         Y09443         alkydilycerone phosphate synthase           AF1Q         U16954         ALL1-fused gene from chromosome 1q           G2AN         D42041         alpha glucosidase II alpha subunit           KIAA1017         AB023234         alpha integrin binding protein 63           alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S.         cerevisiae)					aldo-keto reductase family 1, member B1	aldo-keto reductase family 1, member B1
AKR1C3	95	36589_at	AKR1B1	X15414	(aldose reductase)	(aldose reductase)
(3-alpha hydroxysteroid dehydrogenase, type II)   aldo-keto reductase family 7, member A2   AKR7A2   AF026947   (aflatoxin aldehyde reductase)   AGPS   Y09443   alkydiycerone phosphate synthase   AF1Q   U16954   ALL1-fused gene from chromosome 1q   G2AN   D42041   alpha glucosidase II alpha subunit   AB023234   alpha integrin binding protein 63   alpha thalassemia/mental retardation   syndrome X-linked (RAD54 homolog, S. ATRX   U72936   cerevisiae)					aldo-keto reductase family 1, member C3	
AKR1C3         D17793         type il)           AKR7A2         AF026947         (aflatoxin aldehyde reductase)           AGPS         Y09443         alkylglycerone phosphate synthase           AF1Q         U16954         ALL1-fused gene from chromosome 1q           G2AN         D42041         alpha glucosidase il alpha subunit           KIAA1017         AB023234         alpha integrin binding protein 63           alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S.         syndrome X-linked (RAD54 homolog, S.					(3-alpha hydroxysteroid dehydrogenase,	aldo-keto reductase family 1, member C3 (3-
AKR7A2 AF026947 (aflatoxin aldehyde reductase) AGPS Y09443 alkylglycerone phosphate synthase AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. ATRX U72936 cerevisiae)	96	37399_at	AKR1C3	D17793	type II)	alpha hydroxysteroid dehydrogenase, type II)
AKR7A2       AF026947       (aflatoxin aldehyde reductase)         AGPS       Y09443       alkylglycerone phosphate synthase         AF1Q       U16954       ALL1-fused gene from chromosome 1q         G2AN       D42041       alpha glucosidase II alpha subunit         KIAA1017       AB023234       alpha integrin binding protein 63         alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S.         ATRX       U72936					aldo-keto reductase family 7, member A2	
AGPSY09443alkylglycerone phosphate synthaseAF1QU16954ALL1-fused gene from chromosome 1qG2AND42041alpha glucosidase II alpha subunitKIAA1017AB023234alpha integrin binding protein 63alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S.ATRXU72936cerevisiae)	26	32510_at	AKR7A2	AF026947	(aflatoxin aldehyde reductase)	aflatoxin aldehyde reductase AFAR
AGPS       Y09443       alkylglycerone phosphate synthase         AF1Q       U16954       ALL1-fused gene from chromosome 1q         G2AN       D42041       alpha glucosidase II alpha subunit         KIAA1017       AB023234       alpha integrin binding protein 63         alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S.         ATRX       U72936						alkyl-dihydroxyacetonephosphate synthase
AF1Q U16954 ALL1-fused gene from chromosome 1q G2AN D42041 alpha glucosidase II alpha subunit KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. ATRX U72936 cerevisiae)	98	39225 at	AGPS	Y09443	alkylglycerone phosphate synthase	precursor
G2AN   D42041 alpha glucosidase II alpha subunit	66		AF1Q	U16954	ALL1-fused gene from chromosome 1q	AF1Q protein
KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. ATRX U72936 cerevisiae)	8	37040 at	GZAN	D42041	alpha glucosidase II alpha subunit	alpha glucosidase II alpha subunit
alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. Orrewisiae)	101	35223_at	KIAA1017	AB023234	alpha integrin binding protein 63	KIAA1017 protein
Syndrome X-linked (RAD54 homolog, S. U72936 cerevisiae)					alpha thalassemia/mental retardation	
ATRX (U72936 cerevisiae)					syndrome X-linked (RAD54 homolog, S.	putative DNA dependent ATPase and
	102	39147_g_at	ATRX	U72936	cerevisiae)	helicase

	٨	В	ပ	O	บ
				alpha thalassemia/mental retardation	
				syndrome X-linked (RAD54 homolog, S.	putative DNA dependent ATPase and
103	818_s_at	ATRX	U72936	cerevisiae)	helicase
				afternative translation initiation; H.sapiens	
			•	HLTF gene for helicase-like transcription	
5	104 34327_at	HLTF	246606	factor.	helicase-like transcription factor
				aminoadipate-semialdehyde	
				dehydrogenase-phosphopantetheinyl	
105	35761_at	AASDHPPT	AL050073	transferase	hypothetical protein
<del>2</del>	106 39431_at	NPEPPS	AJ132583	aminopeptidase puromycin sensitive	puromycin sensitive aminopeptidase
107	107 41338_at	AES	Al951946	amino-terminal enhancer of split	
108	108 36996_at	6-SO	U41635	amplified in osteosarcoma	OS-9 precurosor
				amylo-1, 6-glucosidase, 4-alpha-	
				glucanotransferase (glycogen	
				debranching enzyme, glycogen storage	
109	38253_at	AGL	U84011	disease type III)	głycogen debranching enzyme isoform 6
				amyloid beta (A4) precursor protein	amyloid beta (A4) precursor protein
110	110 41136_s_at	APP	Y00264	(protease nexin-II, Alzheimer disease)	(protease nexin-II, Alzheimer disease)
				amyloid beta (A4) precursor protein-	
11	40148_at	APBB2	U62325	binding, family B, member 2 (Fe65-like)	FE65-like protein
				amyloid beta precursor protein	
112	38471_r_at	APPBP2	D86981	(cytoplasmic tail) binding protein 2	KIAA0228 protein
				amyloid beta precursor protein	
=	113 38470_i_at	APPBP2	D86981	(cytoplasmic tail) binding protein 2	KIAA0228 protein
				amyloid beta precursor protein binding	:
114	35364_at	APPBP1	U50939	protein 1, 59KU	amyloid precursor protein-binding protein 1
				amyotrophic lateral sclerosis 2 (juvenile)	
115	40064_at	ALS2CR3	AB011121	chromosome region, candidate 3	KIAA0549 protein
				androgen receptor (dihydrotestosterone	
				receptor; testicular feminization; spinal	
				and bulbar muscular atrophy; Kennedy	
116	1577_at	AR	M23263	disease)	androgen receptor
117	38842_at	AMOTL2	AB023206	angiomotin like 2	angiomotin like 2
118	39315_at	ANGPT1	D13628	angiopoietin 1	angiopoietin 1
119	1929_at	ANGPT1	U83508	angiopoietin 1	angiopoietin-1

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	В	O	0	E
	ANK3	U13616	lankyrin 3, node of Hanvier (ankyrin G)	ankyrın G
	ANXA1	80650X	annexin A1	annexin l
	ANXA11	L19605	annexin A11	56K autoantigen
	ANXA2	D00017	annexin A2	lipocortin II
<del>†                                    </del>	ANXA2P1	M62896	annexin A2 pseudogene 1	
<u> </u>	ANXA2P3	M62895	annexin A2 pseudogene 3	
	ANXAA	Masana	annexin A4	annexin IV (placental anticoagulant protein  }}
$\overline{}$	ANXA7	J04543	annexin A7	annexin VII isoform 1; annexin VII isoform 2
	MIC2	M16279	antigen identified by monoclonal antibodies 12E7, F21 and O13	antigen
1	C4: API	21: AU75686	APP-1; Homo sapiens polyadenylate binding protein mRNA, complete cds.	polyadenylate binding protein
	ARCN1	X81198	archain 1	archain
	RERE	AB007927	arginine-glutamic acid dipeptide (RE)	KIAA0458 protein
	RARS	S80343	arginyl-tRNA synthetase	arginyl-tRNA synthetase
	ARIH2	AF099149	ariadne homolog 2 (Drosophila)	TRIAD1 type I
	ARIH1	AJ009771	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila) putative RING finger protein	putative RING finger protein
1	ALEX2	AB011084	armadillo repeat protein ALEX2	KIAA0512 protein
]	ACTEIA	Y8220R	ARP1 actin-related protein 1 homolog A,	aloha-centractin
			ARP2 actin-related protein 2 homolog	
	ACTR2	A1935551	(yeast)	
			ARP2 actin-related protein 2 homolog	(
	ACTR2	AF006082	(yeast)	Arp2
			ARP3 actin-related protein 3 homolog	
	ACTR3	AF006083	(yeast)	Arp3
	AHR	L19872	aryl hydrocarbon receptor	AH-receptor
	ASNS	M27396	asparagine synthetase	asparagine synthetase
1	NARS	D84273	asparaginyl-tRNA synthetase	Asparaginyl tRNA Synthetase
	DNPEP	AF005050	aspartyl aminopeptidase	aspartyl aminopeptidase
	AGA	X55330	aspartylglucosaminidase	aspartylglucosaminidase

Fig 21

	¥	8	ပ	Q	Ш
145	37229_at	ATR	U49844	ataxia telangiectasia and Rad3 related	FRAP-related protein
146	146 34817_s_at	A2LP	U70671	ataxin 2 related protein	ataxin-2 related protein
				ATP binding protein associated with cell	
147	379_at	APACD	AB006679	differentiation	ATP binding protein
148	40881_at	ACLY	X64330	ATP citrate lyase	ATP-citrate (pro-S-)-lyase
				ATP synthase, H+ transporting,	
				mitochondrial F0 complex, subunit b,	
149	149 41228_r_at	ATP5F1	X60221	isoform 1	H+-ATP synthase subunit b
				ATP synthase, H+ transporting,	
				mitochondrial F0 complex, subunit c	mitochondrial ATP synthase subunit 9
150	34811_at	ATP5G3	U09813	(subunit 9) isoform 3	precursor
				ATP synthase, H+ transporting,	
151	35760_at	ATP5H	AF087135	mitochondrial F0 complex, subunit d	F1FO-type ATPase subunit d
				ATP synthase, H+ transporting,	
152	38751_i_at	ATP51	<b>Ā</b> A426364	mitochondrial F0 complex, subunit e	
				ATP synthase, H+ transporting,	
153	36107_at	ATP5J	AA845575	mitochondrial FO complex, subunit F6	
				ATP synthase, H+ transporting,	
154	154 38693_at	ATPSL	AA917672	mitochondrial F0 complex, subunit g	
				ATP synthase, H+ transporting,	
				mitochondrial F1 complex, gamma	
155	155 40115_at	ATP5C1	D16562	polypeptide 1	ATP synthase gamma-subunit
				ATPase, Ca++ transporting, cardiac	ATPase, Ca++ transporting, cardiac muscle,
156	39791_at	ATP2A2	M23114	muscle, slow twitch 2	slow twitch 2
				ATPase, Ca++ transporting, cardiac	ATPase, Ca++ transporting, cardiac muscle,
157	39790_at	ATP2A2	M23115	muscle, slow twitch 2	slow twitch 2
				ATPase, Ca++ transporting, type 2C,	
158	38684_at	ATP2C1	AJ010953	member 1	putative Ca2+-transporting ATPase
159	35831_at	ATP9A	AB014511	ATPase, Class II, type 9A	KIAA0611 protein
<del>1</del> 8		ATP10D	AI478147	ATPase, Class V, type 10D	
161	36635_at	ATP11B	AB023173	ATPase, Class VI, type 11B	KIAA0956 protein
				ATPase, Cu++ transporting, alpha	
162	36523_at	ATP7A	L06133	polypeptide (Menkes syndrome)	Cu++-transporting P-type ATPase
46.5	220EA	ATDOM	A A 07770E	ATPase, H+ transporting, lysosomal	
3	163 33634_81	A : Fow	AA8///95	(vacuolar proton pump)	

	A	В	ပ	O	IJ
Γ				somal	
<u>2</u>	37395_at	ATP6S14	D49400		vacuolar A i Pase
				somal	
165	36994_at	ATP6L	M62762		vacuolar H+ ATPase proton channel subunit
				somai	
166	36167_at	ATP6F	D89052		proton-ATPase-like protein
Γ				somal	
167	37367_at	ATPEE	X76228	-	vacuolar H+ ATPase E subunit
				ATPase, H+ transporting, lysosomal	
168	37948_at	ATP6C	J05682	(vacuolar proton pump) 42kD	H+ -ATPase C subunit
				ATPase, H+ transporting, lysosomal	
169	33875_at	ATP6H	AI547262	(vacuolar proton pump) 9kD	
				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump) membrane sector	
170	40903_at	ATP6M8-9	AL049929	associated protein M8-9	hypothetical protein
				ATPase, H+ transporting, hysosomal	
				(vacuolar proton pump), alpha	
171	34889_at	ATP6A1	AA056747	polypeptide, 70kD, isoform 1	
				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump), beta polypeptide,	
172	40568_at	ATP6B2	L35249	56/58kD, isoform 2	vacuolar H+-ATPase 56,000 subunit
				ATPase, H+ transporting, lysosomal	
173	35770_at	ATP6S1	D16469	(vacuolar proton pump), subunit 1	ORF
				ATPase, Na+/K+ transporting, beta 1	
174	37669_s_at	ATP1B1	U16799	polypeptide	Na,K-ATPase beta subunit
				ATPase, Na+/K+ transporting, beta 3	sodium/potassium-transporting A l Pase beta-
175	32563_at	ATP1B3	U51478	polypeptide	3 subunit
L				ATP-binding cassette, sub-family A	
176	35717_at	ABCA8	AB020629	(ABC1), member 8	KIAA0822 protein
				ATP-binding cassette, sub-family C	
177		ABCC3	AF085692	(CFTR/MRP), member 3	multidrug resistance-associated protein 3B
178	35648	KIAA0442	AB007902	autism-related protein 1	autism-related protein 1
179	3806	AMFR	M63175	autocrine motility factor receptor	autocrine motility factor receptor
180	38433	AXL	M76125	AXL receptor tyrosine kinase	tyrosine kinase receptor
					hypothetical protein DKFZp586F1122 similar
181	35268_at	АХОТ	AL050171	axotrophin	to axotrophin

	⋖		ပ		·
182	35350_at	GALNAC4S-6ST	AB011170		KIAA0598 protein
				B lymphoma Mo-MLV insertion region	murine leukemia viral (bmi-1) oncogene
88	41562_at	BMI1	L13689		homolog
				B lymphoma Mo-MLV insertion region	murine leukemia viral (bmi-1) oncogene
<del>2</del> 8	1728_at	BMI1	L13689	(esnom)	homolog
188	185 36578 at	BIRC2	U37547	baculoviral IAP repeat-containing 2	MIHB
186	186 41278 at	BAF53A	AF041474	BAF53	BAF53a
187	33175_at	BBS4	AA156237	Bardet-Biedl syndrome 4	
				basic helix-loop-helix domain containing,	
188	40790_at	BHLHB2	AB004066	class B, 2	29O-1
189	40108_at	BZAP45	D13630	basic leucine-zipper protein BZAP45	basic leucine-zipper protein BZAP45
				basic transcription element binding protein	
190	40202_at	BTEB1	D31716		GC box binding protein
191	35055_at	ВТЕЗ	X53281	basic transcription factor 3	general transcription factor
192	38364_at	BCE-1	AF068197	BCE-1 protein	BCE-1
				B-cell CLL/lymphoma 6 (zinc finger protein	
193	40091_at	BCL6	U00115	51)	zinc-finger protein
				B-cell translocation gene 1, anti-	
194	37294_at	BTG1	X61123	proliferative	B-cell translocation protein 1
				BCL2/adenovirus E1B 19kD interacting	BCL2/adenovirus E1B 19kD-interacting
195	32060_at	BNIP2	U15173	protein 2	protein 2
				BCL2/adenovirus E1B 19kD interacting	
196	38010_at	BNIP3	AF002697	protein 3	E1B 19K/Bcl-2-binding protein Nip3
L				BCL2/adenovirus E1B 19kD interacting	BCL2/adenovirus E1B 19kDa-interacting
197	39436_at	BNIP3L	AF079221	protein 3-like	protein 3a
				-	glucocortoid receptor-associated protein
198	198 34798_at	BAG1	Z35491	BCL2-associated athanogene	RAP46
199	199 35291_at	BAG2	AL050287	BCL2-associated athanogene 2	hypothetical protein
8	200 36463 at	BAG5	AB020680	BCL2-associated athanogene 5	KIAA0873 protein
201	38050_at	BTF	D79986	Bcl-2-associated transcription factor	KIAA0164 gene product
202	38101_at	BDG-29	AB011151	BDG-29 proten	KIAA0579 protein
				beclin 1 (coiled-coil, myosin-like BCL2	
203	39378_at	BECN1	U17999	interacting protein)	
				beta subunit; Human pyruvate	
204	204 39160 at	PDHB	D90086	gene, exons 1-10.	pyruvate dehydrogenase (lipoamide) beta

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205	34644_at	B2M	AB021288		beta 2-microglobulin
206	40601_at	BBP	Al057115	beta-amyloid binding protein precursor	
				beta-hexosaminidase alpha chain; Human	
				beta-hexosaminidase alpha chain (HEXA)	
207	39340_at	HEXA	M16424	gene, exon 14.	hexosaminidase A preproprotein
208	208 38126 at	BGN	J04599	biglycan	biglycan preproprotein
602	209 33198 at	BART1	AA206524	binder of Arl Two	
				biotin-amide amidohydrolase; Homo	
				sapiens biotindase (BTD) gene, exons 2,	
210	210 37274_at	Btd	AF018631		biotinidase
				biphenyl hydrolase-like (serine hydrolase;	
				breast epithelial mucin-associated	
211	211 40912_s_at	BPHL	X81372	antigen)	biphenyl hydrolase-related protein
212	212 35267 g at	BLCAP	AL049288	bladder cancer associated protein	bladder cancer associated protein
213	213 35266 at	BLCAP	AL049288	bladder cancer associated protein	bladder cancer associated protein
214	214 37700 at	BLMH	X92106	bleomycin hydrolase	bleomycin hydrolase
				ne morphogenetic protein receptor, type	
215	39565_at	BMPR1A	Z22535		ALK-3
216	39551_at	BHC80	V98667	BRAF35/HDAC2 complex (80 kDa)	
				brain abundant, membrane attached	
217	32607_at	BASP1	AF039656	signal protein 1	neuronal tissue-enriched acidic protein
				brain abundant, membrane attached	
218	32606_at	BASP1	AA135683	signal protein 1	
219	37945 at	ВАСН	U91316	brain acyl-CoA hydrolase	acyl-CoA thioester hydrolase
220	37958 at	BCMP1	AL049257	brain cell membrane protein 1	brain cell membrane protein 1
221	40023_at	BDNF	X60201	brain-derived neurotrophic factor	brain-derived neurotrophic factor
				branched chain keto acid dehydrogenase	
				E1, beta polypeptide (maple syrup urine	branched chain alpha-ketoacid
222	41683_i_at	ВСКОНВ	U50708	disease)	dehydrogenase E1 beta subunit
					breast cancer antiestrogen resistance 3
223	36812_at	<b>BCAR3</b>	U92715	breast cancer anti-estrogen resistance 3	protein
				brefeldin A-inhibited guanine nucleotide-	
224	38306_at	BIG1	AA477576	exchange protein 1	
225	37947_at	BRD3	D26362	bromodomain containing 3	bromodomain containing protein 3
200	23 24 80E at	ВАСИ	ABOOSBOS	BTB and CNC homology 1, basic leucine zinner transcription factor 1	BTB and CNC homology 1, basic leucine zipper transcription factor 1
877	31032_al	חסאם	ADOUGLOOS	tippol nationalization india.	

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_		1			DICO
_	36634_at	B1G2	072649		0192
228	37218_at	BTG3	D64110		ANA
				BUB3 budding uninhibited by	
229	41547_at	BUB3	AF047472	benzimidazoles 3 homolog (yeast)	spleen mitotic checkpoint BUB3
230	34783_s_at	BUB3	AF047473	benzimidazoles 3 homolog (yeast)	testis mitotic checkpoint BUB3
234	32781 f at	BPAG1	AA058762	bullous pemphigoid antigen 1 (230/240kD)	
_					
232	32780_at	BPAG1	AB018271	bullous pemphigoid antigen 1 (230/240kD) KIAA0728 protein	KIAA0728 protein
233	32629_f_at	BTN3A1	U90552	butyrophilin, subfamily 3, member A1	butyrophilin
234	234 39357_at	C2F	U72514	C2f protein	CZł
235	40709_at	LOC58502	W27601	C2H2 (Kruppel-type) zinc finger protein	
236	37031_at	C9orf10	D80005	C9orf10 protein	C9orf10 protein
237	33856_at	CXX1	Y13374	CAAX box 1	putative prenylated protein
				cadherin 11, type 2, OB-cadherin	
238	36976_at	CDH11	D21255	(osteoblast)	OB-cadherin-2
				cadherin 11, type 2, OB-cadherin	
239	2087_s_at	CDH11	D21254	(osteoblast)	OB-cadherin-1
240	240 2053 at	CDH2	M34064	cadherin 2, type 1, N-cadherin (neuronal)	cadherin 2, type 1 preproprotein
				calcium/calmodulin-dependent protein	
241	31670_s_at	CAMK2G	U81554	kinase (CaM kinase) II gamma	CaM kinase II isoform
				calcium/calmodulin-dependent protein	
242	38716_at	CAMKK2	AB018330	kinase kinase 2, beta	KIAA0787 protein
L				calcium/calmodulin-dependent serine	
243	31854_at	CASK	AF035582	protein kinase (MAGUK family)	CASK
244	41738_at	CALD1	M64110	caldesmon 1	caldesmon
245	41739_s_at	CALD1	M83216	caldesmon 1	caldesmon
				calmodulin 1 (phosphorylase kinase,	
246	41288_at	CALM1	AL036744	delta)	
_				calmodulin 2 (phosphorylase kinase,	
247	/ 911_s_at	CALM2	M19311	delta)	calmodulin 2 (phosphorylase kinase, delta)
248	3 40125_at	CANX	L10284	calnexin	calnexin
249	37001_at	CAPN2	M23254	calpain 2, (m/II) large subunit	neutral protease large subunit
250	36138	CAPNS1	X04106	calpain, small subunit 1	calpain, small subunit 1

A 252 33385_g_ 253 40953_at	٧	8	ပ	3	U
251 4125 252 3338 253 4095		100			
252 3338 253 4095		CAST	D16217	calpastatin	caipastatin
253 4095	at	CAST	U31346	calpastatin	calpastatin
		CNN3	S80562	calponin 3, acidic	acidic calponin
254 3734		CALU	AF013759	calumenin	calumein
					cAMP responsive element binding protein 1,
255 3753	37535 at	CREB1	M27691	cAMP responsive element binding protein	Isolorm A, CAMP responsive element pinding protein 1, isoform B
				cAMP responsive element binding protein	
256 408	40849_s_at	CREB3	U88528		transcription factor LZIP
				ponsive element binding protein-	
257 3943	39438_at	CREBL2	AF039081	like 2	Cre binding protein-like 2
					cyclic AMP-responsive element modulator
258 3206	32065_at	CREM	S68134	cAMP responsive element modulator	beta isoform
259 32067_at	67_at	CREM	S68271	cAMP responsive element modulator	cyclic AMP-responsive element modulator
-					cyclic AMP-responsive element modulator
260 3200	32066_g_at	CREM	S68134	cAMP responsive element modulator	beta isoform
_				capping protein (actin filament) muscle Z-	
261 409	40910_at	CAPZA1	U56637	line, alpha 1	capping protein alpha subunit isoform 1
_				capping protein (actin filament) muscle Z-	•
262 36641	41_at	CAPZA2	U03851	line, alpha 2	capping protein alpha
				capping protein (actin filament) muscle Z-	
263 370	37012_at	CAPZB	U03271	line, beta	F-actin capping protein beta subunit
_				carbohydrate (chondroitin 6)	
264 320	32094_at	CHST3	AB017915	suffotransferase 3	chondroitin 6-sulfotransferase
265 414	41447_at	CHSY1	AB023207	carbohydrate (chondroitin) synthase 1	KIAA0990 protein
				carbohydrate (keratan sulfate Gal-6)	
266 413	41395_at	CHST1	AB003791	sulfotransferase 1	keratan sulfate Gal-6-sulfotransferase
-				carbohydrate (N-acetylglucosamine-6-0)	N-acetylglucosamine-6-O-sulfotransferase
267 379	37960_at	CHST2	AB014679	sulfotransferase 2	(GicNAc6ST)
268 36454_at	54_at	CA12	AF037335	carbonic anhydrase XII	carbonic anhydrase precursor
269 348	34876_at	CPD	U65090	carboxypeptidase D	carboxypeptidase D
270 366	36606_at	CPE	X51405	carboxypeptidase E	carboxypeptidase E precursor
				Cas-Br-M (murine) ectropic retroviral	
	35632_at	CBLB	U26710	transforming sequence b	cpl-b
272 401	40184_at	CSNK1A1	L37042	casein kinase 1, alpha 1	casein kinase I-alpha
273 365	36949_at	CSNK1D	U29171	casein kinase 1, delta	casein kinase I delta

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274	38019_at	CSNK1E	L37043		casein kinase I-epsilon
275	1211_s_at	CRADD	U84388	CASP2 and RIPK1 domain containing adaptor with death domain	death domain containing protein CRADD
276	1867_at	CFLAR	AF005775	CASP8 and FADD-like apoptosis regulator	CASP8 and FADD-like apoptosis regulator caspase-like apoptosis regulatory protein 2
				caspase 4, apoptosis-related cysteine	
277	195_s_at	CASP4	U28014		cysteine protease
978	33774 at	CASPR	X98172	caspase 8, apoptosis-related cysteine	MACH-alpha-1
				catenin (cadherin-associated protein),	
279	279 41156 g at	CINNA1	003100	alpha 1 (102KU)	alphaz(E)-cateriiri
280	280 41155_at	CTNNA1	U03100	catenin (cadherin-associated protein), alpha 1 (102kD)	alpha2(E)-catenin
281	2085 s at	CTNNA1	D14705	catenin (cadherin-associated protein), alpha 1 (102kD)	'human alpha-catenin'
6	1000	OTNINA 4	1 22005	catenin (cadherin-associated protein),	alcha 1 (E). catanin
787	2069_s_at	CINNAI	CDRCZ	alpha i (iozku)	מוחום ו (ב)-כמום וווו
283	35331_at	CTNNAL1	U97067	catenin (cadherin-associated protein), alpha-like 1	alpha-catenin-like protein
				catenin (cadherin-associated protein),	
284	284 40777_at	CTNNB1	X87838	beta 1 (88kD)	beta-catenin
				catenin (cadherin-associated protein),	
285	40444_s_at	CTNND1	AB002382	delta 1	
286	38466_at	CTSK	X82153	cathepsin K (pycnodysostosis)	Cathepsin O
287	37391_at	CTSL	X12451	cathepsin L	pro-(cathepsin L)
288	36915_at	CTSO	A1810485	cathepsin O	
289	36119_at	CAV1	AF070648	caveolin 1, caveolae protein, 22kD	
290	339_at	CAV2	AF035752	caveolin 2	caveolin-2
291	33113 at	CITED2	U65093	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	msg-related gene 1
292	1052 s at	CEBPD	M83667	CCAAT/enhancer binding protein (C/EBP), delta	NF-IL6-beta protein
293	293 39219_at	CEBPG	U20240	CCAAT/enhancer binding protein (C/EBP), gamma	C/EBP gamma

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	A		ار	U	U
		0.100		CCR4-NOT transcription complex, subunit	
234	33861_8[	CNOIZ	A1123426	7	
				CCR4-NOT transcription complex, subunit	
295   3		CNOT4	U71267		potential transcriptional repressor IVO 14mp
96 3	٠	CD164	D14043	CD164 antigen, sialomucin	MGC-24 precursor
297 3	34699 at	CD2AP	AL050105	CD2-associated protein	hypothetical protein
T					
				CD36 antigen (collagen type I receptor,	
				thrombospondin receptor)-like 2	
298 3	33823_at	CD36L2	D12676	(lysosomal integral membrane protein II)	85kDa human lysosomal sialoglycoprotein
T				CD44 antigen (homing function and Indian	
299 2	2036_s_at	CD44	M59040	blood group system)	cell adhesion molecule
T				CD81 antigen (target of antiproliferative	
300	35282_r_at	CD81	M33680	antibody 1)	CD81 antigen
8	39389_at	CD9	M38690	CD9 antigen (p24)	CD9 antigen
T				CDC10 cell division cycle 10 homolog (S.	
305	32175_at	CDC10	S72008	cerevisiae)	cell division cycle 10
				CDC16 cell division cycle 16 homolog (S.	
303	40404_s_at	CDC16	U18291	cerevisiae)	CDC16Hs
				CDC23 (cell division cycle 23, yeast,	
304	31877_at	CDC23	AF053977	. (Bolomou	cell division cycle protein 23
305	40690 at	CKS2	X54942	CDC28 protein kinase 2	Cks1 protein homologue
306	33362 at	CEP3	AF094521	Cdc42 effector protein 3	MSE55-related protein
307	32833_at	CLK1	M59287	CDC-like kinase 1	
	41535 at	CDK2AP1	AF006484	CDK2-associated protein 1	putative oral tumor suppressor protein
Γ				CDP-diacylglycerol synthase	
<del>0</del> 000	41343_at	CDS2	Y16521	(phosphatidate cytidytyttransferase) 2	CDS2 protein
				CDP-diacyfglycerolinositol 3-	
-				phosphatidyftransferase	
310	310 33397 at	CDIPT	AL050383	(phosphatidylinositol synthase)	
311	40591 at	CDC27	S78234	cell division cycle 27	H-NUC
				cell growth regulatory with ring finger	
312	450 g at	CGR19	U66469	domain	cell growth regulator CGR19
				cell growth regulatory with ring finger	
313	313 36514_at	CGR19	U66469	domain	cell growth regulator CGH19

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T					sollings and property of E1A ctimulated games
		0	00000		Cellular repressor of ETA-still unated gorles
5 4	33311_at	CHEG	AFU84523	cellular repressor of ETA-stimulated genes CHEG	כאפים
315	41333_at	CENTB2	D26069	centaurin, beta 2	centaurin, beta 2
	34676_at	CENTG2	AB029022	centaurin, gamma 2	KIAA1099 protein
317	38410_at	CETN2	X72964	centrin, EF-hand protein, 2	caltractin
				centrin, EF-hand protein, 3 (CDC31	
318	35232_f_at	CETN3	A1056696	homolog, yeast)	
319	31894_at	CENPC1	M95724	centromere protein C 1	centromere autoantigen C
	33805_at	CAP350	AB007949	centrosome-associated protein 350	KIAA0480 protein
				cerebellar degeneration-related protein	
321	36190_at	CDR2	M63256	(62kD)	major Yo paraneoplastic antigen
322	32262_at	CGI-01	AL049669	CGI-01 protein	hypothetical protein
323	323 40931_at	LOC50999	AL080084	CGI-100 protein	
324	38500_at	LOC51014	AB002450	CGI-109 protein	
325	325 34359_at	LOC51020	AA524058	CGI-130 protein	
326	38667_at	LOC51031	AA189161	CGI-150 protein	
327	327 41824_at	LOC51096	A1140114	CGI-48 protein	
328	328 34862_at	LOC51097	AA005018	CGI-49 protein	
329	37199_at	LOC51626	AI760932	CGI-60 protein	
	41411_at	LOC51103	AI566877	CGI-65 protein	
331	39814_s_at	LOC51635	AI052724	CGI-86 protein	
_				chaperonin containing TCP1, subunit 2	chaperonin-containing TCP-1 beta subunit
332	35759_at	CCT2	AF026166	(beta)	homolog
				chaperonin containing TCP1, subunit 3	
333	40774_at	ССТЗ	X74801	(gamma)	gamma subunit of CCT chaperonin
				chaperonin containing TCP1, subunit 4	chaperonin containing t-complex polypeptide
334	32594_at	CCT4	AF026291	(delta)	1, delta subunit
				chaperonin containing TCP1, subunit 6A	
335	38416_at	CCT6A	127706	(zeta 1)	chaperonin-like protein
				chaperonin containing TCP1, subunit 7	chaperonin containing t-complex polypeptide
336	38720_at	CC17	AF026292	(eta)	I, ela subumit
		-		chaperonin containing TCP1, subunit 8	chaperonin containing ICP1, subunit 8
33/	39767_at	8133	D1362/	(meta)	(111914)
338	338 41000_at	CHES1	U68723	checkpoint suppressor 1	checkpoint suppressor 1
339	37855_at	CTBS	M95767	chitobiase, di-N-acetyl-	di-N-acetylchitobiase

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38732_at	CLNS1A	X91788	chloride channel, nucleotide-sensitive, 1A Icin protein	Icin protein
_at	CLIC4	AL080061	chloride intracellular channel 4	
342 32363_at	CH25H	AF059214	cholesterol 25-hydroxylase	cholesterol 25-hydroxylase
			chondroitin sulfate proteoglycan 2	
38112_g_at	CSPG2	X15998		chondroitin sulfate proteoglycan 2 (versican)
			chondroitin sulfate proteoglycan 2	
_at	CSPG2	X15998	(versican)	chondroitin sulfate proteoglycan 2 (versican)
			chondroitin sulfate proteoglycan 6	
at	CSPG6	AF020043	(bamacan)	chromosome-associated polypeptide
			chromobox homolog 1 (HP1 beta homolog	
at Ta	CBX1	U35451	Drosophila )	heterochromatin protein p25
			chromobox homolog 3 (HP1 gamma	
38085_at	CBX3	AI740522	homolog, Drosophila)	
			chromobox homolog 3 (HP1 gamma	
348 38084_at	CBX3	AA648295	homolog, Drosophila)	
			chromodomain helicase DNA binding	
36137_at	CHD4	X86691	protein 4	Mi-2 protein
			chromodomain protein, Y chromosome-	
at	CDYL	AL050164	like	hypothetical protein
39550_at	Clorf17	AB011156	chromosome 1 open reading frame 17	KIAA0584 protein
39033_at	C1orf8	Z78368	chromosome 1 open reading frame 8	
32217_at	C12orf22	AF052105	chromosome 12 open reading frame 22	TGF-beta induced apotosis protein 12
40979_at	C14orf3	AJ243310	chromosome 14 open reading frame 3	C14orf3 protein
355 40045_g_at	C18orf1	AF009425	chromosome 18 open reading frame 1	clone 22
at	C19orf7	AB028987	chromosome 19 open reading frame 7	KIAA 1064 protein
34287_at	C21orf80	AB023175	chromosome 21 open reading frame 80	KIAA0958 protein
at	C22orf2	AL050345	chromosome 22 open reading frame 2	hypothetical protein
33778_at	C22orf4	AL096779	chromosome 22 open reading frame 4	hypothetical protein
41758_at	C22orf5	AL096879	chromosome 22 open reading frame 5	hypothetical protein
38690_at	C3orf4	AL080097	chromosome 3 open reading frame 4	hypothetical protein
36013_at	C4orf1	AF006621	chromosome 4 open reading frame 1	embryonic lung protein
36955_at	C5orf8	U10362	chromosome 5 open reading frame 8	GP36b glycoprotein
41375_at	C6orf28	AJ245416	chromosome 6 open reading frame 28	G7b protein
	C6orf34	W27949	chromosome 6 open reading frame 34	
36130 at	25.00	41.0000	a character of one of the former	The mathematical managerin

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					0 10 motors and and 0 10 motors
<u>ر</u> اود	35193_at	CHCJL	AF060219		ACCI-IIKE G exchanging factor RLG
368 3	34292_at	CXorf12	X92475	chromosome X open reading frame 12	chromosome X open reading frame 12
369	11314_at	SS	AF047042		citrate synthase
370 4	41159_at	CLTC	D21260	clathrin, heavy polypeptide (Hc)	clathrin heavy chain
-					clathrin, light polypeptide A, isoform a;
371 3	38657_s_at	CLTA	M20471	clathrin, light polypeptide (Lca)	clathrin, light polypeptide A, isoform b
				cleavage and polyadenylation specific	
372 3	35743_at	CPSF4	U79569	factor 4, 30kD subunit	no arches
_				cleavage stimulation factor, 3' pre-RNA,	
373 3	32723_at	CSTF1	L02547	subunit 1, 50kD	cleavage stimulation factor
				cleavage stimulation factor, 3' pre-RNA,	
	41183_at	CSTF3	U15782	subunit 3, 77kD	cleavage stimulation factor 77kDa subunit
375 3	38711_at	CLASP2	AB014527	CLIP-associating protein 2	KIAA0627 protein
376	36017_at	LOC57213	AF055016	CLLL6 protein	CLLL6 protein
一				clusterin (complement lysis inhibitor, SP-	clusterin (complement lysis inhibitor, SP-
				40,40, sulfated glycoprotein 2,	40,40, sulfated glycoprotein 2, testosterone-
				testosterone-repressed prostate message repressed prostate message 2,	repressed prostate message 2,
377	36780_at	CLU	M25915	2, apolipoprotein J)	apolipoprotein J)
378	35180_at	LOC113251	AL050205	c-Mpl binding protein	
379	40811_at	COASTER	AB011148	coactivator for steroid receptors	KIAA0576 protein
280	38052 at	F13A1	M14539	coagulation factor XIII A1 polypeptide	coagulation factor XIII A1 subunit precursor
381	36972 at	PNP24	X92098	coated vesicle membrane protein	transmembrane protein
_	34326 at	COPB	X82103	coatomer protein complex, subunit beta	beta-Coat protein
				coatomer protein complex, subunit beta 2	
383	36677_at	COPB2	X70476	(beta prime)	subunit of coatomer complex
384	35205	COBRA1	AL050280	cofactor of BRCA1	hypothetical protein
				cofactor required for Sp1 transcriptional	
385	36648_at	CRSP9	AF031383	activation, subunit 9 (33kD)	hMed7
386	386 33659_at	CFL1	X95404	cofilin 1 (non-muscle)	cofilin
387	40879_at	BICD2	AB014599	coiled-coil protein BICD2	KIAA0699 protein
388	388 39864_at	CIRBP	D78134	cold inducible RNA binding protein	CIRP
389	39839_at	CSDA	M24069	cold shock domain protein A	cold shock domain protein A
330	390 32307_s_at	COL1A2	V00503	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein
391	32306_g_at	COL1A2	J03464	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein
392	392 32305 at	COL1A2	J03464	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein



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				Anllocan trace III clube 1 (Eblore-Donloc	
393	32488 at	COL3A1	X14420	syndrome type IV, autosomal dominant)	prepro-alpha-1 type 3 collagen
394	36659	COL4A2	X05610	collagen, type IV, alpha 2	alpha (2) chain
395	38420	COL5A2	Y14690	collagen, type V, alpha 2	procollagen alpha 2(V)
	38722_at		X15880	collagen, type VI, alpha 1	alpha-1 collagen VI (AA 574-1009)
397	38077		X52022	collagen, type VI, alpha 3	collagen type VI, alpha 3 chain
398	37459_at		X57527	collagen, type VIII, alpha 1	alpha 1(VIII) collagen
					alpha 1 type XI collagen, isoform A
					preproprotein; alpha 1 type XI collagen,
					isoform B preproprotein; alpha 1 type XI
399	37892 at	COL11A1	J04177	collagen, type XI, alpha 1	collagen, isoform C preproprotein
400	35168_f_at	COL16A1	M92642	collagen, type XVI, alpha 1	alpha-1 type XVI collagen
401	37668 at	C10BP	M69039	complement component 1, q	complement component 1, q subcomponent binding protein precursor
				complement component 1, r	
402	39409_at	C1R	M14058	subcomponent	complement component 1, r subcomponent
				complement component 1, s	
403	403 40496_at	C1S	J04080	subcomponent	complement component 1, s subcomponent
404	404 36638_at	CTGF	X78947	connective tissue growth factor	connective tissue growth factor
				conserved gene amplified in	
405	41202_s_at	0S4	AF000152	osteosarcoma	OS-4 protein
ا				conserved helix-loop-helix ubiquitous	
406	33770_at	CHUK	AF009225	Kinase	IKB Kinase alpha subunit
				COP9 constitutive photomorphogenic	
407	1789_at	COPS5	U65928	homolog subunit 5 (Arabidopsis)	Jun activation domain binding protein
8	32539_at	COP9	U51205	COP9 homolog	COP9 signalosome subunit 1 CSN1
404	409 40138 at	MOV34-34KD	1170735	COP9 subunit 6 (MOV34 homolog, 34 kD)	34 kDa Mov34 homolog
4	410 40452 at	CPNE1	U83246	copine l	copine I
<u>±</u>	39706_at	CPNE3	AB014536	copine III	KIAA0636 protein
				coproporphyrinogen oxidase	
412	37999_at	CPO	D16611	(coproporphyria, harderoporphyria)	coproporphyrinogen oxidase
413	37026_at	COPEB	AF001461	core promoter element binding protein	Kruppel-like zinc finger protein 219
414	41175_at	CBFB	120298	core-binding factor, beta subunit	transcription factor
415	32803_at	CNIL	AF104398	cornichon-like	comichon



					ц
			Š	COX11 homolog cytochrome c oxidese	
416	416 34723_at	COX11	U79270	assembly protein (yeast)	COX11 homolog
[ ]	i de	L C		CpG island protein; Human nested gene	rictory bottomore IIIV retails and reliable
4	417 37907_at	F8A; UXS522E	M345//	protein gene, complete cas.	coagulation lactor viii-associated protein
418	38664_at	CFDP1	AB009285	craniofacial development protein 1	craniofacial development protein 1
	,	; ;		CREB binding protein (Rubinstein-Taybi	
419	33831_at	CREBBP	U47741	syndrome)	CREB-binding protein
420	420 36948_at	CRI1	AL109701	CREBBP/EP300 inhibitory protein 1	C15orf3
421	38148_at	CRY1	D83702	cryptochrome 1 (photolyase-like)	photolyase
422	422 37902_at	CRYZ	L13278	crystallin, zeta (quinone reductase)	zeta-crystallin
423	423 40167_s_at	LOC55884	AF038187	CS box-containing WD protein	
				CSE1 chromosome segregation 1-like	
424	38804_at	CSE1L	AF053641	(yeast)	cellular apoptosis susceptibility protein
425	1768_s_at	CSK	X59932	c-src tyrosine kinase	c-src-kinase
426	426 41309_g_at	CTBP1	U37408	C-terminal binding protein 1	phosphoprotein CtBP
427	427 40780_at	CTBP2	AF016507	C-terminal binding protein 2	C-terminal binding protein 2
428	428 39723_at	CUL1	AF062536	cullin 1	cullin 1
429	40141_at	CUL4B	AB014595	cullin 4B	KIAA0695 protein
L				cut-like 1, CCAAT displacement protein	
<u>왕</u>	31823_at	CUTL1	M74099	(Drosophila)	cut-like 1, CCAAT displacement protein
431	36872_at	ARPP-19	AL120559	cyclic AMP phosphoprotein, 19 kD	
				cyclin D binding myb-like transcription	cyclin D binding myb-like transcription factor
432	432 41808_at	DMTF1	AF052102	factor 1	
				cyclin D1 (PRAD1: parathyroid	
433	433 38418_at	CCND1	X59798	adenomatosis 1)	cyclin
				cyclin D1 (PRAD1: parathyroid	
43	2020_at	CCND1	M73554	adenomatosis 1)	bcl-1
<u> </u>	36650_at	CCND2	D13639	cyclin D2	cyclin D2
<u>송</u>	40225_at	GAK	D88435	cyclin G associated kinase	HsGAK
437	437 37723_at	CCNG2	U47414	cyclin G2	cyclin G2
438	1913_at	CCNG2	U47414	cyclin G2	cyclin G2
439	439 1924_at	CCNH	U11791	cyclin H	cyclin H
44	440 1836_at	CCNI	D50310	cyclin I	cyclin I
441	1792_g_at	CDK2	M68520.	cyclin-dependent kinase 2	cdc2-related protein kinase

(7 Si)

42         33317_at         CDK7         Cyclin-dependent kinas of Minase of				Č		
CDK7		<	В	)	O.	u
1,000					cyclin-dependent kinase 7 (MO15	
1989 s. at   CDK7   L20320   Kinase    CDK1   CDK2   Cyclin-dependent kinase 7 (MO15   Cyclin-dependent kinase 8   Coltar   CDK8   R59697   Cyclin-dependent kinase and bibitor 1A (p21, cyclin-dependent kinase inhibitor 1A (p21, cyclin-dependent kinase inhibitor 1A (p21, cyclin-dependent kinase inhibitor 1B (p27, cyclin-dependent kinase inhibitor 2C (p18, cyclin-dependent kinase inhibitor 1B (p27, cyclin-dependent kinase inhibitor 2C (p18, cyclin-dependent c					homolog, Xenopus laevis, cdk-activating	
1969 s at CDK7	442	33317_at	CDK7	120320	kinase)	protein serine/threonine kinase
1969 s_at   CDK7   X77743   Kinase)   CDK8   R59697   Cyclin-dependent kinase and plate to CDK8   R59697   Cyclin-dependent kinase inhibitor 1A (p21, cyclin-dependent kinase inhibitor 1B (p27, cyclin-dependent cyclin-de					cyclin-dependent kinase 7 (MO15	
1969_s_at   CDK7					homolog, Xenopus laevis, cdk-activating	
193140_at   CDK8   R59697   Cyclin-dependent kinase inhibitor 14 (p21, cyclin-dependent kinase inhibitor 14 (p21, cyclin-dependent kinase inhibitor 18 (p27, cyclin-dependent kinase inhibitor 2 (p18, cyclin-dependent kinase inhibitor 2 (p21, cyclin-dependent coxidase subunit VII (p21, cyclin-dependent kinase inhibitor 2 (p21, cyclin-dependent coxidase subunit VII (p21, cyclin-dep	443	1969_s_			kinase)	CDK activating kinase
COENTIA   U03106   Cip1   Cip1	444			R59697	cyclin-dependent kinase 8	
CDKN1A   U03106   Cip1					cyclin-dependent kinase inhibitor 1A (p21,	
COKN1B	445	2031	CDKN1A	U03106	Cip1)	cyclin-dependent kinase inhibitor 1A
CDKN1B					cyclin-dependent kinase inhibitor 1B (p27,	
36053_at   CDKN2C   AF041248   inhibits CDK4    inhibit	446	33847	CDKN1B		Kip1)	
36053_at         CDKN2C         AF041248         inhibits CDK4)           38700_at         CSRP1         M33146         cysteine and glycine-rich protein 1           41401_at         CSRP2         U57646         cysteine and glycine-rich protein 2           41401_at         CSRP2         U57646         cysteine and glycine-rich protein 2           40936_at         CSRP2         U57646         cysteine-rich, angiogenic inducer, 61           40936_at         CRRM1         Al651806         cysteine-rich, angiogenic inducer, 61           40408_at         CYR61         Y11307         cysteinyl-tRNA synthetase           40408_at         CARS         L06845         cysteinyl-tRNA synthetase           40408_at         CMAH         D08224         N-acetylneuraminic acid hydroxylase (CMP-Actylneuraminic acid hydroxylase (CMP-Actylneuraminic acid hydroxylase (CMP-Actylneuraminic acid hydroxylase)           41206_rat         COX5B         Al526089         cytochrome c oxidase subunit VIIa           41760_at         COX7A2         AA978033         polypeptide c					cyclin-dependent kinase inhibitor 2C (p18,	
38700_at         CSRP1         M33146         cysteine and glycine-rich protein 1           41401_at         CSRP2         U57646         cysteine and glycine-rich protein 2           40936_at         CRIM1         Al651806         cysteine-rich motor neuron 1           38772_at         CYR61         Y11307         cysteine-rich motor neuron 1           40936_at         CARS         L06845         cysteine-rich, angiogenic inducer, 61           40408_at         CARS         L06845         cysteine-rich, angiogenic inducer, 61           40408_at         CARS         L06845         cysteinyl-tRNA synthetase           40408_at         CARS         L06845         cysteinyl-tRNA synthetase           40408_at         CARAH         D86324         N-acetylneuraminate monoxygenase)           A4170_at         CMAH         D86324         N-acetylneuraminate monoxygenase)           A4170_at         CMAH         AA173896         membrane precursor           39921_at         CXX6         AA1526089         cytochrome c oxidase subunit VIc           41206_r         AA152406         cytochrome c oxidase subunit VIla           41760_at         COX7A2         AA978033         polypeptide 1 (muscle)           34381_at         COX7C         AA9708039         cytoc	447		CDKN2C	AF041248	inhibits CDK4)	cyclin-dependent kinase inhibitor
41401_at         CSRP2         U57646         cysteine and glycine-rich protein 2           40936_at         CRIM1         Al651806         cysteine-rich motor neuron 1           38772_at         CYR61         Y11307         cysteine-rich motor neuron 1           40408_at         CYR61         Y11307         cysteine-rich, angiogenic inducer, 61           40408_at         CARS         L06845         cysteine-rich, angiogenic inducer, 61           40408_at         CARS         L06845         cysteine-rich, angiogenic inducer, 61           40408_at         CARS         L06845         cysteinyl-tRNA synthetase           59317_at         CMAH         D86324         N-acetylneuraminate monooxygenase)           34340_at         CYMAH         D86324         N-acetylneuraminate monooxygenase)           34340_at         CYMAH         AA173896         membrane precursor           35818_at         HCS         D00265         cytochrome coxidase subunit VIB           39921_at         COX64         W51774         cytochrome coxidase subunit VIB           39031_at         COX7A1         AA978033         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34381_at         COX7C         AI708889 <th>448</th> <td>38700</td> <td>CSRP1</td> <td>M33146</td> <td>cysteine and glycine-rich protein 1</td> <td>cysteine and glycine-rich protein 1</td>	448	38700	CSRP1	M33146	cysteine and glycine-rich protein 1	cysteine and glycine-rich protein 1
40936_at         CRIM1         Al651806         cysteine-rich motor neuron 1           38772_at         CYR61         Y11307         cysteine-rich, angiogenic inducer, 61           40408_at         CARS         L06845         cystein-rich, angiogenic inducer, 61           40408_at         CARS         L06845         cysteinyl-tRNA synthetase           40408_at         CARS         L06845         cysteinyl-tRNA synthetase           39317_at         CMAH         D86324         N-acetylneuraminate monooxygenase)           34340_at         CYBS-M         A4173896         membrane precursor           35818_at         HCS         D00265         cytochrome be outer mitochondrial           35921_at         COX5B         A1526089         cytochrome c oxidase subunit VIa           36165_at         COX6A1         A1526089         cytochrome c oxidase subunit VIa           36165_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2         AB907618         polypeptide 2 (liver)           34381_at         COX7A2         AB007618         cytochrome c oxidase subunit VIIa           34381_at         COX7A2         AB007618	449	41401_at	CSRP2	U57646	cysteine and glycine-rich protein 2	cysteine and glycine-rich protein 2
38772_at         CYR61         Y11307         cysteine-rich, angiogenic inducer, 61           40408_at         CARS         LO6845         cysteinyl-tRNA synthetase           39317_at         CAMH         D86324         cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-acetylneuraminic acidase subunit VII acetylneuraminic acidase subun	450	40936	CRIM1	AI651806	cysteine-rich motor neuron 1	
40408_at         CARS         LO6845         cysteinyl-tRNA synthetase           39317_at         CMAH         D86324         N-acetylneuraminate monooxygenase)           34340_at         CYB5-M         AA173896         Membrane precursor           35818_at         HCS         D00265         cytochrome could see subunit Vb           35818_at         HCS         D00265         cytochrome coxidase subunit Vb           39921_at         COX5B         A1526089         cytochrome coxidase subunit Vla           41206_r_at         COX6C         W51774         cytochrome coxidase subunit Vla           36165_at         COX6C         W51774         cytochrome coxidase subunit Vlla           39031_at         COX7A1         AA152406         cytochrome coxidase subunit Vlla           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2         AB007618         polypeptide 2 like           34381_at         COX7C         A1708889         cytochrome coxidase subunit Vllc	451	38772	CYR61	Y11307	cysteine-rich, angiogenic inducer, 61	CYR61 protein
CONTAL   CONTAL   CONTAL	452		CARS	L06845	cysteinyl-tRNA synthetase	cysteinyl-tRNA synthetase
CONTAL   CONTAL   CONTAL   CONTAL						
39317_at         CMAH         D86324         N-acetylneuraminic acid hydroxylase (CMP-Acetylneuraminate monooxygenase)           34340_at         CYB5-M         AA173896         Membrane b5 outer mitochondrial membrane precursor           35818_at         HCS         D00265         cytochrome c oxidase subunit Vb cytochrome c oxidase subunit Vla           41206_r_at         COX6A1         AI526089         cytochrome c oxidase subunit Vla           36165_at         COX6A1         AI540925         polypeptide 1           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         AI708889         cytochrome c oxidase subunit Vllc					cytidine monophosphate-N-	
39317_at         CMAH         D86324         N-acetylneuraminate monooxygenase)           34340_at         CYB5-M         AA173896         membrane precursor           35818_at         HCS         D00265         cytochrome c           39921_at         COX5B         AI526089         cytochrome c oxidase subunit Vb           41206_r_at         COX6A1         AI540925         polypeptide 1           36165_at         COX6C         W51774         cytochrome c oxidase subunit Vlc           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         AI708889         cytochrome c oxidase subunit Vllc					acetylneuraminic acid hydroxylase (CMP-	
34340_at         CYB5-M         AA173896         membrane precursor           35818_at         HCS         D00265         cytochrome c           39921_at         COX5B         AI526089         cytochrome c oxidase subunit Vb           41206_r_at         COX6A1         AI540925         polypeptide 1           36165_at         COX6C         W51774         cytochrome c oxidase subunit Vla           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         AI708889         cytochrome c oxidase subunit Vllc	453		СМАН	D86324	N-acetylneuraminate monooxygenase)	CMP-N-acetylneuraminic acid hydroxylase
34340_at         CYB5-M         AA173896         membrane precursor           35818_at         HCS         D00265         cytochrome c           39921_at         COX5B         AI526089         cytochrome c oxidase subunit Vb           41206_r_at         COX6A1         AI540925         polypeptide 1           36165_at         COX6C         W51774         cytochrome c oxidase subunit Vla           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         AI708889         cytochrome c oxidase subunit Vllc					cytochrome b5 outer mitochondrial	
35818_at         HCS         D00265         cytochrome c oxidase subunit Vb           39921_at         COX5B         Al526089         cytochrome c oxidase subunit Vb           41206_r_at         COX6A1         Al540925         polypeptide 1           36165_at         COX6C         W51774         cytochrome c oxidase subunit Vla           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         AI708889         cytochrome c oxidase subunit Vilc	454	34340_at	CYB5-M	AA173896	membrane precursor	
39921_at         COX5B         AI526089         cytochrome c oxidase subunit Vb           41206_r_at         COX6A1         AI540925         polypeptide 1           36165_at         COX6C         W51774         cytochrome c oxidase subunit Vla           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34331_at         COX7A2L         AB007618         polypeptide 2 like           34331_at         COX7A2L         AI708889         cytochrome c oxidase subunit Vllc	455	35818_at	HCS	D00265	сутоснготе с	cytochrome c
41206_r_at COX6A1 Al540925 polypeptide 1  36165_at COX6C W51774 cytochrome c oxidase subunit VIa  39031_at COX7A1 AA152406 polypeptide 1 (muscle)  41760_at COX7A2 AA978033 polypeptide 2 (liver)  34330_at COX7A2L AB007618 polypeptide 2 like  34381_at COX7C Al708889 cytochrome c oxidase subunit VIIa	456	39921_at	COX5B	AI526089	cytochrome c oxidase subunit Vb	
41206_r_at         COX6A1         Al540925         polypeptide 1           36165_at         COX6C         W51774         cytochrome c oxidase subunit VIIa           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         Al708889         cytochrome c oxidase subunit VIIc					cytochrome c oxidase subunit Vla	
36165_at         COX6C         W51774         cytochrome c oxidase subunit VIIa           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 (liker)           34330_at         COX7A2L         AB007618         polypeptide 2 liker           34381_at         COX7A2         AI708889         cytochrome c oxidase subunit VIIc	457	41206_r_at	COX6A1	AI540925	polypeptide 1	
39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         AI708889         cytochrome c oxidase subunit VIIc	458	36165_at	coxec	W51774	cytochrome c oxidase subunit VIc	
39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7A2C         AI708889         cytochrome c oxidase subunit VIIc					cytochrome c oxidase subunit VIIa	
41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7A2L         AI708889         cytochrome c oxidase subunit VIIc	459		COX7A1	AA152406	polypeptide 1 (muscle)	
41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         AI708889         cytochrome c oxidase subunit VIIc					cytochrome c oxidase subunit VIIa	
34330_at COX7A2L AB007618 polypeptide 2 like 34381_at COX7C AI708889 cytochrome c oxidase subunit VIIc	<del>4</del>	41760_at	COX7A2	AA978033	polypeptide 2 (liver)	
34330_at COX7A2L AB007618 polypeptide 2 like a 4381_at COX7C Al708889 cytochrome c oxidase subunit VIIc					cytochrome c oxidase subunit VIIa	
_at   COX7C   AI708889	46	34330	COX/A2L	AB007618	polypeptide 2 like	COA/HP
	462		COX7C	AI708889	cytochrome c oxidase subunit VIIc	

			ě		U
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_	<u> </u>	COXB	A1525665	cytochrome c oxidase subunit VIII	
\$	35819_at	CYC1	X06994	cytochrome c-1	cytochrome c-1
				cytochrome P450, 51 (lanosterol 14-alpha-	
465	33389_at	CYP51	U23942	demethylase)	lanosterol 14-demethylase cytochrome P450
				cytochrome P450, subfamily I (dioxin-	
				inducible), polypeptide 1 (glaucoma 3,	
466	859_at	CYP1B1	U03688	primary infantile)	cytochrome P450
				cytochrome P450, subfamily I (dioxin-	
		•		inducible), polypeptide 1 (glaucoma 3,	
467	40071_at	CYP1B1	U03688	primary infantile)	cytochrome P450
468	37509_at	CRLF3	AF046059	cytokine receptor-like factor 3	cytokine receptor related protein 4
469	37306_at	KIAA0068	D38549	cytoplasmic FMRP interacting protein 1	
				cytoplasmic; Human Ser/Thr protein	
470	1706_at	A-RAF-1	U01337	kinase (A-RAF-1) gene, complete cds.	Ser/Thr protein kinase
471	34338_at	CKAP1	D49738	cytoskeleton-associated protein 1	cytoskeleton associated protein
472	32529_at	CKAP4	X69910	cytoskeleton-associated protein 4	P63 protein
473	40282_s_at	PF	M84526	D component of complement (adipsin)	adipsin/complement factor D
474	40877_s_at	MN7	AF041080	D15F37 (pseudogene)	
				damage-specific DNA binding protein 2	
475	1243_at	DDB2	U18300	(48kD)	DDBb p48
476	476 36616_at	DAZAP2	D31767	DAZ associated protein 2	DAZ associated protein 2
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
477	37663_at	DDX1	X70649	polypeptide 1	member of DEAD box protein family
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
478	35306_at	DDX15	AB001636	polypeptide 15	ATP-dependent RNA helicase #46
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
479	40490_at	DDX21	U41387	polypeptide 21	Gu protein
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
480	39744_at	DDX3	AF000982	polypeptide 3	dead box, X isoform
				DEAD/H (Asp-Glu-Ala-Asp/His) box	DEAD/H (Asp-Glu-Ala-Asp/His) box
481	34647_at	DDXS	X52104	polypeptide 5 (RNA helicase, 68kD)	polypeptide 5
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
				polypeptide 9 (RNA helicase A, nuclear	
482	36153_at	6XQQ	L13848	DNA helicase II; leukophysin)	RNA helicase A
483	483 41872 at	DFNA5	AF073308	deafness, autosomal dominant 5	nonsyndromic hearing impairment protein

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J		8	<u>ن</u>	0	
					ionizing radiation resistance conterning
	$\neg$	DAP3	U18321	death associated protein 3	protein
		UEPP	AR022718	decidual protein induced by progesterone	ОЕРР
	T	DOCK1	D50857	_	DOCK180 protein
l	T	DAD1	D15057	ath 1	DAD-1
	Τ			deficient in late-infantile neuronal ceroid	
				lipofuscinosis; Homo sapiens lysosomal	
		CI No	AF039704		lysosomal pepstatin insensitive protease
	Т			atocyte homolog, lipid	
		DEGS	AF002668		MLD
ŀ		DEK	X64229	nding)	putative oncogene
		DLC1	AF035119		deleted in liver cancer-1
33791 at		DLEU1	Y15227	deleted in lymphocytic leukemia, 1	deleted in lymphocytic leukemia, 1
38744 at		DSS1	N95406	Deleted in split-hand/split-foot 1 region	
				delta sleep inducing peptide,	
	_	DSIPI	AI635895	immunoreactor	
35814 at	ĺ	GA17	AF064603	dendritic cell protein	GA17 protein
38385 at		DSTN	S65738	destrin (actin depolymerizing factor)	actin depolymerizing factor
	1			development and differentiation enhancing	development and differentiation enhancing development- and differentiation-enhancing
39410 at		DDEF2	AB007860	factor 2	factor 2
498 39044 s at	1	DGKD	D73409	diacylglycerol kinase, delta (130kD)	diacylglycerol kinase delta
499 38003 s at		DGKZ	U94905	diacylglycerol kinase, zeta (104kD)	diacylglycerol kinase zeta
33920 at		DIAPH1	AF051782	diaphanous homolog 1 (Drosophila)	diaphanous 1
				diazepam binding inhibitor (GABA	
J				receptor modulator, acyl-Coenzyme A	
at		DBI	AI557240	binding protein)	
	1			dihydrolipoamide S-acetyftransferase (E2	
				component of pyruvate dehydrogenase	:
502 39041_at		DLAT	Y00978	complex)	PDC-E2 precursor (AA -54 to 561)
503 40607 at		DPYSL2	U97105	dihydropyrimidinase-like 2	N2A3
504 36149 at		DPYSL3	D78014	dihydropyrimidinase-like 3	dihydropyrimidinase related protein-3
505 39503 s at		DPYSL4	AB006713	dihydropyrimidinase-like 4	dihydropyrimidinase related protein 4
-		DPYD	U20938	dihydropyrimidine dehydrogenase	dihydropyrimidine dehydrogenase
507 40485 at	ļ	HSA249128	AA176780	DIPB protein	
1					

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A	L	8	0	Q	ш
479_at DAB2 U53446		U53446		disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	Doc-2
				discoidin domain receptor family, member	
509 36643_at DDR1 L20817		120817		1	tyrosine protein kinase
510 40575_at DLG5 AB011155		AB011155		discs, large (Drosophila) homolog 5	KIAA0583 protein
				dishevelled associated activator of	
511 33753_at   DAAM1 AB014566		AB014566		morphogenesis 1	KIAA0666 protein
3150_at SAS10 Al126004		A1126004		disrupter of silencing 10	
				dJ635G19.1 (LAMR1 (Laminin Receptor 1	
				(67kD) (RPSA, 40S Ribosomal Protein	
				SA, P40)) pseudogene); match: cDNAs:	
				Em:X15005 Em:J03799 Em:X61156	
-				Em:M64923 Em:X06406 Em:AF140348	
		•		Em:J02870 Em:L16589 Em:Z22749	
.)_	1	1		Em:D25224 Em:M14199 Em:M27798;	
40916_at dJ635G19.1 AL035494		AL035494	ı	match: ESTs: Em:AA642	dJ635G19.2.1 (novel protein (isoform 1))
				dJ734P14.1 (KRAB box and C2H2 Zinc	
				finger domain protein pseudogene) match:	
				cDNAs: Em:M27878 Em:M29580	
				Em:U27186 Em:D31763 Em:AB007872	
				Em:U09366 Em:U09413 Em:X17617	
_	_			Em:AF011573 Em:AF020591 Em:X78925	
				match: proteins: Sw:P52736 Sw:Q06730	
				Sw.P51523 Tr.Q14585 Sw.P15620	
				Sw:Q02386 Sw:P51786 Sw:Q99676	
				Tr:O60792 Sw:Q03923 Sw:O75820	dJ734P14.2.1 (snRNP (smail nuclear
514 38456 s_at dJ734P14.1 AL049650		AL049650		Tr:Q61116 Tr:Q64247	ribonucleoprotein particle) protein B)

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515	38455_at	dJ734P14.1	AL049650	dJ734P14.1 (KRAB box and C2H2 Zinc finger domain protein pseudogene) match: cDNAs: Em:M27878 Em:M29580 Em:U27186 Em:D31763 Em:AB007872 Em:U09366 Em:U09413 Em:X17617 Em:AF011573 Em:AF020591 Em:X78925 match: proteins: Sw:P52736 Sw:Q06730 Sw:Q51523 Tr:Q14585 Sw:P15620 Sw:Q03923 Sw:Q05820 Tr:Q60792 Sw:Q03923 Sw:O75820	dJ734P14.2.1 (snRNP (small nuclear
516	516 35809_g_at	dJ862K6.4	AL031681	dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:Q57731 Sw:P40558	dJ862K6.2.2 (splicing factor, arginine/serine- rich 6 (SRP55-2)(isoform 2))
517	35808_at	dJ862K6.4	AL031681	dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:P21590 Sw:Q57731 Sw:P40558	dJ862K6.2.2 (splicing factor, arginine/serine- rich 6 (SRP55-2)(isoform 2))
518	518 32433 at	dJ90 <u>L</u> 6.1	297353	dJ90L6.1 (RPL15 (60S Ribosomal Protein L15) pseudogene); match: proteins: Sw:O74895 Sw:P51417 Sw:P39030 Sw:O77445 Sw:P54780 Sw:O23515 Sw:O65050 Wp:CE12148 Sw:P30736 Sw:P641051 Sw:P54060 Sw:O65082 Sw:P52818 Sw:P5924 Sw:P05748; Human DNA sequence from clone RP1-90L6 on chromosome 22q11.21-11.23 Contains an RPL15 (60S Ribosomal Protein L15) pseudogene, ESTs, STSs and GSSs, complete sequence.	·

Fig 21

	V	9			Ц
-		٦,		1	the mothering a protein
	04100 at	DNFZF434C171			ilypoinement protein
	40801_at	UNF2P434C212 AA64306		UNFZF434CZ1Z protein	
	38400_at	DKFZP434D1335		<b>=</b>	
522	33392_at	4	AL080155		hypothetical protein
523	39411_at	4	AL080156		hypothetical protein
524	40564_at	ದ		DKFZP564A043 protein	
525	37000_at	DKFZP564B167			hypothetical protein
526	33433_at	DKFZP564F0522 AL049943			hypothetical protein
527	41437_at	DKFZP564F1123			hypothetical protein
528	39442_at	DKFZP564G0222 AL080115			hypothetical protein
529	529 40437_at	DKFZP564G2022		DKFZP564G2022 protein	hypothetical protein
530	530 36456_at	DKFZP5641052	AL080063	DKFZP5641052 protein	hypothetical protein
531	38033_at	DKFZP564M1416 AL049934		DKFZP564M1416 protein	hypothetical protein
532	36078_at	DKFZP56400423 AL080120		DKFZP56400423 protein	hypothetical protein
533	38256_s_at	DKFZP5640092 W21827	W21827	DKFZP5640092 protein	
534	39034_at	DKFZP5640123	AL080122	DKFZP5640123 protein	hypothetical protein
535	41662_at	_	AL050272	DKFZP566B183 protein	hypothetical protein
536	32807_at	DKFZP566C134	AF004292	DKFZP566C134 protein	
232	38687_at		AL050051	DKFZP566D193 protein	hypothetical protein
538	33776_at	DKFZP566K023	AL050062	DKFZP566K023 protein	hypothetical protein
539	539 41335_at	DC8	AL050084	DKFZP56601646 protein	hypothetical protein
540	36961_at	DKFZP586A011	AL050286	DKFZP586A011 protein	hypothetical protein
541	38717_at	DKFZP586A0522 AL050159	AL050159	DKFZP586A0522 protein	hypothetical protein
542	40831_at	DKFZP586B0923 AL050190	AL050190	DKFZP586B0923 protein	hypothetical protein
543	34821_at	DKFZP586D0623 AL050197	AL050197	DKFZP586D0623 protein	hypothetical protein
544	39986_at	DKFZP586D0919 AL050100	AL050100	DKFZP586D0919 protein	hypothetical protein
545	34269_at	DKFZp586F1019 AL050102	AL050102	DKFZp586F1019 protein	hypothetical protein
546	546 35736_at	DKFZP586F1918 AL050091	AL050091	DKFZP586F1918 protein	hypothetical protein
547	547 40832_s_at	DKFZP586G011	AL050126	DKFZP586G011 protein	hypothetical protein
548	36007_at	DKFZP586L151	AL050137	DKFZP586L151 protein	hypothetical protein
549	34833_at	DKFZP58600120	120 AL050157	DKFZP586O0120 protein	hypothetical protein
550	37333_at	DNMT1	X63692	DNA (cytosine-5-)-methyttransferase 1	DNA (cytosine-5-)-methyftransferase
				DNA segment on chromosome X (unique)	-
551	40891_f_at	DXS9879E	X92896	9879 expressed sequence	ITBA2 protein
				DNA segment on chromosome X and Y	DNA segment on chromosome X and Y
552	552 34215_at	DXYS155E	L03426	(unique) 155 expressed sequence	(unique) 155 expressed sequence

	Y	89	ပ	D	ш
, L		0.00	27 2029	DNA segment, single copy probe LNS-	rie transfer proposed arratein
553	1252_at	<b>D55346</b>	M73547	CAVLNS-CAII (deleted in polyposis	polyposis iocus-ericoded protein
				DNA segment, single copy, probe pH4	DNA segment, single copy, probe pH4
554	37162_at	D10S170	S72869	(transforming sequence, thyroid-1,	(transforming sequence, thyroid-1,
				DnaJ (Hsp40) homolog, subtamily A,	•
555	39118_at	DNAJA1.	690807	member 1	DNAJ homologue-2
				DnaJ (Hsp40) homolog, subfamily A,	
556	276_at	DNAJA1	F08069	member 1	DNAJ homologue-2
				DnaJ (Hsp40) homolog, subfamily B,	
557	41233_at	DNAJB6	AB014888	member 6	MRJ
				DnaJ (Hsp40) homolog, subfamily B,	
558	35799_at	DNAJB9	AL080081	member 9	hypothetical protein
				DnaJ (Hsp40) homolog, subfamily C,	
559	36166_at	DNAJC8	AF083190	member 8	SPF31
				docking protein 1, 62kD (downstream of	
560	816_g_at	DOK1	U70987	tyrosine kinase 1)	GAP binding protein p62dok
	-			docking protein 1, 62kD (downstream of	
561	34433_at	DOK1	AF035299	tyrosine kinase 1)	docking protein 1
				dolichyl-phosphate mannosyliransierase	esettavs escape metabolación lodoilob
299	34879_at	UFM1	AF00/8/5	polypeptide 1, catalytic suburit	מפוויווס פפטייוושים מייים אייים איייוויים איייים
563	38957_at	DCAMKL1	AB002367	doublecortin and CaM kinase-like 1	doublecortin and CaM kinase-like 1
564	32168_s_at	DSCR1	U85267	Down syndrome critical region gene 1	Down syndrome critical region protein 1
999		DSCR2	AJ006291	Down syndrome critical region gene 2	leucine rich protein
999	35166_at	DSCR3	D87343	Down syndrome critical region gene 3	DCRA
				down-regulator of transcription 1, TBP-	TATA binding protein-associated
267		DR1	M97388	binding (negative cofactor 2)	phosphoprotein
268	37981_at	DBN1	D17530	drebrin 1	drebrin E
				dual specific protein; Homo sapiens	
				tyrosine phosphatase (cdc14B) mRNA,	
569	40920_at	cdc14B	AF023158	complete cds.	tyrosine phosphatase
				dual specificity phosphatase 11	
570	39727_at	DUSP11	AF023917	(RNA/RNP complex 1-interacting)	PIR1
571	38272_at	DUSP14	AF038844	dual specificity phosphatase 14	MKP-1 like protein tyrosine phosphatase
572	41225 at	Edsi IU	A! 049417	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	
3		0.000	201011		

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	A	8	ပ	Q	u
573	41193_at	DUSP6	AB013382	dual specificity phosphatase 6	DUSP6
				dual-specificity tyrosine-(Y)-	
574	36946_at	DYRK1A	D86550	phosphorylation regulated kinase 1A	serine/inreonine protein kinase
575	1512 at	DYRK14	086550	dual-specificity tyrosine-(Y)- phosphorvlation regulated kinase 1A	serine/threonine protein kinase
3	1015-41	213112	2000		
-				dual-specificity tyrosine-(Y)-	dual-specificity tyrosine-(Y)-phosphorylation
929	760 at	DYRK2	Y09216	inase 2	regulated kinase 2 isoform 1
				dual-specificity tyrosine-(Y)-	
577	39931_at	DYRK3	Y12735	phosphorylation regulated kinase 3	Dyrk3 protein
578	38368_at	DUT	U31930	dUTP pyrophosphatase	deoxyuridine nucleotidohydrolase
579	38475 at	DCTN2	U50733	dynactin 2 (p50)	dynamitin
580	34891_at	PIN	AI540958	dynein, cytoplasmic, light polypeptide	
581	34829 at	DKC1	U59151	dyskeratosis congenita 1, dyskerin	Cbf5p homolog
$\overline{}$				dystonia 1, torsion (autosomal dominant;	
582	32234_at	DYT1	AF007871		torsinA
				dystroglycan 1 (dystrophin-associated	
583	36989_at	DAG1	L19711	glycoprotein 1)	dystroglycan
				dystrophin (muscular dystrophy,	
584	584 40488_at	DMD	M18533	Duchenne and Becker types)	dystrophin
585	585 40106 at	E18-AP5	AJ007509	E1B-55kDa-associated protein 5	E1B-55kDa-associated protein
586	33354_at	SMURF2	AA630312	E3 ubiquitin ligase SMURF2	
587	40375 at	EGR3	X63741	early growth response 3	transcription factor
588	36135 at	EBNA18P2	U86602	EBNA1 binding protein 2	nucleolar protein p40
589	37730 at	p100	U22055	EBNA-2 co-activator (100kD)	100 kDa coactivator
590		EVIS	AF008915	ecotropic viral integration site 5	EVI-5 homolog
				ectodermal-neural cortex (with BTB-like	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
591	39542_at	ENC1	AF059611	domain)	nuclear matrix protein NRP/B
				ectonucleotide	
				pyrophosphatase/phosphodiesterase 2	•
592	41124_r_at	ENPP2	L35594	(autotaxin)	autotaxin
				ectonucleotide	
				pyrophosphatase/phosphodiesterase 2	
593	41123_s_at	ENPP2	L35594	(autotaxin)	autolaxiii
202	504 32551 at	EEEMP1	U03877	EGF-containing fibulin-like extracellular matrix protein 1	extracellular protein
3	10500 July	- 11111			

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	¥	В	ပ	O	ú
595	36488_at	EGFL5	AB011542	EGF-like-domain, multiple 5	MEGF9
				electron-transfer-flavoprotein, alpha	electron transfer flavoprotein, alpha
596	40509_at	ETFA	J04058	polypeptide (glutaric aciduria II)	polypeptide
				electron-transfer-flavoprotein, beta	
282	36881_at	ETFB	X71129	polypeptide	electron transfer flavoprotein beta subunit
	,			elongation factor EF-1-alpha; Human	
				elongation factor EF-1-alpha gene,	eukaryotic translation elongation factor 1
598	598 1288_s_at	EEF1A	J04617	complete cds.	alpha 1
599	599 31853_at	EED	AF080227	embryonic ectoderm development	embryonic ectoderm development protein
				ems1 sequence (mammary tumor and	
				squamous cell carcinoma-associated	
8	39861_at	EMS1	M98343	(p80/85 src substrate)	amplaxin
				end of last exon based on GENSCAN	
				prediction presumably this gene and	
				dJ477H23.2 are part of the same gene	
601	41478_at	dJ477H23.1	AL033538	match: ESTs: Em:AA354647	dJ477H23.1 (novel protein)
				endocytic receptor (macrophage mannose	
602	37408_at	ENDO180	AB014609	receptor family)	KIAA0709 protein
				endosome-associated FYVE-domain	
603	37914_at	ENDOFIN	AB002303	protein	endosome-associated FYVE-domain protein
604	39010_at	ENSA	A1658639	endosultine alpha	
				endothelial differentiation,	
				lysophosphatidic acid G-protein-coupled	
605	40387_at	EDG2	U80811	receptor, 2	lysophosphatidic acid receptor homolog
909	40874_at	EDF1	AJ005259	endothelial differentiation-related factor 1	endothelial differentiation-related factor 1
				enhancer of rudimentary homolog	human protein homologous to DROER
607	39079_at	EBH	D85758	(Drosophila)	protein
88	608 2035_s_at	ENO1	M55914	enolase 1, (alpha)	c-myc binding protein
609	34335 at	EFNB2	AI765533	ephrin-82	
				epidermal growth factor receptor pathway	epidermal growth factor receptor pathway
610	37731_at	EPS15	Z29064	substrate 15	substrate 15
				epidermal growth factor receptor pathway	epidermal growth factor receptor kinase
611	611 1467_at	EPS8	U12535	substrate 8	substrate
612	612 37762_at	EMP1	Y07909	epithelial membrane protein 1	progression associated protein
613	613 39631_at	EMP2	U52100	epithelial membrane protein 2	XMP

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	A	8	၁	O	'n
				EPM1 disease gene; cysteine protease	
				an cystatin B gene,	1
614	35816_at	cystatin B	U46692	complete cds.	cystatin B
				embrane protein band 4.1-	
615	32585_at	EPB41L2	AF027299		protein 4:1-G
616	616 38375 at	ESD		esterase Diformylglutathione hydrolase	esterase D
				estrogen receptor binding site associated,	
617	38283_at	EBAG9	AB007619	antigen, 9	EBAG9
618	618 37161 at		W28948	ESTs	
619	619 40885 s at		N30151	ESTs	
830	620 33328 at	C1S		ESTs	
621	33453 at	ATP6S1	AI400326	ESTs	
622	31801_at		AI808712	ESTs	
623	623 41598 at		AA890010	ESTs	
				ESTs, Highly similar to RS21_HUMAN	
		_		40S RIBOSOMAL PROTEIN S21	
624	32744 at	RPS21	AI526078	[H.sapiens]	
				ESTs, Moderately similar to	
				ALUS HUMAN ALU SUBFAMILY SX	
				SEQUENCE CONTAMINATION	
625	39750 at		W61005	WARNING ENTRY [H.sapiens]	
				ESTs, Moderately similar to	
				GLK5_HUMAN GLUTAMATE	
				RECEPTOR, IONOTROPIC KAINATE 5	
626	34906 o at		AA977136	PRECURSOR [H.sapiens]	
				ESTs, Moderately similar to T46365	
				hypothetical protein DKFZp434A1518.1	
627	35787 at		A1986201	[H.sapiens]	
	_			ESTs, Weakly similar to 0903209A	
628	628 41463 at		AL042729	peptide PD,basic Pro rich [H.sapiens]	
				ESTs, Weakly similar to N-WASP	·
629	629 41273 at	-	AL046940	[H.sapiens]	
83	630 38097 at	PIG8	AF010313	etoposide-induced mRNA	Pig8
3	1 00007	EE 51 A 1	W/28170	eukaryotic translation elongation factor 1	
3	631 40666 I at	EELIAI	W20170		

(Fig 21

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1	<	۵	ر	D	
	,			eukaryotic translation elongation factor 1	
632	35175_f_at	EEF1A2	X70940	alpha 2	elongation factor 1 alpha-2
633	35748 at	EEF182	X60489	eukaryotic translation elongation factor 1 beta 2	elongation factor-1-beta
	1			eukaryotic translation elongation factor 1	
634	41256_at	EEF1D	Z21507	protein)	human elongation factor-1-delta
6.3E	1676 c at	בכבזפ	MEEADO	eukaryotic translation elongation factor 1	pancraatic fumor-related protein
3 8			244000	7	point of the state
စ္တ	3026/_at	EEFZ	769117	eukaryong translation elongation factor z	חתוומון פוסוקמוסו ומכנסו כ
637	663_at	EIF1A	L18960	eukaryotic translation initiation factor 1A	protein synthesis factor
638	638 34278_at	EIF1A	L18960	eukaryotic translation initiation factor 1A	protein synthesis factor
639	639 1154 at	EIF2S1	J02645	eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD)	eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kD )
				eukaryotic translation initiation factor 2B,	eukaryotic translation initiation factor 2B,
640	640 40515_at	EIF2B2	AF035280	subunit 2 (beta, 39kD)	subunit 2 (beta, 39kD)
641	1644 at	FIE3S2	136764	eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)	TGF-beta receptor interacting protein 1
				eukaryotic translation initiation factor 3,	
642	35327_at	EIF3S3	U54559	subunit 3 (gamma, 40kD)	translation initiation factor eIF3 p40 subunit
643	32576 at	FIF3S5	1194855	eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD)	translation initiation factor 3 47 kDa subunit
				eukaryotic translation initiation factor 3,	murine mammary tumor integration site 6
44	38681_at	EIF3S6	U62962	subunit 6 (48kD)	(oncogene homolog)
940	25.000 04	GIC967	1 154550	eukaryotic translation initiation factor 3,	translation initiation factor alF3 n66 subunit
3	22530 at	Cir 207	22	eukaryotic translation initiation factor 3,	
946	35323_at	EIF3S9	U78525	subunit 9 (eta, 116kU)	eukaryotic translation initiation factor
				eukaryotic translation initiation factor 4	•
87	41785_at	EIF4G2	U73824	gamma, 2	/Ad
648	648 33907 at	EIF4G3	AF012072	eukaryotic translation initiation factor 4 gamma, 3	elF4GII
	2000				

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	A	8	3		
649	1430 5 24	EIEAAO	חשטפט	eukaryotic translation initiation factor 4A, isoform 2	eukaryotic initiation factor 4All
ŝ		17.	200000		
650	37752 at	EIF4E	M15353		cap-binding protein
				eukaryotic translation initiation factor 4E	
651	35263_at	EBP2	N73769		
652	167_at	EIF5	U49436	eukaryotic translation initiation factor 5	translation initiation factor 5
653	37318 at	ETE1	X81625	eukarvotic translation termination factor 1	C11 protein
				1	excision repair cross-complementing rodent
				rodent repair deficiency, complementation	rodent repair deficiency, complementation repair deficiency, complementation group 3
				group 3' (xeroderma pigmentosum group	(xeroderma pigmentosum group B
654	654 1885 at	ERCC3	M31899		complementing)
				excision repair cross-complementing	
			)	rodent repair deficiency, complementation	
	•			group 5 (xeroderma pigmentosum,	
				complementation group G (Cockayne	
655	2063 at	ERCCS	120046	syndrome))	excision repair protein
				exons 1-4 beyond this clone; match:	dJ434O14.1 (Hydroxysteroid (11-beta)
929	656 33734_at	HSD11B1	AL022398	proteins P28845 P50172 P51975 Q29608	
657	657 222 at	EXT1	879639	exostoses (multiple) 1	exostoses (multiple) 1
658	36526 at	EXTL2	AF000416	exostoses (multiple)-like 2	EXT-like protein 2
629	38809 s at	EXTL3	AB011091	exostoses (multiple)-like 3	KIAA0519 protein
099	37729 at	XPO1	Y08614	exportin 1 (CRM1 homolog, yeast)	exportin 1
				exportin, tRNA (nuclear export receptor for	
661	38753_at	XPOT	AF039022	(RNAs)	exportin t
				extracellular matrix protein 2, female	
662	39673 i at	ECM2	AB011792	organ and adipocyte specific	extracellular matrix protein
				extracellular matrix protein 2, female	
663	39674_r_at	ECM2	AB011792	organ and adipocyte specific	extracellular matrix protein
<b>8</b>	1 35226 at	EYA2	U71207	eyes absent homolog 2 (Drosophila)	Eab1
				family with sequence similarity 8, member	
965	5 38318_at	FAM8A1	AL050128	A1	
				far upstream element (FUSE) binding	S cietare ecipie 3
99	666 31879_at	FUBP3	U69127	protein 3	TOOL DINGING PROCESS OF

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	A	В	<u>ر</u>	O	
			•	farnesyl diphosphate synthase (famesyl	farnesyl diphosphate synthase (farnesyl
				pyrophosphate synthetase,	pyrophosphate synthetase,
					dimethylallyltranstransferase,
299	37325_at	FDPS	D14697		geranyftranstransferase)
				nesyltransferase	
899	34848_at	FDFT1	X69141		farnesyl-diphosphate farnesyltransferase
699	1499_at	FNTA	L10413	famesyltransferase, CAAX box, alpha	farnesyl-protein transferase alpha-subunit
				Fas (TNFRSF6)-associated via death	
670	38755_at	FADD	X84709	domain	mediator of receptor induced toxicity
				fasciculation and elongation protein zeta 1	
671	37743_at	FEZ1	09009N	(zygin I)	FEZ1
				fasciculation and elongation protein zeta 2	
672	38651_at	FEZ2	U60061	(zygin li)	FEZ2
				FAT tumor suppressor homolog 1	
673	673 40454_at	FAT	X87241	(Drosophila)	homologue of Drosophila Fat protein
				fatty-acid-Coenzyme A ligase, long-chain	•
674	674 40082_at	FACL2	D10040	2	long-chain acyl-CoA synthetase
27.0		200	Deores	fatty-acid-Coenzyme A ligase, long-chain	Acvi-GoA synthetase 3
0/0	3366U_at	racks			
				fatty-acid-Coenzyme A ligase, long-chain	
	33881_at	FACL3		3	
<i>LL</i> 9	33360_at	FBXL11	AB023221	F-box and leucine-rich repeat protein 11	KIAA1004 protein
678	37205_at	FBXL7	AB020647	F-box and leucine-rich repeat protein 7	KIAA0840 protein
629	32854_at	FBXW1B	AB014596	F-box and WD-40 domain protein 1B	KIAA0696 protein
680	32169 at	FBX021	AB020682	F-box only protein 21	KIAA0875 protein
681	35337_at	FBX07	AL050254	F-box only protein 7	hypothetical protein
				ERBNP: hataronaneous ribonucleoprotein	
				homolog. This segment comes from Fig.	
				3: D10S102≡FBRNP (human, fetal brain.	
682	33817 at	D10S102	S63912	mRNA, 3043 nt].	FBRNP
683	1877	High	HG1103-HT1103 Fe protein	Fe protein	dinitrogenase reductase
88	34678 at	FER1L3	AL096713	fer-1-like 3, myoferlin (C. elegans)	hypothetical protein
				FERM, RhoGEF (ARHGEF) and pleckstrin	-
685	685 32148_at	FARP1	AI701049	domain protein 1 (chondrocyte-derived)	

Fig 2)

П		В	0	D formin home not be and info	E E
	FIM1		106227	remin, neavy polypeptide 1	Terriin neavy cnain fotal Alzheimer antigen
688 32535 at FBN1	FBN1		X63556	ome)	fibrillin
	FAP		U09278	fibroblast activation protein, alpha	fibroblast activation protein
	FGF7		M60828	fibroblast growth factor 7 (keratinocyte growth factor)	keratinocyte growth factor
					fibroblast growth factor receptor 1, isoform 1 precursor; fibroblast growth factor receptor 1, isoform 2 precursor; fibroblast growth
					factor receptor 1, isoform 3 precursor; fibroblast growth factor receptor 1, isoform 4
					precursor, fibroblast growth factor receptor
					1, isotorm 5 precursor; fibroblast growin factor receptor 1, isoform 6 precursor;
					fibroblast growth factor receptor 1, isoform 7
				fibroblast growth factor receptor 1 (fms- related tyrosine kinase 2. Pfeiffer	precursor; fibroblast growth factor receptor 1 isoform 8 precursor: fibroblast growth
691 2057 g at FGFR1 M		Σ	M34641	syndrome)	factor receptor 1, isoform 9 precursor
		<u> </u>			fibronectin 1, isoform 1 preproprotein;
at FN1		2	M10905	fibronectin 1	fibronectin 1, isoform 2 preproprotein
31719_at FN1		×	X02761	fibronectin 1	fibronectin precursor
		-		fibronectin leucine rich transmembrane	fibronectin feucine rich transmembrane
FLRT2		٩	AB007865	protein 2	protein 2
FBLN1		7	U01244	fibulin 1	(ibulin-1D
		3	AF093118	fibulin 5	UP50
697 38078_at FLNB			AF042166	filamin B, beta (actin binding protein 278)	beta-filamin
			AA487755	FK506 binding protein 9 (63 kD)	
FMO3		-	M83772	flavin containing monooxygenase 3	flavoprotein
FLN29		+	AB007447	FLN29 gene product	Fln29
1-00		-	1410481	follistatin precursor; Human follistatin	follistatin isoform FST317 precursor;
/01 30000 at 1501		7	VI 1340 I	igano, excit o.	

Fig 21

	٧	В	C	O	ij
				forkhead (Drosophila)-like 7; FREAC3;	
				×-like	and and and holiv like transcription
	1007	1	000001	actor / (FNTL/) gene,	Total Autor 7
3		FKHL/	AFU/8096		
<u>8</u>	36319_at	FOXF2	U13220	forkhead box F2	forkhead protein FREAC-2
					cio contrar de la contrar de l
ş	405/U_at	FUXUIA	AFUSZ883	(Inabdolliyosalcollia)	ioinipad pioteiii
705	34740_at	FOXO3A	AF032886		forkhead protein
90/	32542_at	FHL1	AF063002	four and a half LIM domains 1	LIM protein SLIMMEH
707	38422 s_at	FHL2	U29332	four and a half LIM domains 2	heart protein
708	41649_at	FHX	AF038177	FOXJ2 forkhead factor	
709	709 34997 r at	FZD5	U43318	frizzled'homolog 5 (Drosophila)	transmembrane receptor
710	34472 at	FZD6	AB012911	frizzled homolog 6 (Drosophila)	Frizzled-6
711	711 33222 at	FZD7	AB017365	frizzled homolog 7 (Drosophila)	frizzled-7
712	712 38923 at	FRG1	L76159	FSHD region gene 1	FSHD region gene 1
713	713 38139 at	FPGT	AF017445	fucose-1-phosphate guanylytransferase	GDP-L-fucose pyrophosphorylase
714	41814 at	FUCA1	M29877	fucosidase, alpha-L- 1, tissue	fucosidase, alpha-L- 1, tissue
				Fukuyama type congenital muscular	
715	715 40022_at	FCMD	AB008226	dystrophy (fukutin)	fukutin
716	716 32546_at	击	U59309	fumarate hydratase	fumarase precursor
717	36145 at	SIAHBP1	151586	fuse-binding protein-interacting repressor	siah binding protein 1
	15 - C				
718	718 40480_s_at	FYN	M14333	FYN oncogene related to SRC, FGR, YES	FYN oncogene related to SRC, FGR, YES FYN oncogene related to SRC, FGR, YES
719	719 2039 s at	FYN	M14333	FYN oncogene related to SRC, FGR, YES	FYN oncogene related to SRC, FGR, YES FYN oncogene related to SRC, FGR, YES
720	34288_at	RDC1	U67784	G protein-coupled receptor	orphan G protein-coupled receptor
721	37308 at	GPR107	A1888084	G protein-coupled receptor 107	
722	37298	GABARAP	AF044671	GABA(A) receptor-associated protein	MM46
				GABA(A) receptor-associated protein like	
723	35785_at	GABARAPL1	W28281	-	
				GABA(A) receptor-associated protein-like	
724	724 35767_at	GABARAPL2	AI565760	2	
725	725 37825_at	GALK2	M84443	galactokinase 2	galactokinase
726	726 37742_at	GLB1	M34423	galactosidase, beta 1	galactosidase, beta 1

	A	<b>B</b>	ပ	O	L L
				ase,	
727	37263_at	GGH	U55206		human gamma-glutamyl hydrolase
				gap junction protein, alpha 1, 43kD	
728	32531_at	GJA1	X52947	(connexin 43)	connexin 43
				GCN1 general control of amino-acid	
729	36603_at		D86973	synthesis 1-like 1 (yeast)	
		GDI2	Y13286	GDP dissociation inhibitor 2	GDP dissociation inhibitor beta
				gene predicted from cDNA with a	gene predicted from cDNA with a complete
731	39386_at	KIAA0110	D14811		coding sequence
				riants near HD	gene with multiple splice variants near HD
732	32180 s at	RES4-22	AB000461	locus on 4p16.3	locus on 4p16.3
					Bruton's tyrosine kinase-associated protein-
733	466 at	GTF2	U77948	general transcription factor II, i	135
734	734 35450 s at	GTF2I	AF015553	general transcription factor II, i	TFII-I protein
				general transcription factor IIA, 2 (12kD	
735	37010 at	GTF2A2	AI203737	subunit)	
				general transcription factor IIA, 2 (12kD	:
736	869 at	GTF2A2	U14193	subunit)	transcription factor IIA small 12 kDa subunit
				general transcription factor IIE,	
737	37882_at	GTF2E1	X63468	polypeptide 1 (alpha subunit, 56kD)	TFIIE-alpha
				general transcription factor IIE,	
738	37295_at	GTF2E2	X63469	polypeptide 2 (beta subunit, 34kD)	TFIIE-beta
				general transcription factor IIH,	
739	38782_at	GTF2H1	M95809	polypeptide 1 (62kD subunit)	basic transcription factor 62kD subunit
				general transcription factor IIH,	
740	40754 at	GTF2H3	Z30093	polypeptide 3 (34kD subunit)	basic transcription factor 2, 35 kD subunit
177	10 00100 17	CTCOA	N32257	deneral transcription factor IIIA	Xenopus transcription factor IIIA homologue
1	747 35296 at	15055	AR019036	geranylderanyl diphosphate synthase 1	geranylgeranyl pyrophosphate synthase
743	743 763 at	GMFB	AB001106	glia maturation factor, beta	glia maturation factor
744	39793 at	GBAS	AF029786	glioblastoma amplified sequence	GBAS
				glucan (1,4-alpha-), branching enzyme 1	
				(glycogen branching enzyme, Andersen	
				disease, glycogen storage disease type	
745	745 32643_at	GBE1	L07956	(2)	1,4-alpha-glucan branching enzyme
746	746 34332_at	GNPI	D31766	glucosamine-6-phosphate isomerase	glucosamine-o-phosphate isomerase

İ					
	A	8	ပ	Ω	. 1
				glucosaminyl (N-acetyl) transferase 1,	
		٠		core 2 (beta-1,6-N-	
747	38218_at	GCNT1	M97347	acetylglucosaminyttransferase)	beta-1,6-N-acetylglucosaminyttransferase
748	39122_at		K03515		neuroleukin
749	38986 at	GRP58	Z49835		protein disultide isomerase
750	38042 at			glucose-6-phosphate dehydrogenase	glucose-6-phosphate dehydrogenase
751	33308 at	GUSB		glucuronidase, beta	glucuronidase, beta
		GLUD1	M20867	glutamate dehydrogenase 1	glutamate dehydrogenase 1
753	a	GRM4	X80818	glutamate receptor, metabotropic 4	metabotropic glutamate receptor type 4
				glutamate-ammonia ligase (glutamine	
754	40522_at	פרחר	X59834	synthase)	glutamateammonia ligase
				glutamate-cysteine ligase, catalytic	
755	31850_at	CCLC	M90656	subunit	gamma-glutamylcysteine synthetase
				glutamate-cysteine ligase, modifier	gamma-glutamylcysteine synthetase light
756	33163_r_at	GCLM	L35546	subunit	subunit
				glutamic-oxaloacetic transaminase 1,	
757	35343 at	GOT1	M37400	soluble (aspartate aminotransferase 1)	aspartate aminotransferase 1
				glutamic-oxaloacetic transaminase 2,	
			_	mitochondrial (aspartate aminotransferase	
758	758 40764_at	GOT2	M22632	(2)	aspartate aminotransferase 2 precursor
759	759 34719_at	GLS	AB020645	glutaminase	KIAA0838 protein
				glutamine-fructose-6-phosphate	glutamine:fructose-6-phosphate
760	32626_at	GFPT1	M90516	transaminase 1	amidotransferase
L				glutamine-fructose-6-phosphate	Glutamine:fructose-6-phosphate
761	39640_at	GFPT2	AB016789	transaminase 2	amidotransferase
762	762 35300_at	EPRS	X54326	glutamyl-prolyf-tRNA synthetase	glutaminyl-tRNA synthetase
763	763 34311_at	GLRX	X76648	glutaredoxin (thiottransferase)	glutaredoxin
76	764 37033 s at	GPX1	X13710	glutathione peroxidase 1	
765	765 40508 at	GSTA4	AF025887	glutathione S-transferase A4	glutathione S-transferase A4-4
766	38386 r at	GSS	U34683	glutathione synthetase	glutathione synthetase
				glutathione-S-transferase like; glutathione	
767	824_at	<b>GSTTLp28</b>	U90313	transferase omega	glutathione-S-transferase homolog
L				glyceraldehyde-3-phosphate	
768	AFFX-HUMGAP(GAPD	GAPD	M33197	dehydrogenase	glyceraldehyde-3-phosphate dehydrogenase
	10000	O V D	1134005	glyceraldehyde-3-phosphate	
e e	709 33902 S at	GALD	004333		

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18	770 AFFX-HUMGAP(GAPD	(GAPD	M33197	głyceraldehyde-3-phosphate dehydrogenase	glyceraldehyde-3-phosphate dehydrogenase
1	39392 at	GNPAT	A.1002190	olyceronephosphate O-acyltransferase	dihydroxyacetone phosphate acytransferase
:				dycine cleavage system protein H	glycine cleavage system protein H
772	37357 at	GCSH	D00723	(aminomethyl carrier)	(aminomethyl carrier)
773	39665_at	GLRB	U33267	glycine receptor, beta	glycine receptor beta subunit
774	40645 at	GSK3B	L33801	glycogen synthase kinase 3 beta	protein kinase
775	40876 at	GYG	U31525	glycogenin	glycogenin
776	776 35334 at	GYG2	U94362	glycogenin 2	glycogenin-2 alpha
777	38379 at	GPNMB	X76534	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb
778	37251 s at	GPM6B	AF016004	glycoprotein M6B	
779	33126 at	AD-017	L13435	glycosyttransferase AD-017	
780	36582 q at	GARS	U09510	glycyl-tRNA synthetase	glycyl-tRNA synthetase
781	36581 at	GARS	U09510	glycyl-tRNA synthetase	glycyl-tRNA synthetase
782	36201 at	GL01	D13315	głyoxalase I	lactoyl glutathione lyase
				glyoxylate reductase/hydroxypyruvate	
783	783 40133 s at	GRHPR	W28944	reductase	
					guanine nucleotide binding protein (G
					protein), alpha stimulating activity
					polypeptide 1, isoform alpha-s-2;
					neuroendocrine secretory protein 55;
					guanine nucleotide binding protein (G
					protein), alpha stimulating activity
					polypeptide 1, isoform XL-alpha-s; guanine
					nucleotide binding protein (G protein), alpha
					stimulating activity polypeptide 1, isoform
787	784 37449 i at	GNAS	X04409	GNAS complex locus	alpha-s-1
180	785 37448 s at	GNAS	X56009	GNAS complex locus	alpha subunit of GsGTP binding protein
	10 C				

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					guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-2; neuroendocrine secretory protein 55; quanine nucleotide binding protein (G
		·			protein), alpha stimulating activity
					polypeptide 1, isotorm AL-apna-s; guanine nucleotide binding protein (G protein), alpha
					stimulating activity polypeptide 1, isoform
786	786 37450_r_at	GNAS	X04409	GNAS complex locus	alpha-s-1
					ADP-ribosylation factor binding protein 3,
707	27050	<b>S</b>	00000	golgi associated, gamma adaptın ear	isoform short; ADP-ribosylation factor
è	0/ 303	GGAS		כיוויפוסוק פווייסווים זרול, פווויווים	
8	32713_at		U51587	golgi autoantigen, golgin subfamily a, 1	Golgi complex autoantigen golgin-97
789	32150_at		X82834	golgi autoantigen, golgin subfamily a, 4	256 kD golgin
790	36827_at	GOLPH1	AF020762	golgi phosphoprotein 1	unknown protein
791	38620 at	GOSR2	AA905543	golgi SNAP receptor complex member 2	
					putative 13 S Golgi transport complex 90kD
792	34737_at	GOLTC1	AF058718	golgi transport complex 1 (90 kD subunit)	subunit brain-specific isoform
793	793 41767_r_at	KIAA0855	AB020662	golgin-67	KIAA0855 protein
794	36950_at	HSGP25L2G	X90872	gp25L2 protein	
				GPAA1P anchor attachment protein 1	glycosylphosphatidylinositol anchor
795	36035_at	GPAA1	AB002135	homolog (yeast)	attachment 1 (GPAA1)
96/	32595_at	GRSF1	U07231	G-rich RNA sequence binding factor 1	G-rich sequence factor-1
				growth arrest and DNA-damage-inducible,	growth arrest and DNA-damage-inducible, growth arrest and DNA-damage-inducible
797	39822_s_at	GAUD45B	AH078077	Deta	protein GADU450818
		1	1	growth arrest and DNA-damage-inducible,	
798	798 39821_s_at	GADD45B	N95168	beta	
799	799 661_at	GAS1	L13698	growth arrest-specific 1	growth arrest-specific 1
800	800 41839_at	GAS1	L13698	growth arrest-specific 1	growth arrest-specific 1
801	801 37658_at	GAS6	L13720	growth arrest-specific 6	growth-arrest-specific protein
802	802 1598 g_at	GAS6	L13720	growth arrest-specific 6	growth-arrest-specific protein
803	37615_at	GRB10	D86962	growth factor receptor-bound protein 10	growth factor receptor-bound protein 10
80.4	804 41752 at	MIHE	W28190	growth hormone inducible transmembrane protein	
	7113E_CI		1150100		

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	Α	8	3		
805	160030_at		X06562	growth hormone receptor	growth hormone receptor
908	40113 at	155	D87119	GS3955 protein	GS3955
50	27270 ot		110550	GTP binding protein overexpressed in skeletal muscle	meg
	31213_al			ide binding protein (G	
				protein), alpha inhibiting activity	
808	808 33809 at	GNAI1	AL049933	polypeptide 1	hypothetical protein
	•			ein (G	guanine nucleotide binding protein (G
					protein), alpha inhibiting activity polypeptide
808	37307_at	GNAI2	X04828		2
				guanine nucleotide binding protein (G	
810	34608_at	GNB2L1	M24194	protein), beta polypeptide 2-like 1	MHC B complex protein 12.3
				guanine nucleotide binding protein (G	
811	35272_at		AI541042	protein), gamma 5	
812		GNG10	U31383	guanine nucleotide binding protein 10	G protein gamma-10 subunit
				guanylate binding protein 1, interferon-	
813	35735_at	GBP1	M55542	inducible, 67kD	guanylate binding protein isoform l
814	905 at	GUK1	L76200	guanylate kinase 1	guanylate kinase
815	815 32249 at	HFL1	M65292	H factor (complement)-like 1	factor H homologue
816	32250 at	HT	X07523	H factor 1 (complement)	complement factor H
				H.sapiens ACTH-R gene for	candidate adrenocorticotropic hormone
817	420_at	ACTH-R	X65633	adrenocorticotropic hormone receptor.	receptor
818	31673_s_at	sion	regu X65784	H.sapiens CAR gene.	cell matrix adhesion regulator
ο 1 α		CD63: MI A1: MEZ	. ME4X62654	H sapiens gene for Me491/CD63 antigen.	ME491 /CD63 antigen
					ATP synthase, H+ transporting,
				H.sapiens gene for mitochondrial ATP	mitochondrial F0 complex, subunit c (subunit
820	820 38076_at	P1 gene for c sub	sub(X69907	synthase c subunit (P1 form).	9), isoform 1
821	35125 at	95 caq	X67309	H.sapiens gene for ribosomal protein S6.	ribosomal protein S6
					-
822	34646_at	mS7	Z25749	H.sapiens gene for ribosomal protein S7.	nbosomal protein S7
823	823 31510 s at	hH3.3B	748950	H.sapiens hH3.3B gene for histone H3.3.	histone H3.3
3	01010	10.00		X	

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Γ	Α	В	3	0	E
				H.sapiens lactate dehydrogenase B gene	
824	33820 q at	IdhB	X13794	CDS).	lactate dehydrogenase B
				H.sapiens lactate dehydrogenase B gene	
				exon 1 and 2 (EC 1.1.1.27) (and joined	,
825	33819_at	IdhB	X13794	CDS).	lactate dehydrogenase B
	at	ORF1	X93209	H.sapiens mRNA for NRD1 convertase.	NRD1 convertase
				H.sapiens mRNA for PIBF1 protein,	
827	36012_at	PIBF1	Y09631	complete.	PIBF1 protein
				H.sapiens mRNA for tre oncogene (clone	
828	31526_f_at	tre	X63547	213).	oncogene
829	829 40471_at	PXF	Y09048	H.sapiens PxF gene.	PxF protein
				H.sapiens PXMP1 gene, exon 1 (and	70kD peroxisomal integral membrane
830	37038_at	PXMP1	X83467	joined CDS).	protein
				H.sapiens rpS8 gene for ribosomal protein	
831	31583_at	rpS8	X67247	58.	ribosomal protein S8
				H.sapiens SPHAR gene for cyclin-related	•
832	1685_at	SPHAR	X82554	protein.	S-phase response (cyclin-related)
833	38127 at	svndecan-1	748199	H.sapiens syndecan-1 gene (exons 2-5).	syndecan 1
834	834 37310 at	uPA	X02419	H.sapiens uPA gene.	urokinase-plasminogen activator
835	835 34308 at	H2AFL	U90551	H2A histone family, member L	histone 2A-like protein
836	39337 at	H2AFZ	M37583	H2A histone family, member Z	H2A histone family, member Z
837	33458 r. at	H2BFL	AI688098	H2B histone family, member L	
838	40818_at	LOC51580	D14041	H-2K binding factor-2	H-2K binding factor-2
839	839 254_at	H3F3A	M11353	H3 histone, family 3A	H3 histone, family 3A
849	840 39969_at	H4FG	AA255502	H4 histone family, member G	
8	32591 at	HCDI	A1494623	HCDI protein	
842	35215	HDCMA18P	AL049996	HDCMA18P protein	hypothetical protein
				heat shock 10kD protein 1 (chaperonin	
8	843 39353_at	HSPE1	Al912041	10)	
\$	844 37720 at	HSPD1	M22382	heat shock 60kD protein 1 (chaperonin)	mitochondrial matrix protein
				heat shock 70kD protein 5 (glucose-	heat shock 70kD protein 5 (glucose-
845	36614_at	HSPA5	X87949	regulated protein, 78kD)	regulated protein, 78KU)
846	846 41510 c at	HSPA9B	1 15189	heat shock 70kD protein 9B (mortalin-2)	MTHSP75
	41010_0_0	101 730	20103		



-	<	_	•		
247 3	32316 c at	B DODUM	V15183	in 1 alpha	heat shock 90kD protein 1, alpha
		HSPCB	M16660		heat shock 90kD protein 1, beta
849 3	31906_at	HSBP1	AF068754	heat shock factor binding protein 1	heat shock factor binding protein 1 HSBP1
					tumor necrosis factor type 1 receptor
_		TRAP1	U12595	heat shock protein 75	associated protein
851 3	38054_at	HBXIP	AF029890	hepatitis B virus x interacting protein	hepatitis B virus X interacting protein
				hepatoma-derived growth factor (high-	
852 3	38779_r_at	HDGF	D16431	mobility group protein 1-like)	hepatoma-derived GF
853 3	853 35644_at	HEPH	AB014598	hephaestin	KIAA0698 protein
r				heterogeneous nuclear ribonucleoprotein	
854 3	38094_at	HNRPAB	M65028	A/B	hnRNP type A/B protein
				heterogeneous nuclear ribonucleoprotein	
855 3	37334_at	HNRPAO	U23803	A0	heterogeneous ribonucieoprotein AU
_				heterogeneous nuclear ribonucleoprotein	
856 3	856 34987_s_at	HNRPA1	X79536	A1	hnRNPcore protein A1
					heterogeneous nuclear ribonucleoprotein
				heterogeneous nuclear ribonucleoprotein	A2/B1, isoform A2; heterogeneous nuclear
857 3	36654_s_at	HNRPA2B1	M29065	A2/B1	ribonucleoprotein A2/B1, isoform B1
Γ					heterogeneous nuclear ribonucleoprotein C,
				heterogeneous nuclear ribonucleoprotein	isoform b; heterogeneous nuclear
828	33666_at	HNRPC	M16342	C (C1/C2)	ribonucleoprotein C, isoform a
-				heterogeneous nuclear ribonucleoprotein	
-				D (AU-rich element RNA binding protein 1,	
859	38016_at	HNRPD	M94630	37kD)	DNA-binding protein
			-	heterogeneous nuclear ribonucleoprotein	
860	33845_at	HNRPH1	W28483	H1 (H)	
				heterogeneous nuclear ribonucleoprotein	
861	41132_r_at	HNRPH2	U01923	H2 (H')	heterogeneous nuclear ribonucleoprotein H2
				=	heterogeneous nuclear ribonucleoprotein
698	962 41283 at	HOUNH	AE052131	neterogeneous nuciear ribonucieoprotein H3 (2H9)	ns, isolonii a; lietelogeriecus ruciear ribonucleoprotein H3. isoform b
				heterogeneous nuclear ribonucleoprotein	
863	863 40836_s_at	HNRPH3	W26677	H3 (2H9)	

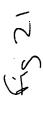
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	Α	В	C	D	
				eterogeneous nuclear ribonucleoprotein	
864	39415_at	HNRPK	X72727	¥	transformation upregulated nuclear protein
				heterogeneous nuclear ribonucleoprotein	
865	35201_at	HNRPL	X16135		heterogeneous nuclear ribonucleoprotein L
				heterogeneous nuclear ribonucleoprotein	
866	37717_at	HNRPM	L03532	. W	M4 protein
867	39792_at	HNRPR	AF000364	heterogeneous nuclear ribonucleoprotein R	heterogeneous nuclear ribonucleoprotein R
				riedorace outro de anotoria en concesso de	
868	38654_at	HNRPU	X65488	literal organization in the control of the control	hnRNP U protein
869	32818_at	НХВ	X78565	hexabrachion (tenascin C, cytotactin)	human tenascin-C
870	39827_at	RTP801	AA522530	HIF-1 responsive RTP801	
074	2450	0000	M64008	high density lipoprotein binding protein	hich density linoprotein hinding protein
6		וותרסג	MONOS	(million)	
872	872 32220_at	HMG1	D63874	high-mobility group (nonhistone chromosomal) protein 1	HMG-1
				high-mobility group (nonhistone	high-mobility group (nonhistone
873	306_s_at	HMG14	J02621	chromosomal) protein 14	chromosomal) protein 14
				high-mobility group (nonhistone	
874	35738_at	HMG17L3	AI347088	chromosomal) protein 17-like 3	
L				high-mobility group (nonhistone	high-mobility group (nonhistone
875		HMG2	X62534	chromosomal) protein 2	chromosomal) protein 2
876		HMG2L1	AL079310	high-mobility group protein 2-like 1	hypothetical protein
877		HPCAL1	AF070616	hippocalcin-like 1	BDP-1 protein
878	1009 at	HINT	U51004	histidine triad nucleotide binding protein 1	protein kinase C inhibitor
879	3423	HBOA	AF074606	histone acetyltransferase	histone acetyltransferase
88	41855	HAT1	AF030424	histone acetyftransferase 1	histone acetyttransferase 1
88		HDAC1	D50405	histone deacetylase 1	RPD3 protein
882	34368	HDAC2	U31814	histone deacetylase 2	transcriptional regulator homolog RPD3
883	3 38271_at	HDAC4	AB006626	histone deacetylase 4	KIAA0288 protein
88	39046	H2AV	AL049324	histone H2A.F/Z variant	
88	39092	H2AV	AW007731	histone H2A.F/Z variant	
988	38824_at	HTATIP2	AF039103	HIV-1 Tat interactive protein 2, 30 kD	Tat-interacting protein TIP30
887	7 40220_at	HIS1	AB021179	HMBA-inducible	HEXIM1 protein

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888	39809_at	HBP1	AF019214	HMG-box containing protein 1	HMG box containing protein 1
				HMG-domain containing protein which is the 57 kd subunit within SWVSNF-related	
				BAF complexes; contains a proline-rich N-	
		· •		terminus, a kinesin-like coiled-coil region,	
				and a highly acidic c-terminus; Homo	
		-		sapiens BAF57 (BAF57) gene, complete	
889	33828_at	BAF57	AF035262		BAF57
				HMT1 hnRNP methyltransferase-like 1 (S.	-
890	39348_at	HRMT1L1	X99209		arginine methyltransferase
				NP methyltransferase-like 2 (S.	
891	32825_at	HRMT1L2	Y10805		arginine methyttransferase
				HNRNP Core Protein A1 LIKE	
				pseudogene; match: proteins P04256	
				Q28521 P49312 P09651 P51991 P51992	
892	31463 s at	dJ256G22.1	AL022097	P51968 P17130 P22626	
				holocytochrome c synthase (cytochrome c	
893	38943_at	HCCS	U36787		holocytochrome c-type synthetase
894	39610_at	HOXB2	X16665		homeo box B2
895	40674 s at	HOXCe	S82986	hormeo box C6	homeo box C6
				:	£
896	38233_at	HOMER-3	AF093265	Homer, neuronal immediate early gene, 3 homer-3	nomer-3
				Homo sapiens (clone f17252) ubiquinol	
1	10000	199000	720021	cytochrome c reductase Rieske iron-	Bieske Fe-S protein
ò	State at	Coursi	116707	Homo sapiens (clone FFE-7) type II	
				inosine monophosphate dehydrogenase	
				(IMPDH2) gene, exons 1-13, complete	inosine monophosphate dehydrogenase type
888	36624_at	IMPDH2	L33842	cds.	
				Homo sapiens aldehyde oxidase (AOX1)	
899	37599_at	AOX1	AF017060	gene, exon 35 and complete cds.	aldehyde oxidase
[ 8	20740 2 04	Q Q	A E05/197	Homo sapiens alpha NAC mRNA,	aloha NAC
3	300 337 40 3 at	2022	101101	con const	

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_	17 00200	•	4 705 44 07	Homo sapiens alpha NAC mRNA,	O N O H
5	39/39 BI	NACA	AFU5418/	compiete cas.	alpha IMO
902	902 41154 r_at	CTNNA1	AF102803	Homo sapiens alphaE-catenin (CTNNA1) gene, exon 18 and complete cds.	• alphaE-catenin
903	41153_f_at	CTNNA1	AF102803	Homo sapiens alphaE-catenin (CTNNA1) gene, exon 18 and complete cds.	alphaE-catenin
3				Homo sapiens cDNA FLJ10784 fis, clone NT2RP4000448, highly similar to Homo	
908	39324_al		ALUSUU/8	Homo sapiens cDNA FLJ13267 fis, clone	
905	35310_at		D45288	OVARC1000964	
906	906 35754_at		L40391	Homo sapiens cDNA FLJ13553 fis, clone PLACE1007454	
				Homo sapiens cDNA FLJ14821 fis, clone	
				OVARCTUODSSE, fighry similar to RIBOSOMAL PROTEIN SE KINASE II	
907	33325_at		W26667	ALPHA 2 (EC 2.7.1)	
808	38102_at		W28575	Homo sapiens cDNA FLJ25016 fis, clone CBL01574	
606	909 41253 s at		A1983043	Homo sapiens cDNA FLJ30436 fis, clone BRACE2009037	
910	39162 at		AA156987	Homo sapiens cDNA FLJ30544 fis, clone BRAWH2001412	
911	41807_at		AL040137	Homo sapiens cDNA FLJ31959 fis, clone NT2RP7007422	•
912			W87466	Homo sapiens cDNA FLJ33151 fis, clone UTERU2000263	
913	34246 at		AA418437	Homo sapiens cDNA: FLJ21175 fis, clone CAS11071	
914	914 40813_at		AI768188	Homo sapiens cDNA: FLJ21243 fis, clone COL01164	



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915	915 40923 at		A A 290994	Homo sapiens cDNA: FLJ21449 fis, clone COL04483, highly similar to AF010235 Homo sapiens mRNA from chromosome 5531-33 region	
916	916 38993 r at		W27522	Homo sapiens cDNA: FLJ21904 fis, clone HEP03585	
917	917 38093 at		60606N	Homo sapiens cDNA: FLJ21927 fis, clone HEP04178, highly similar to HSU90909 Human clone 23722 mRNA sequence	
918	34840_at		AI700633	Homo sapiens cDNA: FLJ22642 fis, clone HSl06970	
				Homo sapiens cDNA: FLJ23324 fis, clone HEP12482, highly similar to HUMMYOHCB Human nonmuscle myosin smooth muscle myosin heavy chain isoform	в myosin heavy chain isoform
919	919 32838_at	smooth muscle m S67247	S67247	heavy chain-B (MYH10) mRNA SMemb	
920	33737 f at		A1871359	Homo sapiens cervical cancer suppressor- 1 mBNA, complete cds	
				Homo sapiens clone 23570 mRNA	
128	921 41663_at		AFU38202	Homo sapiens clone 23700 mRNA	
922	36815_at		AF038185	sequence	
923	923 41841 at		AF052138	Homo sapiens clone 23718 mRNA sequence	
700	2770A at		AE035281	Homo sapiens clone 23903 mRNA	
175	10			Homo sapiens clone 23938 mRNA	
925	38/64_at		AF007142	Homo sapiens clone 24416 mRNA	
956	926 35342_at		AF052159	sequence	
927	31867 at		AF052174	Homo sapiens clone 24630 mRNA sequence	
928	928 36758 at		AF070578	Homo sapiens clone 24674 mRNA sequence	
929	929 41864_at		AF052181	Homo sapiens clone 24790 mRNA sequence	

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				Homo sapiens clone FBD3 Cri-du-chat	
930	38070_at		AL080234	critical region mRNA	
				Homo sapiens cofactor A protein mRNA,	
931	34773_at	TBCA	AF038952	complete cds.	cofactor A protein
	-			Homo sapiens cytochrome c oxidase	
				subunit IV precursor (COX4) gene,	
				nuclear gene encoding mitochondrial	
932	932 39027_at	COX4	AF017115		cytochrome c oxidase subunit IV precursor
				Homo sapiens D15F37 pseudogene, S4	
933	40878_f_at	D15F37	AF041081	allefe, mRNA sequence.	
				Homo sapiens deoxycytidylate deaminase	
934	631_g_at	DCTD	L39874	_	deóxycytidylate deaminase
				Homo sapiens deoxycytidylate deaminase	
935	935 630_at	DCTD	L39874	gene, complete cds.	deoxycytidylate deaminase
				Homo sapiens DNA for	
				galactocerebrosidase, exon 17 and	
936	33936_at	GALC	D86181		galactocerebrosidase
				Homo sapiens F1Fo-ATPase synthase f	
937	40134_at	ATP5J2; ATP5JL; AF047436	AF047436	subunit mRNA, complete cds.	F1Fo-ATPase synthase f subunit
				Homo sapiens gene for LD78 alpha	
938	938 36103_at	SCYA3; LD78ALP	ALP D90144	precursor, complete cds.	LD78 alpha precursor
				Homo sapiens GOS28/P28 protein	
939	939 40725_at	GOSR1; P28; GS	GS2AF047438	mRNA, complete cds.	GOS28/P28 protein
				Homo sapiens GTP binding protein	
940	38708_at	RAN; TC4; ARA24	RA24AF054183	mRNA, complete cds.	GTP binding protein
				Homo sapiens H beta 58 homolog mRNA,	
941	35790_at	VPS26; HB58; HB AF054179	AF054179	complete cds.	H beta 58 homolog
				Homo sapiens histone macroH2A1.2	
942	942 36576 at	HZAFY; HZA.y; HZ	.y; H2AF054174	mRNA, complete cds.	histone macroH2A1.2
				Homo sapiens insulin induced protein 1	
943	35303_at	INSIG1	U96876	(INSIG1) gene, complete cds.	insulin induced protein 1
				Homo sapiens interferon-gamma receptor	
	,		!	alpha chain gene, exon / and complete	ciedo edolo xotacos caracos accopactai
944	944 1038_s_at	interferon-gamma U19247	U19247	cds.	Imerieron-garinna receptor apria citalin

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945	945 21	<u>u</u>	19686	Ното sapiens macrophage migration inhibitor factor (MIF) gene. complete cds.	macrophage migration inhibitory factor
	15 - O.O.			Homo sapiens mitochondrial proteolipid	
				68MP homolog mRNA, nuclear gene	
		_		encoding mitochondrial protein, complete	
946	38967_at	C14orf2; MP68; P AF054175		cds.	mitochondrial proteolipid 68MP homolog
Γ				Homo sapiens mRNA for Hmob33 protein,	
947	31881_at		Y14155	3' untranslated region	
948	948 34677_f_at	11132	AJ012755	Homo sapiens mRNA for TL132	TL132 protein
				Homo sapiens mRNA full length insert	
949	38786_at		AL079279	cDNA clone EUROIMAGE 248114	
Γ				Homo sapiens mRNA; cDNA	
				DKFZp434A012 (from clone	
920	33418_at		AL096752	DKFZp434A012)	
				Homo sapiens mRNA; cDNA	
				DKFZp434B102 (from clone	
951	38630_at		AL080192	DKFZp434B102)	
				Homo sapiens mRNA; cDNA	
-				DKFZp434M162 (from clone	
952	952 41529 g at		W72239	DKFZp434M162)	
				Homo sapiens mRNA; cDNA	
				DKFZp434M245 (from clone	
953	953 36451_at		AI743299	DKFZp434M245)	
				Homo sapiens mRNA; cDNA	
				DKFZp564A026 (from clone	
954	954 36821_at	DKFZp564A026	AL050367	DKFZp564A026)	hypothetical protein
				Homo sapiens mRNA; cDNA	
				DKFZp564A072 (from clone	
955	37366 at	_	AL049969	DKFZp564A072)	
				Homo sapiens mRNA; cDNA	
				DKFZp564B222 (from clone	
926	39506_at		AA933984	DKFZp564B222)	
				Homo sapiens mRNA; cDNA	
				DKFZp564D016 (from clone	
957	957 39748_at		AL050021	DKFZp564D016)	

Fig 21

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				Homo sapiens mRNA; cDNA	
				DKFZp564D156 (from clone	
958	38357_at		AL049321	DKFZp564D156)	
				Homo sapiens mRNA; cDNA	
				DKFZp564E122 (from clone	
959	33716_at		N95443	DKFZp564E122)	
				Homo sapiens mRNA; cDNA	
				DKFZp564E2222 (from clone	
960	35301_at		AL049941	DKFZp564E2222)	
				Homo sapiens mRNA; cDNA	
				DKFZp564F053 (from clone	
961	35842 at		AL049265	DKFZp564F053)	
Γ				Homo sapiens mRNA; cDNA	
				DKFZp564F112 (from clone	
962	40552_s_at		AL049987	DKFZp564F112)	
				Homo sapiens mRNA; cDNA	
				DKFZp564J0323 (from clone	
963	39170_at		AL049957	DKFZp564J0323)	
				Homo sapiens mRNA; cDNA	
				DKFZp564L0822 (from clone	
964	34303 at		AL049949	DKFZp564L0822)	
				Homo sapiens mRNA; cDNA	
				DKFZp564L222 (from clone	
965	36509_at		AL049998	DKFZp564L222)	
				Homo sapiens mRNA; cDNA	
			_	DKFZp564P0823 (from clone	
996	966 40353_at		AL049962	DKFZp564P0823)	
				Homo sapiens mRNA; cDNA	
				DKFZp566J2146 (from clone	
967	35290 at		AL050081	DKFZp566J2146)	
				Homo sapiens mRNA; cDNA	
_				DKFZp586B0918 (from clone	
968	38079_at		AL049367	DKFZp586B0918)	
				Homo sapiens mRNA; cDNA	
				DKFZp586B1922 (from clone	
696	969 32195_at		AL049450	DKFZp586B1922)	

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				Homo sapiens mRNA; cDNA	
				DKFZp586C1019 (from clone	
970	39379_at		AL049397	DKFZp586C1019)	
				Homo sapiens mRNA; cDNA	
				DKFZp586C1723 (from clone	
971	37575_at		AL050192	DKFZp586C1723)	
				Homo sapiens mRNA; cDNA	
				DKFZp586F071 (from clone	
972	34283_at		AL050125	DKFZp586F071)	
				Homo sapiens mRNA; cDNA	
				DKFZp586G1922 (from clone	
973	39600_at		AL080110	DKFZp586G1922)	
[				Homo sapiens mRNA; cDNA	
				DKFZp586G2222 (from clone	
974	34752_at		AL080111	DKFZp586G2222)	
				Homo sapiens mRNA; cDNA	
				DKFZp58610523 (from clone	
975	39103_s_at		H98552	DKFZp586l0523)	
				Homo sapiens mRNA; cDNA	
				DKFZp58611823 (from clone	
926	36092_at		AL080213	DKFZp586l1823)	
				Homo sapiens mRNA; cDNA	
				DKFZp586K1123 (from clone	
977	35187_at		AL080216	DKFZp586K1123)	
				Homo sapiens mRNA; cDNA	
				DKFZp586K2322 (from clone	
978	35363_at	DDX17	AL080113	DKFZp586K2322)	
				Homo sapiens mRNA; cDNA	
				DKFZp586M2022 (from clone	
979	41013 at		AL080114	DKFZp586M2022)	
				Homo sapiens mRNA; cDNA	
				DKFZp586N012 (from clone	
980	41690_at		AL049471	DKFZp586N012)	
				Homo sapiens mRNA; cDNA	
				DKFZp586N1720 (from clone	
981	981 40349_at		AL049442	DKFZp586N1720)	

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		,		Homo sapiens mRNA; cDNA	
				DKFZp586N1918 (from clone	
982	32672_at		AL049387	DKFZp586N1918)	
				me b5	
983	36668_at	DIA1	M28713		NADH-cytochrome b5 reductase
				Homo sapiens nucleophosmin	
			•	phosphoprotein (NPM) gene, 3' flanking	
984	38542_at		U89322	sequence.	
				Homo sapiens p18 protein mRNA,	
985	40587_s_at	EEF1E1; P18	AF054186	complete cds.	p18 protein
				Homo sapiens PAC clone RP1-170019	even-skipped homeo box 1 (homolog of
986	986 41448_at	HOXA4	AC004080	from 7p15-p21, complete sequence.	Drosophila)
				Homo sapiens prion protein (PrP) gene,	•
987	36159_s_at	PrP	U29185	complete cds.	prion protein
				Homo sapiens putative dienoyl-CoA	
				isomerase (ECH1) gene, exons 7-10, and	
988	988 32756_at	ECH1	AF030249	complete cds.	putative dienoyl-CoA isomerase
				Homo sapiens RP58 gene, complete	
989	989 35824_at	RP58	AJ223321	CDS.	RP58 protein
				Homo sapiens Sec61 gamma mRNA,	
990	990 39169_at	SEC61G	AF054184	complete cds.	Sec61 gamma
				Homo sapiens signal transducer and	•
		-		activator of transcription 6 (STAT6) gene,	signal transducer and activator of
991	991 41222_at	STATE	AF067575	exons 15 through 23 and complete cds.	transcription 6
				Homo sapiens sperm acrosomal protein	
992	38817_at	SPAG7; ACRP; F	IP; F\$AF047437	mRNA, complete cds.	sperm acrosomal protein
L				Homo sapiens splicing factor,	
				arginine/serine-rich 12 (SFRS12) mRNA,	
993	36033_at		AL049309	complete cds	
				Homo sapiens thymosin beta-10 gene,	
994	31481_s_at	TMSB10	M92383	3'end.	thymosin beta-10
				Homo sapiens TIMP gene for tissue	
905	005 1603 c at	TIMP	D11139	inhibitor of metalloproteinases, partial cds. tissue inhibitor of metalloproteinases	tissue inhibitor of metalloproteinases
200	1030 3 01	1 11411			

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				Homo sapiens transaldolase-related	
				protein gene, exons 3-8 and complete	•
966	37311_at	TALDO1; TAL-H;  AF010400		cds.	transaldolase-related protein
				Homo sapiens translation initiation factor	
997	32229 at	EIF4EL3; 4EHP; 4	HP: 4 AF038957	4e mRNA, complete cds.	translation initiation factor 4e
998	1323 at	UBB	X04803	Homo sapiens ubiquitin gene.	ubiquitin
666		UBB	U49869	Homo sapiens ubiquitin gene.	ubiquitin
8	38372 at		U66042	Homo sapiens unknown mRNA	
				Homo sapiens vacuolar H(+)-ATPase	
1001	1001 38814_at	ATP6V1G1; ATP6	ATP6AF038954	subunit mRNA, complete cds.	vacuolar H(+)-ATPase subunit
				Homo sapiens vesicle trafficking protein	
1002	1002 41597_s_at	SEC22L1; SEC22	EC22 AF047442	sec22b mRNA, complete cds.	vesicle trafficking protein sec22b
1003		XSL	Y18504	Homo sapiens X5L gene.	XAP-5-like protein
				Homo sapiens, clone IMAGE:3028427,	
1004	1004 38662 at		AL047596	mRNA, partial cds	
				Homo sapiens, clone IMAGE:3140802,	
1005	1005 38312 at		AL050002	mRNA	
				Homo sapiens, clone IMAGE:3855224,	
1006	1006 33388 at		AL080223	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4132509,	
1007	1007 38676 at		AA059408	mRNA	
				Homo sapiens, clone IMAGE:4150198,	
1008	1008 40238 at		AI674208	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4182947,	
100	1009 32119_at		AL049423	mRNA	
				Homo sapiens, clone IMAGE:4183312,	
1010	1010 38650 at	IGFBP5	127560	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4183312,	
101	1011 1396 at	IGFBP5	127560	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4391536,	
1012	1012 40432 at	-	AA522891	mRNA	
				Homo sapiens, Similar to RNA helicase-	
			·	related protein, clone MGC:9246	
101	1013 36130_f_at	MT1E	R92331	IMAGE:3892441, mHNA, complete cds	

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				Homo sapiens, Similar to serine (or	
	•			cysteine) proteinase inhibitor, clade E	
	•			(nexin, plasminogen activator inhibitor	
				type 1), member 2, clone MGC:23129	
1014	1014 41246_at	. •	AI743134	IMAGE:4578406, mRNA, complete cds	
				Homo sapiens, similar to unknown, clone	
				MGC:39325 IMAGE:5440447, mRNA,	
1015	1015 41533 at		U79298		
				-inducible, endoplasmic	homocysteine-inducible, endoplasmic
					reticulum stress-inducible, ubiquitin-like
1016	1016 39733_at	HERPUD1	AF055001		domain member 1
				homolog of yeast mutL gene; Human	
				_	
1017	1017 525 g at	hPMS1	U13695		postmeiotic segregation 1
				homologous to mouse Rsu-1; putative;	
				Human RSU-1/RSP-1 mRNA, complete	
1018	1018 32545_r_at	RSU-1	L12535		ras suppressor protein 1
				homologous to mouse Rsu-1; putative;	
				Human RSU-1/RSP-1 mRNA, complete	
1019	1019 32544_s_at	RSU-1	L12535	cds.	ras suppressor protein 1
1020	1020 39800_s_at	HAX1	U68566	HS1 binding protein	HAX-1
				Human 2,4-dienoyl-CoA reductase gene,	
1021	1021 38104 at	DECR1; NADPH	U78302		2,4-dienoyl-CoA reductase
L				Human alcohol dehydrogenase chi	
			٠.	polypeptide (ADH5) gene exons 8-9,	
1022	1022 37708 r at	ADHS	M81118	complete cds.	alcohol dehydrogenase
				Human alcohol dehydrogenase chi	
				polypeptide (ADH5) gene exons 8-9,	
1023	1023 37707 i at	ADHS	M81118	complete cds.	alcohol dehydrogenase
				Human alpha-1 collagen type IV gene,	
1024	1024 39333_at	COL4A1	M26576	exon 52.	alpha-1 type IV collagen
				ANG TO COOM A COOR TO COME TO	MAD American (AMDO) AMD AMD Assistant assistant and an american and american variant
20 10 10 10 10	1025 3841 /_at	AMPUZ	Majora	numan Aivir dearningse (Aivii DE) minno.	
1026	1026 37747 at	ANXS	105770	Human annexin V (ANX5) gene, exon 13.	annexin V
	15-12-12-12	200			

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1027	1027 41143_at	CALM1	U12022	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds.	calmodulin
1028	1028 239_at	CTSD	M63138	Human cathepsin D (catD) gene, exons 7, 8, and 9.	cathepsin D
3				Human cellular oncogene c-fos (complete v-fos FBJ murine osteosarcoma viral	v-fos FBJ murine osteosarcoma viral
1029	1029 1916_s_at	c-tos	V01512	sequence).	oncogene nomolog
1030	1030 1915_s_at	c-fos	V01512	Human cellular oncogene c-los (complete la lacemente la munne osteosarcoma viral sequence).	V-los FBJ munne osteosarcoma viral oncogene homolog
1031	1031 32583_at	NOC	J04111	Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1.	v-jun avian sarcoma virus 17 oncogene homolog
1032	1032 1895_at	NON	J04111	Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1.	v-jun avian sarcoma virus 17 oncogene homolog
1033	1033 41604_at		U79297	Human clone 23589 mRNA sequence	
1034	1034 32185_at		U00946	Human clone A9A2BRB5 (CAC)n/(GTG)n repeat-containing mRNA	
1035	1035 33667_at	PPIA	X52851	Human cyclophilin gene for cyclophilin (EC 5.2.1.8).	peptidylprolyl isomerase
1036	1036 38459_g_at	CYB5	L39945	Human cytochrome b5 (CYB5) gene, exon 6 and complete cds.	cytochrome b5
1037	1037 38458_at	CYB5	L39945	Human cytochrome b5 (CYB5) gene, exon 6 and complete cds.	cytochrome b5
1038	1038 36163_at	3. 13.	D; DUL13761	Human dihydrolipoamide dehydrogenase gene, exon 14.	dihydrolipoamide dehydrogenase
1039	1039 1424_s_at		HA1{D78577	Human DNA for 14-3-3 protein eta chain, exon2 and complete cds.	14-3-3 protein eta chain
				Human DNA sequence from clone 73H22 on chromosome 6q23, complete	
1040	1040 31797_at	dJ73H22.1	AL035699	sequence.	dJ73H22.1 (TBP-like protein)
1041	1041 40193_at	EN02	X51956	Human ENO2 gene for neuron specific (gamma) enolase.	human gamma enolase
1042	1042 38326_at	G0S2	M69199	Human G0S2 protein gene, complete cds. G0S2 protein	G0S2 protein
1043	1043 40567_at	TUBA3; FLJ25113X01703	X01703	Human gene for alpha-tubulin (b alpha 1). alpha-tubulin	alpha-tubulin

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	A	В	C	D	'n
1044	1044 39775_at	SERPING1; C1IN	11N X54486	Human gene for C1-inhibitor.	C1 inhibitor
				gene for creatine kinase B (EC	1
1045	1045 40862_i_at	скв; сквв	X15334		creatine kinase B
				Human gene for hepatitis C-associated	
				microtubular aggregate protein p44, exon	hepatitis C-associated microtubular
1046	1046 37641_at	IF144; p44; MTAP4	TAP4D28915		aggregate protein p44
				Human gene for heterogeneous nuclear	
				ribonucleoprotein (hnRNP) core protein	
1047	1047 40211_at	HNRPA1; HNRNP	RNPX12671	A1.	hnrnp a1 protein
				Human gene for melanoma growth	melanoma growth stimulatory activity
1048	1048 408 at	MGSA	X54489	1	preprotein
				Human gene for omithine decarboxylase	
1049	1049 36203_at	00001	X16277	ODC (EC 4.1.1.17).	omithine decarboxylase (ODC)
				Human gene for very low density	
1050	1050 36873_at	VLDLR	D16532	lipoprotein receptor, exon 19.	very low density lipoprotein receptor
1051	1051 34759_at		U68494	Human hbc647 mRNA sequence	
				Human hepatic dihydrodiol	
1052	1052 32805_at	AKR1C1; DD1; DQU05861	U05861	dehydrogenase gene, exon 9.	hepatic dihydrodiol dehydrogenase
				Human HMG-17 gene for non-histone	
1053	1053 41231_f_at	HMG17; MGC562 X13546	X13546	chromosomal protein HMG-17.	put. HMG-17 protein
				Human HOX 5.1 gene for HOX 5.1	
1054	1054 38294_at	HOXD4; HOX4; H X17360	X17360	protein.	hox 5.1 protein
				Human hsc70 gene for 71 kd heat shock	
1055	1055 40637_at	HSP73 HSC70 H\$Y00371	Y00371	cognate protein.	71 Kd heat shock cognate protein
1056	1056 232 at	I AMB2	M55210	Human laminin B2 chain gene, exon 28.	laminin B2 chain
				Human lipoprotein-associated coagulation	
				inhibitor (LACI) gene, exon 9 and	
1057	1057 40767_at	TFPI	M59499	complete cds.	lipoprotein-associated coagulation inhibitor
				500	
1058	1058 38637_at	LOX	L16895	Human lysyl oxidase (LOA) gene, exon 7. liysyl oxidase	lysyl Oxidase
				Human medium-chain acyl-CoA	4 - C
<del>5</del>	1059 37532_at	MCAD	M91432	dehydrogenase (MCAD) gene, exon 12.	medium-chain acyi-coa denyurogenase
1060	1060 870 f at	MT3: GIF: GIFB	M93311	Human metallothionein-til gene, complete cds.	metallothionein-III
	72.2-7-2	11 15 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			

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				Human metaxin (MTX) gene, complete	•
1061	1061 40890_at	MTX	U46920	cds.	metaxin
				Human mRNA for erythrocyte adducin	
1062	1062 32145_at	ADD1	X58141	alpha subunit.	erythrocyte alpha adducin
				Human mRNA for general transcription	
1063	1063 37381_g_at	TF2B	X59268	factor IIB.	IIB protein
98	1064 33683_at	H	D50525	Human mRNA for TI-227H.	
				hancer factor	myocyte-specific enhancer factor 2A, C9
					form; myocyte-specific enhancer factor 2A,
1065	1065 41747_s_at	MEF2A	U49020	complete cds.	C4 form
				Human NAD(P)H:quinone oxireductase	
1066	1066 38066_at	NG01	M81600	gene, exon 6.	NAD(P)H:quinone oxireductase
				Human natural killer cell enhancing factor	
1067	1067 39729_at	NKEFB	L19185	(NKEFB) mRNA, complete cds.	enhancer protein
				Human nonmuscle/smooth muscle alkali	non-muscle myosin light chain; smooth
1068	1068 33994_g_at	MLC	M22919	myosin light chain gene, complete cds.	muscle myosin light chain
				Human nucleic acid binding protein gene,	
1069	1069 32841_at	9; DM2;	CNB(U19765	complete cds.	nucleic acid binding protein
1070	32590_at	NCL	M60858	Human nucleolin gene, complete cds.	nucleolin
				Human oncoprotein 18 (Op18) gene,	
1071	1782_s_at	Op18	M31303	complete cds.	oncoprotein 18
L				Human prostaglandin D2 synthase gene,	
1072	1072 216_at	PTGDS	M98539	exon 7.	prostaglandin D2 synthase (21kD, brain)
				Human protein phosphatase 2A catalytic	protein phosphatase-2A catalytic subunit-
1073	1073 237_s_at	PPP2CA	M60483	subunit-alpha gene, complete cds.	alpha
				Human protein phosphatase inhibitor 2	
1074	1074 812 at	PPP1R2	U68111	(FFFINZ) gene, exun o and complete cds.	protein phosphatase inhibitor 2
				Human protein phosphatase inhibitor 2 (PPD1R2) gene exon 6 and complete	
1075	1075 33180 at	PPP1R2	U68111	cds.	protein phosphatase inhibitor 2
1076	1076 35356 at		W21884	Human putative ribosomal protein S1 mRNA	
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1	<	0	,		
				Human receptor tyrosine phosphatase	
				gamma (PTPHG) gene, exon 30 and	
71	1077 491_at	PTPRG	U46116		receptor tyrosine phosphatase gamma
				Human receptor tyrosine phosphatase	
078	1078 492 g at	PTPRG	U46116		receptor tyrosine phosphatase gamma
				ill-type low molecular weight	
					red cell-type low molecular weight acid
979	1079 36611 at	ACP1	U25849		phosphatase
				Human SH3 domain-containing protein	
080	1080 174 s_at	SH3P18	U61167	SH3P18 mRNA, complete cds	SH3 domain-containing protein SH3P18
				Human spermidine synthase gene,	
081	1081 241 g at	SRM	M64231	complete cds.	spermidine synthase
				Human sterol carrier protein-X/sterol	
				carrier protein-2 (SCP-X/SCP-2) gene,	
082	36688 at	SCP-X/SCP-2	U11313	exon 16, and complete cds.	sterol carrier protein-X/sterol carrier protein-2
083	1083 32587_at	ZFP36L2; BRF2; (U07802	U07802	Human Tis11d gene, complete cds.	Tis11d
084	1084 31680 at	TOP1P2	M55630	Human topoisomerase I pseudogene 2.	
				Human transformation-related protein	
1085	1085 36446 s at	HMG1L2	124521	mRNA, 3' end	transformation-related protein
				Human transmembrane protein (CD59)	
980	1086 39351_at	CD59	M84349	gene, exon 4.	CD59 protein
1087	1087 38727_at	THE	M23161	Human transposon-like element mRNA	
				Human vascular cell adhesion molecule-1	
1088	1088 41433 at	VCAM1	M73255	(VCAM1) gene, complete CDS.	vascular cell adhesion molecule-1
1089	1089 40121 at	HIP2	U58522	huntingtin interacting protein 2	huntingtin interacting protein
1000		НУРН	AB023163	Huntingtin interacting protein H	KIAA0946 protein
1091	1091 40196 at	HYA22	D88153	HYA22 protein	HYA22
				A company of book seek.	
				dehydrogenase/3-ketoacyl-Coenzyme A	enoyl-CoA hydratase/3-hydroxyacyl-CoA
5	20000	800	D16480	thiolase/enoyl-Coenzyme A hydratase	dehydrogenase alpha-subunit of triunctional protein
1082	1092 36952_at	ארוטארו	340		

(Fig 2)

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Ι Ξ	НАОНВ	D16481	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	3-ketoacyl-CoA thiolase beta-subunit of trifunctional protein
	HSD17B4	X87176	hydroxysteroid (17-beta) dehydrogenase 4 17beta-hydroxysteroid dehydrogenase	17beta-hydroxysteroid dehydrogenase
			Hypothetical protein of unknown function; Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypotetical proteins encoded by (Z81122) T13F2.1 [Caenorhabditis elegans] and (Z70271) W08D2.4 [Caenorhabditis elegans]; DNA structure-specific endonuclease FEN1; FLAP ENDONUCLEASE-1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN; Hypothetical human Best's macular dystrophy relatedprotein; Simulated translation extends ORF of previously reported partial coding sequence for Best's macular dystrophy related protein (AF038536); Homo	
	, i	0.7770	sapiens chromosome 11, BAC CII-HSP- 311e8 (BC269730) containing the hFEN1	BC269730_1; BC269730_2; FEN1_HUMAN;
		AC004/10	gene, compiete sequence.	- no reading

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											•														_	hypothetical protein CG018		hypothetical protein AF038182	
			Hypothetical protein of unknown function;	Hypothetical 52 kDa protein; Hypothetical	profein exhibits similarity to motifs found in	(1)79010) delta 6 desaturase, a	handhatical cytochrome b5 containing	fusion protein and hypotetical proteins	proded by (781122) T13F2.1	(770271)	Caenomabouts eregains and (2)	W08D2.4 [Caenorhabditis elegans]; UNA	structure-specific endonuclease FEN1;	EL AP ENDONUCI EASE-1:	MATION FACTOR 1 (MF1): DNase	MAIOTATION TANDING TO THE PROPERTY OF THE PROP	IV; RAD2_HUMAN; Hypothetical numan	Rest's macular dystrophy relatedprotein;	Simulated translation extends ORF of	previously reported partial coding	segmence for Best's macular dystrophy	related protein (AF038536); Homo	saniens chromosome 11, BAC CIT-HSP-	311e8 (BC269730) containing the hFEN1	gene complete seguence.	the chalical gane CG018	Inypollience going case of	Inypoinetical general supported by	AFU3818Z; BU003ZU3
C	,								•						<u>-</u>										0.7770	20000	12c0c0	-	AF038182
-	۵																								-		CG018	<u> </u>	LOC90355
1	4						-					-														1096 34224_at	1097 1527_s_at		1098 33466_at
-		-			_	_		_									_		····		_					1096	1097		1098

Fig 21

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Ų	יט	R32184_1; R32184_3		hypothetical protein, similar to (AC007017) putative RNA helicase A (Arabidopsis	thaliana			
	O	Hypothetical human protein (partial CDS); CDS constructed from combination of BLASTX, EST matches and Xgrail predictions. N-terminus of protein likely encoded in flanking cosmid R29942. Predicted protein exhibits weak similarity to hypothetical protein PIDIe1226191 (ALO21106) from Drosophila melanogaster, Hypothetical human protein most similar to Rat ionotropic glutamate receptor (L34938); CDS constructed primarily from XGRAIL predictions and BLASTX similarity to (L34938) ionotropic glutamate receptor [Rattus norvegicus] and gil2160125 (U29873) NMDAR-L [Rattus norvegicus]. Also exhibits similarity to PIDIe258718 (Z78413) T01C3.10 [Caenorhabdritis elegans]. C-terminus of hypothetical protein is iil-defined at this point; definition will require identification and characterization of appropriate cDNAs; Hypothetical 59.8 kDa human protein; CDS constructed from EST matches and Xgrail predictions. C- terminus of predicted protein not fully confirmed by EST or cDNA coverage. Hypothetical protein exhibits no significant database similarities when queried against R32184_3; R32184_3;	hypothetical protein			hypothetical protein	hypothetical protein 23851	hypothetical protein 24636
	ပ		AA015605		AL079292	AF007130	AF035313	A1651368
	В	MGC2436	FLJ20811		LOC54505	LOC54104	LOC56007	LOC55977
	A	1099 35983_at	1100 38440 s at		1101 39140_at	1102 37819_at	a	1104 41561_s_at
		1096	E		110	10	110	2



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1105 41128	1128_at	LOC92703	AF070537	hypothetical protein BC013073	
11063	1106 38972_at	LOC115207	AF052169	hypothetical protein BC013764	
11073	1107 34864 at	CGI-57	AF070638	hypothetical protein CGI-57	hypothetical protein CGI-57
11083	1108 39960_at	CL640	AF091086	hypothetical protein CL640	hypothetical protein CL640
1109 38837	8837_at	DJ971N18.2	W26226	hypothetical protein DJ971N18.2	
11103	111035142_at	DKFZP564D172	AF070617	hypothetical protein DKFZp564D172	
11113	1111 34830_at	DKFZP564K0822 W25986	W25986	hypothetical protein DKFZp564K0822	
11123	1112 31852_at	DKFZP5640043	AL050390	hypothetical protein DKFZp5640043	
11133	1113 33895_at	DKFZP586F1318 AL050373	AL050373	hypothetical protein DKFZP586F1318	hypothetical protein
11143	1114 39692_at	DKFZP586F2423	23 AL080209	hypothetical protein DKFZp586F2423	
11153	1115 35682_at	FLB6421	AI133727	hypothetical protein FLB6421	
11163	1116 36647_at	FLJ10326	AA526812	hypothetical protein FLJ10326	
11173	1117 34804_at	FLJ10618	AL049246	hypothetical protein FLJ10618	
11183	1118 36840_at	FLJ10737	AF052158	hypothetical protein FLJ10737	
11193	1119 35283_at	FLJ10738	H05692	hypothetical protein FLJ10738	
11203	1120 37610_at	FLJ10803	AI765280	hypothetical protein FLJ10803	
11213	1121 33173 g at	FLJ10849	T75292	hypothetical protein FLJ10849	
1122 39923	39923_at	FLJ10971	Al935420	hypothetical protein FLJ10971	
				hypothetical protein FLJ11021 similar to	
1123	1123 38105_at	FLJ11021	W26521	splicing factor, arginine/serine-rich 4	
1124	1124 33394_at	FLJ11126	AA034074	hypothetical protein FLJ11126	
1125	1125 35709_at	FLJ11149	AF038172	hypothetical protein FLJ11149	
1126	1126 38141_at	FLJ11193	AF038176	hypothetical protein FLJ11193	
1127	1127 40859_at	FLJ11806	Al561196	hypothetical protein FLJ11806	
1128	1128 41177_at	FLJ12443	AW024285	hypothetical protein FLJ12443	
1129	1129 41434_at	FLJ12552	AF070557	hypothetical protein FLJ12552	hypothetical protein FLJ12552
1130	1130 36580_at	FLJ13910	AL050139	hypothetical protein FLJ13910	hypothetical protein FLJ13910
1131	1131 32222_at	FLJ14639	AA152202	hypothetical protein FLJ14639	
1132	1132 38710_at	FLJ20113	AL096714	hypothetical protein FLJ20113	
1133	1133 38652_at	FLJ20154	AF070644	hypothetical protein FLJ20154	
1134	1134 40868_at	FLJ20274	AA442799	hypothetical protein FLJ20274	
1135	1135 34739_at	FLJ20275	W26023	hypothetical protein FLJ20275	
1136	1136 34857_at	FLJ20986	Z24724	hypothetical protein FLJ20986	
1137	1137 32251_at	FLJ21174	AA149307	hypothetical protein FLJ21174	
1138	1138 40615_at	FLJ21439	AA780049	hypothetical protein FLJ21439	
1139	1139 33915_at	FLJ23027	W22655	hypothetical protein FLJ23027	

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1140 35198	5198_at	LOC57146	AF070596	4796	hypothetical protein from clone 24795
1141 38483	8483 at	HSA011916	AJ011916		hypothetical protein
11424	1142 41236 at	HSU79252	U79252		hypothetical protein HSU79252
11433	1143 38443 at	MGC14433	U79291	hypothetical protein MGC14433	
11443	1144 39811 at	MGC2749	AA402538	hypothetical protein MGC2749	
				hypothetical protein MGC2840 similar to a	
11453	1145 32051 at	MGC2840	AJ224875	putative glucosyltransferase	glucosyttransferase
11463	5219 at	MGC3047		hypothetical protein MGC3047	
11474	1147 41696 at	MGC3077	AI620381	hypothetical protein MGC3077	
				hypothetical protein MGC4276 similar to	hypothetical protein MGC4276 similar to
1148	1148 41147 at	MGC4276	AF038186	CG8198	CG8198
1149	1149 37242 at	MGC5149	U79260	hypothetical protein MGC5149	
1150	1150 36975 at	MGC8721	W26659	hypothetical protein MGC8721	
1151	1151 35677 at	MGC9084	AL035369	hypothetical protein MGC9084	hypothetical protein
1152	32504 at	MY014	AW024812	hypothetical protein My014	
1153	1153 38106_at	YR-29	AJ012409	hypothetical protein YR-29	hypothetical protein
1154	1154 37640 at	HPRT1	M31642	hypoxanthine phosphoribosytransferase 1 (Lesch-Nyhan syndrome)	hypoxanthine phosphoribosyttransferase 1
	in-010				
1155	1155 1039_s_at	HIF1A	U22431	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) hypoxia-inducible factor 1 alpha	hypoxia-inducible factor 1 alpha
				IGF binding protein-4; Human insulin-like	`
1156	1156 39781 at	IGFBP4	U20982	growth factor binding protein-4 (IGFBF4) gene, promoter and complete cds.	insulin-like growth factor binding protein-4
1157		ᆂ	AJ005579	IK cytokine, down-regulator of HLA II	Prer protein
1158	1158 218_at	¥	S74221	IK cytokine, down-regulator of HLA II	IK factor
1159	1159 37690 at	ILVBL	U61263	ivB (bacterial acetolactate synthase)-like	acetolactate synthase homolog
1160	1160 36097_at	ETR101	M62831	immediate early protein	immediate early protein
1161	1161 1237_at	IER3	S81914	immediate early response 3	immediate early response 3, isoform short; immediate early response 3, isoform long
1162	1162 34391 at	IGBP1	Y08915	immunoglobulin (CD79A) binding protein 1 alpha 4 protein	l alpha 4 protein

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				perfamily containing	
1163	1163 38636_at	ISLR	AB003184	leucine-rich repeat	ISLR
				IMP (inosine monophosphate)	IMP (inosine monophosphate)
1164	1164 40695 at	IMPDH1	J05272	dehydrogenase 1	dehydrogenase 1
1165	1165 36875 at		AL050018	inhibitor of Bruton's tyrsoine kinase	hypothetical protein
	5			inhibitor of DNA binding 1, dominant	inhibitor of DNA binding 1, dominant
1166	1166 36617 at	Ō	X77956	negative helix-loop-helix protein	negative helix-loop-helix protein
				inhibitor of DNA binding 2, dominant	,
1167	1167 41215_s_at	ID2	D13891	negative helix-loop-helix protein	Id-2H
				inhibitor of kappa light polypeptide gene	
				enhancer in B-cells, kinase complex-	
1168	1168 34344 at	IKBKAP	AF044195	associated protein	IkappaB kinase complex associated protein
				inner membrane protein, mitochondrial	
1169	1169 37659 at	IMMI	L42572	(mitofilin)	transmembrane protein
					human type 1 inositol 1,4,5-trisphosphate
1170	1170 755 at	ITPR1	D26070	inositol 1,4,5-triphosphate receptor, type 1	receptor
					human type 1 inositol 1,4,5-trisphosphate
1171	1171 32778 at	ITPR1	D26070	inositol 1,4,5-triphosphate receptor, type 1	receptor
11/2	1172 36154 at	IHPK1	D87452	inositol hexaphosphate kinase 1	KIAA0263 protein
	1				lithium-sensitive myo-inositol
1173	1173 32697_at	IMPA1	AF042729	inositol(myo)-1(or 4)-monophosphatase 1	monophosphatase A1
[ ]	17.4 36.40E at	IMPA?	AE014398	inositol(mvo)-1 (or 4)-monophosphatase 2	myo-inositol monophosphatase 2
117	1175 35833 at	LOC51141	AL080184	insulin induced protein 2	
12	1176/41049 at	IRS1	S62539	insulin receptor substrate 1	insulin receptor substrate-1
11/2	177 851 s at	IRS1	S62539	insulin receptor substrate 1	insulin receptor substrate-1
				insulin-like growth factor 1 (somatomedin	•
117	1178 38737_at	IGF1	X57025	(2)	insulin-like growth factor I
				insulin-like growth factor 1 (somatomedin	
117	1179 1501_at	IGF1	X57025	(0)	insulin-like growth factor I
138	1180 160027_s_at	IGF2R	Y00285	insulin-like growth factor 2 receptor	
	1			insulin-like growth factor binding protein 2	insulin-like growth factor binding protein 2
<u></u>	1181 40422_at	IGFBP2	X16302	(30KU)	(cuc)
118	1182 1737 s at	IGFBP4	M62403	insulin-like growth factor binding protein 4	insulin-like growth factor binding protein 4 insulin-like growth factor binding protein 4

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1183	11R3 2062 at	IGEBP7	19182	insulin-like growth factor binding protein 7	
	'·\ _			internal mombines and to in t	integral membrane protein 1
1184 3799	3/991_at	[W]	L38861	megrai membrane protein i	anografia month and anografia
				integral membrane protein; swiss-prot accession: O04901; may play role in cell	
1185	1185 37326_at	-	U93305	differentiation in intestinal epithelium	LIM domain only 6
188	1186 41163 at	P24B	AL109672	integral type I protein	p24B protein
					integrin beta 1 isoform 1A precursor, integrin
					beta 1 isotorm 18 precursor; integrin beta 1 isotorm 1C-1 precursor integrin beta 1
				integrin beta 1 subunit precursor; Human	isoform 1D precursor; integrin beta 1 isoform
1187	1187 32808_at	ITGB1; CD29; FN	FN(X07979	mRNA for integrin beta 1 subunit.	1C-2 precursor
				integrin cytoplasmic domain-associated	integrin cytoplasmic domain associated
1188	1188 1195_s_at	ICAP-1A	AF012024	protein 1	protein
1189	1189 120_at		X68742	integrin, alpha 1	
1190	1190 37484 at		X68742	integrin, alpha 1	
1191	1191 36892 at	ITGA7	AF032108	integrin, alpha 7	integrin alpha-7
				integrin, alpha V (vitronectin receptor,	integrin, alpha V (vitronectin receptor, alpha
1192	1192 39071_at	ITGAV	M14648	alpha polypeptide, antigen CD51)	polypeptide, antigen CD51)
1193	39754_at	ITGB5	X53002	integrin, beta 5	
1194	1194 2058 s at	ITGB5	M35011	integrin, beta 5	integrin, beta 5
				integrin, beta-like 1 (with EGF-like repeat	
1195	1195 40681_at	ITGBL1	AB008375	domains)	osteoblast specific cysteine-rich protein
1196	1196 35365 at	놀	U40282	integrin-linked kinase	integrin-linked kinase
				interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; long form; interacts with adenovirus E3-14.7KDa, a TNF-alpha cytolysis antagonist; leucine zipper protein; alternatively translated; short form; Homo sapiens FIP2 atternatively translated	
1197	1197 41743 i.at	OPTN; NRP; FIP2	FIP2 AF061034	mRNA, complete cds.	FIP2

(Fig 21

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				interacts with adenovirus E3-14.7KDa, a	
				TNF-alpha cytolysis antagonist; leucine	
				zipper protein; alternatively translated;	
				long form; interacts with adenovirus E3-	-
				14.7KDa, a TNF-alpha cytolysis	
				antagonist; leucine zipper protein;	
				atternatively translated; short form; Homo	
1198	1198 41742 s at	OPTN; NRP; FIP2	FIP2 AF061034	mRNA, complete cds.	FIP2
				interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 1
1199	1199 676_g_at	IFITM1	J04164	1 (9-27)	(9-27)
				interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 1
1200	1200 675_at	IFITM1	J04164	1 (9-27)	(9-27)
				interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 3
1201	1201 41745_at	IFITM3	X57352	3 (1-8U)	(1-8U)
1202	1202 1456_s_at	IF116	M63838	interferon, gamma-inducible protein 16	interferon-gamma induced protein
1203	925_at	IF130	J03909	interferon, gamma-inducible protein 30	interferon, gamma-inducible protein 30
1204	1204 39728 at	IF130	103909	interferon, gamma-inducible protein 30	interferon, gamma-inducible protein 30
				interferon-induced protein with	interferon-induced protein with
1205	205 32814_at	IFIT1	M24594	tetratricopeptide repeats 1	tetratricopeptide repeats 1
				interferon-related developmental regulator	
1206	1206 37679 at	IFRD1	Y10313	<b>•</b>	PC4 protein
1207	1207 1368 at	IL1R1	M27492	interleukin 1 receptor, type l	interleukin 1 receptor, type l
1208	1208 33228 g at	IL10RB	Al984234	interleukin 10 receptor, beta	
1209	1209 33227 at	IL10RB	AI984234	interleukin 10 receptor, beta	
1210	1210 38969_at	121	Al828168	interleukin 27	
1211	1211 38299 at	IL6	X04430	interleukin 6 (interferon, beta 2)	interleukin 6 (interferon, beta 2)
1212	1212 35372 r at	11.8	M17017	interleukin 8	interleukin 8
				interleukin enhancer binding factor 2,	
1213	1213 36189 at	ILF2	U10323	45kD	NF45 protein
1214	1214 36030 at	DKFZP58612223	AL080214	intermediate filament-like MGC:2625	hypothetical protein
1215	1215 35776_at	ITSN1	AF064243	intersectin 1 (SH3 domain protein)	intersectin short form
1216	1216 41431_at	ICK	AB023153	intestinal cell kinase	KIAA0936 protein
		0	14000	IQ motif containing GTPase activating	rae G.T.Daea-activating-lika protain
121,	1217/1825_at	IGGAPT	L330/5	protein i	ומז כן ו מזפימנוועמוווקיוואס טוטנפוון

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	4	В	ပ	Q	u l
$\dagger$	5			isocitrate dehydrogenase 1 (NADP+),	•
218[3	1218 39023 at	DH1	AF020038		NADP-dependent isocitrate dehydrogenase
		<u>.</u>		incoming dehydrogenese 3 (NAD+) beta	
	1219 40112_at	IDH3B	AA322030	T	NAD+-specific isocitrate dehydrogenase
7000	1220 40111 g at	IDH3B	U49283	īg.	beta precursor
	1221 40478 at	KIAA1162	AL021396	$\neg$	hypothetical protein
222	1222 32695 at	dJ196E23.1	297632	9991	bombesin-like receptor 3
1223	1223 40827 at	IARS	U04953	isoleucine-tRNA synthetase	Isolaucyi-thing syliniblase
1224	1224 36985 at	101	X17025	elta isomerase	isopentenyf-diphosphate delta isomerase
1225	1225 41775 at	ICMT	AF064084	isoprenylcysteine carboxyl methyttransferase	prenylcysteine carboxyl methyttransferase
1926	1926 34877 at	JAK1	AL039831	Janus kinase 1 (a protein tyrosine kinase)	
1227	34318 at	JM4	AJ005896	JM4 protein	JM4 protein
1228	1228 40957 at	JJAZ1	D63881	joined to JAZF1	Joined to JAZF1
1229	1229 41250 at	JTV1	U24169	JTV1 gene	1710
1230	1230 41483_s_at	DNDC	X56681	jun D proto-oncogene	Junio protein
1231	1231 1612 s at	DNDC	X56681	jun D proto-oncogene	Juno protein
1232	1232 40464 g_at	KPNB2	U70322	karyopherin (importin) beta 2	Transporting profein 5
1233	39028_at	KPNB3	Y08890	karyopherin (importin) beta 3	Veryonherin albuh 3
1234	1234 35725_at	KPNA3	D89618	karyopherin alpha 3 (Importin alpria 4)	Oin 1
1235	1235 32487_s_at	KPNA4	AB002533	karyopherin alpha 4 (Importin alpria 3)	
1036	1936 39708 g at	KATNA1	A(191768	Katanin pou (A i rase-comannis) succimi	
123	1937 37386 i at	KDFI R1	X55885	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	KDEL receptor
	200000000000000000000000000000000000000	KDEI B2	M88458	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	KDEL receptor 2
3	23000	1		KDEL (Lys-Asp-Glu-Leu) endoplasmic	hwothetical protein
1235	1239 33402_at	KDELR3	AL035081	reticulum protein retenuori receptor 3	Kelch motif containing protein
12 4 4	1240 37150_at	AB026190	AB026190	Variation bair basic 6 (monilethrix)	type II intermediate filament of hair keratin
124	1241 32329_at	NA I UBO	733145	KH domain containing, RNA binding,	
124%	1242 39346 at	KHDRBS1	M88108	signal transduction associated 1	p62

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ZZZZZZZ	9 D13634 2 D14664	VIA ACCORD STORTIST	1/1 A 0000
		NIAMOUS Gelie product	KIAACCOS gene product
		KIAA0022 gene product	KIAA0022 gene product
	3 D26067	KIAA0033 protein	
		KIAA0062 protein	
XX TILLITIA TILL TO THE STATE OF THE STATE O	7 D38521	KIAA0077 protein	
X IIIIIII BULLET I I I I I I I I I I I I I I I I I I I	6 D43636	KIAA0096 protein	
	7 D43948	KIAA0097 gene product	KIAA0097 protein
		KIAA0098 is a human counterpart of	
		mouse chaperonin containing TCP-1	
	-	gene. Start codon is not identified.	
		ha01413 cDNA clone for KIAA0098 has a	-
		2-bp insertion between 736-737 of the	
		sequence of KIAA0098.; Homo sapiens	
	38 D43950	mRNA for KIAA0098 protein, partial cds.	KIAA0098 protein
	00 D43947	KIAA0100 gene product	KIAA0100 protein
	02 D14658	KIAA0102 gene product	KIAA0102 gene product
	11 D21853	KIAA0111 gene product	KIAA0111 gene product
	21 D50911	KIAA0121 gene product	KIAA0121 protein
to at	36 D50926	KIAA0136 protein	
at	38 D50928	KIAA0138 gene product	KIAA0138 gene product
at at	43 D63477	KIAA0143 protein	
at at	52 D63486	KIAA0152 gene product	KIAA0152 gene product
	57 D63877	KIAA0157 protein	KIAA0157 protein
	70 D79992	KIAA0170 gene product	KIAA0170 gene product
	72   D79994	KIAA0172 protein	
	74 D79996	KiAA0174 gene product	KIAA0174 gene product
	79 D80001	KIAA0179 protein	
	84 D80006	KIAA0184 protein	
	91 D83776	KIAA0191 protein	
	93 D83777	KIAA0193 gene product	KIAA0193 gene product
	95 D83779	KIAA0195 gene product	KIAA0195 gene product
	96 D83780	KIAA0196 gene product	KIAA0196 gene product
		KIAA0202 protein	
		KIAA0217 protein	
1271 38728_at KIAA0225	.25 D86978	KIAA0225 protein	

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a		1	
KIAA0229	D86982	KIAA0229 protein	
KIAA0232	D86985	KIAA0232 gene product	KIAA0232 protein
KIAA0240	D87077	KIAA0240 protein	
KIAA0251	D87438	KIAA0251 protein	
KIAA0256	D87445	KIAA0256 gene product	KIAA0256 protein
KIAA0257	D87446	KIAA0257 protein	
KIAA0265	D87454	KIAA0265 protein	
KIAA0266	D87455	KIAA0266 gene product	KIAA0266 gene product
KIAA0276	D87466	KIAA0276 protein	
KIAA0284	A1828210	KIAA0284 protein	
KIAA0308	AB002306	KIAA0308 protein	
KIAA0321	AB002319	KIAA0321 protein	
KIAA0323	AB002321	KIAA0323 protein	
KIAA0349	AB002347	KIAA0349 protein	
KIAA0350	AB002348	KIAA0350 protein	KIAA0350 protein
KIAA0355	AB002353	KIAA0355 gene product	KIAA0355 gene product
KIAA0365	AB002363	KIAA0365 gene product	
KIAA0367	AB002365	KIAA0367 protein	
KIAA0370	AB002368	KIAA0370 protein	
KIAA0372	AB002370	KIAA0372 gene product	KIAA0372 gene product
KIAA0376	AB002374	KIAA0376 protein	
KIAA0423	AB007883	KIAA0423 protein	
KIAA0433	AB007893	KIAA0433 protein	KIAA0433 protein
KIAA0438	AB007898	KIAA0438 gene product	KIAA0438 gene product
KIAA0440	AB007900	KIAA0440 protein.	KIAA0440 protein
KIAA0446	AB007915	KIAA0446 gene product	KIAA0446 protein
KIAA0447	AB007916	KIAA0447 gene product	KIAA0447 protein
KIAA0451	AB007920	KIAA0451 gene product	KIAA0451 protein
SRGAP2	AB007925	KIAA0456 protein	KIAA0456 protein
KIAA0469	AB007938	KIAA0469 gene product	KIAA0469 protein
KIAA0470	AB007939	KIAA0470 gene product	KIAA0470 protein
KIAA0471	AB007940	KIAA0471 gene product	KIAA0471 protein
KIAA0475	AB007944	KIAA0475 gene product	KIAA0475 protein
KIAA0476	AB007945	KIAA0476 gene product	KIAA0476 protein
KIAA0483	AB007952	KIAA0483 protein	KIAA0483 protein
KIAA0494	AB007963	KIAA0494 gene product	KIAA0494 protein

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KIAA0532 protein
KIAA0537 gene product
KIAA0564 protein
KIAA0592 protein
KIAA0594 protein
KIAA0605 gene product
KIAA0610 protein
KIAA0618 gene product
KIAA0626 gene product
KIAA0630 protein
KIAA0648 protein
KIAA0650 protein
KIAA0662 gene product
KIAA0663 gene product
KIAA0674 protein
KIAA0692 protein
KIAA0697 protein
KIAA0700 protein
KIAA0716 gene product
KIAA0721 protein
KIAA0725 protein
KIAA0729 protein
KIAA0738 gene product
KIAA0740 gene product
KIAA0746 protein
KIAA0747 protein
KIAA0750 gene product
KIAA0769 gene product
KIAA0776 protein
KIAA0779 protein
KIAA0781 protein

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1344	41224_at	KIAA0788	AB018331	KIAA0788 protein	KIAAU/88 protein
1345	1345 34285_at	KIAA0795	AB018338	KIAA0795 protein	KIAA0795 protein
1346	1346 39614_at	KIAA0802	AB018345	KIAA0802 protein	KIAA0802 protein
1347	1347 36588_at	KIAA0810	AB018353	KIAA0810 protein	KIAA0810 protein
1348	1348 40492 at	KIAA0826	AB020633	KIAA0826 protein	KIAA0826 protein
1349	1349 40455 at	KIAA0830	AB020637	KIAA0830 protein	KIAA0830 protein
1350	1350 41372 at	KIAA0831	AB020638	KIAA0831 protein	KIAA0831 protein
1351	1351 36888 at	KIAA0841	AB020648	KIAA0841 protein	KIAA0841 protein
1352	1352 39597_at	KIAA0843	AB020650	KIAA0843 protein	KIAA0843 protein
1353	1353 41503 at	KIAA0854	AB020661	KIAA0854 protein	KIAA0854 protein
1354	1354 38730 at	KIAA0864	AB020671	KIAA0864 protein	KIAA0864 protein
1355	1355 39021 at	KIAA0877	AB020684	KIAA0877 protein	KIAA0877 protein
1356	1356 32215 i at	KIAA0878	AB020685	KIAA0878 protein	KIAA0878 protein
1357	38254 at	KIAA0882	AB020689	KIAA0882 protein	KIAA0882 protein
1358	1358 35720 at	KIAA0893	AB020700	KIAA0893 protein	KIAA0893 protein
1359	1359 40423 at	KIAA0903	AB020710	KIAA0903 protein	KIAA0903 protein
1380	1360 41421 at	KIAA0909	AB020716	KIAA0909 protein	KIAA0909 protein
1361	1361 41498 at	KIAA0911	AB020718	KIAA0911 protein	KIAA0911 protein
1362	1362 39777 at	KIAA0916	AF075587	KIAA0916 protein	protein associated with Myc
1383	1363 32735 at	KIAA0931	AB023148	KIAA0931 protein	KIAA0931 protein
1364	1364 33408 at	KIAA0934	AB023151	KIAA0934 protein	KIAA0934 protein
1385	1365 35369_at	KIAA0937	AB023154	KIAA0937 protein	KIAA0937 protein
1386	1366 33235 at	KIAA0938	AB023155	KIAA0938 protein	KIAA0938 protein
1367	1367 32740 at	Rab11-FIP2	AB023158	KIAA0941 protein	KIAA0941 protein
1366	1368 35794_at	KIAA0942	AB023159	KIAA0942 protein	KIAA0942 protein
138	1369 41595_at	KIAA0947	AB023164	KIAA0947 protein	KIAA0947 protein
137	1370 38649_at	KIAA0970	AB023187	KIAA0970 protein	KIAA0970 protein
137	1371 34396_at	KIAA0978	AB023195	KIAA0978 protein	KIAA0978 protein
137,	1372 32085_at	KIAA0981	AB023198	KIAA0981 protein	KIAA0981 protein
137	1373 35199_at	KIAA0982	AB023199	KIAA0982 protein	KIAA0982 protein
137,	1374 32769_at	KIAA0993	AB023210	KIAA0993 protein	KIAA0993 protein
137	1375 34751_at	KIAA0997	Al970189	KIAA0997 protein	
137	1376 34808_at	KIAA0999	AB023216	KIAA0999 protein	KIAA0999 protein
1377	7 33193_at	KIAA1001	AW052084	KIAA1001 protein	
137	1378 36002_at	KIAA1012	AB023229	KIAA1012 protein	KIAA1012 protein
137	1379 35802_at	KIAA1014	AB023231	KIAA1014 protein	KIAA1014 protein

Fig 21

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1		0 00,1		VIA A 1006 protoin	KIAA 1026 protein
38013	1380 39615_at	KIAA1026	ABUZBS48	NIAM IOZO PIOIGIII	
381 3	1381 34089_at	KIAA1030	AB028953	KIAA1030 protein	KIAA1030 protein
3824	1382 41651 at	KIAA1033	AB028956	KIAA1033 protein	KIAA 1033 protein
383	1383 41708 at	KIAA1034	AB028957	KIAA1034 protein	KIAA1034 protein
384	1384 35163_at	KIAA1041	AB028964	KIAA1041 protein	KIAA1041 protein
385	1385 38778 at	KIAA1046	AB028969	KIAA 1046 protein	KIAA1046 protein
1386	1386 41268 q at	KIAA1049	AB028972	KIAA 1049 protein	KIAA1049 protein
1387	1387 40855 at	KIAA1053	AB028976	KIAA1053 protein	KIAA1053 protein
1388	1388 39400 at	KIAA1055	AB028978	KIAA 1055 protein	KIAA1055 protein
1389	1389 33877 s at	KIAA1067	AB028990	KIAA1067 protein	KIAA1067 protein
1390	1390 34688 at	KIAA1078	AB029001	KIAA1078 protein	KIAA1078 protein
1391	1391 33924 at	KIAA1091	AB029014	KIAA1091 protein	KIAA1091 protein
1392	1392 32508 at	KIAA1096	AL096857	KIAA1096 protein	hypothetical protein
1393	1393 41179 at	KIAA1100	AB029023	KIAA1100 protein	KIAA1100 protein
1394	1394 34839 at	KIAA1104	AB029027	KIAA1104 protein	KIAA1104 protein
1395	1395 33457 at	RAP140	AB029028	KIAA1105 protein	KIAA1105 protein
1396	1396 36814_at	KIAA1109	AB029032	KIAA1109 protein	KIAA1109 protein
1397	1397 34274 at	KIAA1116	AB029039	KIAA1116 protein	KIAA1116 protein
1398	1398 37617 at	KIAA1128	U90912	KIAA1128 protein	
1399	1399 33358 at	KIAA1157	W29087	KIAA1157 protein	
1400	1400 40308_at	KIAA1240	A1830496	KIAA1240 protein	
1401	1401 33811 at	KIAA1254	AI761567	KIAA1254 protein	
1402	38674_at	KIAA1354	AA115140	KIAA1354 protein	
1403	32730 at	KIAA1750	AL080059	KIAA1750 protein	
1404	32171 at	KIAA1856	AL080102	KIAA1856 protein	hypothetical protein
1405	3989	KIAA1966	N36997	KIAA1966 protein	
1406	3284	KTN1	D13629	kinectin 1 (kinesin receptor)	kinectin 1
1407	39057 at	KNS2	L04733	kinesin 2 (60-70kD)	kinesin light chain
1408	32079	KIF13B	AB014539	kinesin family member 13B	KIAA0639 protein
1409	1409 33345 at	KIF3C	AF035621	kinesin family member 3C	kinesin-related protein
1410	1410 34294 at	KIFGS	AL041493	kinesin family member C3	
1411	41474 at	KIF2	Y08319	kinesin heavy chain member 2	kinesin-2
	40779 at	KIFAP3	U59919	kinesin-associated protein 3	SMAP
1413	1413 34216_at	KLF7	AA478904	Kruppel-like factor 7 (ubiquitous)	
,	10000	Contract	Voezen	L-3-hydroxyacyl-Coenzyme A	3-hvdroxvacyl-CoA dehvdrogenase
1414	1414 38/68_at	HADHSC	76/964	deliyalogellase, short chair	

(-1,c 2)

LDHA   X02152   actate dehydrogenase A   LBHR   L25931   amin B receptor   LBHR   L25931   amin B receptor   LBHR   L25931   amin B receptor   LAMB1   M14199   protein SA)   LAMB1   M61916   aminin beta 1   LAMB1   M61916   aminin pera 1   LAMB1   M61916   aminin gardonin growth factor beta 1   LGALS3   AB006780   (galectin 3)   actin galactoside-binding, soluble, 3   call SB   L13210   actin, galactoside-binding, soluble, 3   call SB   L13210   actin, galactoside-binding, soluble, 3   call LCALS8   L13210   actin, galactoside-binding, soluble, 8   actin, galactoside-binding, soluble, 9   actin, caeptor overlapping transcript-II   LAMPI   AF062075   actin, galactoside-binding, soluble, 9   actin, galacto						
41485_at         LDHA         X02152         lactate dehydrogenase A         lamin Breceptor	_	∢	മ	၁		
LBR	14154		LDHA	X02152		lactate dehydrogenase A
Main	14162	288 s at	LBR	125931		lamin B receptor
at         LAMR1         M14199         protein SA)           at         LAMA4         \$78569         laminin, alpha 4         late           t         LAMA4         \$78569         laminin, alpha 4         late           t         LAMB1         M61916         laminin, alpha 4         late           at         LAMB1         M61916         laminin, beta 1           at         LAMCL1         Y11395         like 1 (bacterial)           laterit transforming growth factor beta binding protein 1         latent transforming growth factor beta binding protein 2         latent transforming growth factor beta binding protein 2           at         LGALS1         AB53946         (galectin 1)         lectin, galactoside-binding, soluble, 3						
at         LAMA4         \$78569         laminin, alpha 4         laminin, alpha 4         laminin, alpha 4         laminin, beta 1         lamin, beta 1         lamin, beta 1         lamin, beta 1         lamin, beta	1417 2	256 s at	LAMR1	M14199		laminin receptor 1
LANCL	1418	37671_at	LAMA4	S78569		laminin alpha 4 chain
at         LANCL1         Y11395         like 1 (bacterial)           at         LTBP1         M34057         like 1 (bacterial)           at         LTBP2         Z37976         linding protein 1           at         LGALS1         AB535946         (galectin 3)           at         LGALS3         AB006780         (galectin 3)           at         LGALS3BP         L13210         binding protein 2           at         LGALS3BP         L13210         binding protein           at         LGALS3BP         L13210         binding protein           at         LGALS3BP         L13210         binding protein           at         LGALS8         L78132         (galectin 3)           at         LGALS8         L78132         (galectin 3)           at         LGALS8         L78132         (galectin 3)           at         LGALS9         AW026535         leptin receptor gene-related protein           b. at         LRRFIP1         J69609         protein 1 <td>1419</td> <td>581 at</td> <td>LAMB1</td> <td>M61916</td> <td>laminin, beta 1</td> <td>laminin B1</td>	1419	581 at	LAMB1	M61916	laminin, beta 1	laminin B1
at         LANCL 1         Y11395         like 1 (bacterial)         like 1 (bacterial)         like 1 (bacterial)           at         LTBP1         M34057         binding protein 1         binding protein 1           at         LTBP2         Z37976         binding protein 2         lectin, galactoside-binding, soluble, 1           at         LGALS1         AB535946         (galectin 1)         lectin, galactoside-binding, soluble, 3           at         LGALS3         AB006780         (galectin 3)         galactoside-binding, soluble, 3           at         LGALS3BP         L13210         binding protein         lectin, galactoside-binding, soluble, 3           at         LGALS8         L78132         lectin, galactoside-binding, soluble, 3         lectin, galactoside-binding, soluble, 3           at         LGALS8         L78132         lectin, galactoside-binding, soluble, 3         lectin, galactoside-binding, soluble, 3           at         LGALS8         L78132         lectin, galactoside-binding, soluble, 3         lectin, galactoside-binding, soluble, 3           at         LGALS8         L78132         lectin, galactoside-binding, soluble, 3           at         HSOBRGRP         WW026535         leptin receptor generality           at         HSOBRGRP         Y12670         leptin receptor ge					LanC lantibiotic synthetase component C-	
at LTBP1 M34057 binding protein 1  at LTBP2 Z37976 binding protein 1  LGALS1 AB35946 (galectin 1)  at LGALS3 AB006780 (galectin 1)  at LGALS3 AB006780 (galectin 3)  binding protein 1  at LGALS3 AB006780 (galectin 3)  at HSOBRGRP AW026335 leptin receptor gene-related protein 1  binding protein 3  at HSOBRGRP AW026335 leptin receptor gene-related protein 1  cat LEPROTL1 AF063605 leptin receptor gene-related protein 1  at LDOC1 AB019527 leucine rich repeat (in FLII) interacting 1  at LDC1 AB019527 leucine rich PPR-motif containing 1  at LTA4H J03459 leukocyte-associated lg-like receptor 1  at LTA4H J03459 leukocyte-associated lg-like receptor 1  at LTA4H AF013249 leukocyte-associated lg-like receptor 1  at LTA4H AF013249 leukocyte-associated lg-like receptor 1  at LTA4H AF013249 leukocyte-associated lg-like receptor 1  at LPXN AF062075 leukocyte-associated lg-like receptor 1  at RPS29 Al541542 CDNA 5 menous brain protein E46  Al524873 like mouse brain protein E46	1420	39441 at	LANCL1	Y11395	like 1 (bacterial)	lanthionine synthetase C-like protein 1
LTBP1 M34057 binding protein 1  at LTBP2 Z37976 binding protein 2  binding protein 2  at LGALS1 Ab35946 (galectin 3)  at LGALS3 AB006780 (galectin 3)  at LGALS3BP L13210 binding protein  t LGALS8 L78132 (galectin 8)  t LGALS9BGRP AW026535 leptin receptor gene-related protein  at HSOBRGRP AW026535 leptin receptor gene-related protein  at LEPROTL1 AF063605 leptin receptor gene-related protein  at LDOC1 AB019527 leucine rich repeat (in FLII) interacting brotein 1  at LAIR1 AF013249 leucine-rich PPR-motif containing  at LAIR1 AF013249 leucine-rich PPR-motif containing  at LAIR1 AF013249 leucine-rich PPR-motif containing  at LTA4H J03459 leucine-rich PPR-motif containing  at LPXN AF062075 leucine-rich PPR-motif containing  at LPXN AF062075 leucine-rich Ab4 hydrolase  at LPXN AF062075 leucine-rich Ab4 hydrolase  at LPXN AF062075 leucine-rich PPR-motif containing  at RPS29 Al541542 CDNA 5, mRNA sequence.  at E46, Al524873 lite mouse brain protein E46					latent transforming growth factor beta	latent transforming growth factor beta
at LGALS1 A4535946 binding protein 2  at LGALS1 A4535946 (galectin 1)  at LGALS1 A4535946 (galectin 1)  at LGALS3 AB006780 (galectin 3)  at LGALS3BP L13210 binding protein  t LGALS3BP L13210 binding protein  t LGALS3BP L13210 binding protein  t LGALS3BP L13210 binding soluble, 8  t LGALS3BP L78132 (galectin 8)  r_at LGALS9 AW026535 leptin receptor gene-related protein  at HSOBRGRP AW026535 leptin receptor gene-related protein  at HSOBRGRP Y12670 leptin receptor gene-related protein  at LCDC1 AF063605 leptin receptor overlapping transcript-like 1 is  at LARFIP1 U69609 protein 1  at LARFIP AF013249 leucine rich repeat (in FLII) interacting interact	1421	1495 at	LTBP1	M34057	binding protein 1	binding protein 1 precursor
LGALS1 A4535946 binding protein 2  LGALS1 A4535946 (galectin 1)  LGALS3 AB006780 (galectin 3)  LGALS3BP L13210 binding protein  LGALS3BP L13210 binding protein  LGALS3BP L78132 (galectin 3)  LGALS3BP L78132 (galectin 3)  LGALS3BP L78132 (galectin 3)  LGALS3BP L78132 (galectin 3)  LGALS8 L78132 (galectin 3)  LGALS8 L78132 (galectin 3)  LGALSB L78132 (leptin receptor gene-related protein 1  LDOC1 AF063605 (leptin receptor gene-related protein 1  LDOC1 AB019527 (leucine rich repeat (in FLII) interacting 1  LL LAN AF013249 (leucine rich PPR-motif containing 1  AF0132493 (leucine At hydrolase 1  LDACH AF062075 (leucine At hydrolase 1  LDACH AF0524873 (like mouse brain protein E46					latent transforming growth factor beta	1
LGALS1 A4535946 (galectin 1)  LGALS3 AB006780 (galectin 3)  LGALS3BP L13210 (galectin 3)  LGALS3BP L13210 (galectin 3)  LGALS3BP L13210 (galectin 3)  LGALS8 L78132 (galectin 8)  LGALS8 L78132 (galectin 8)  LGALS8 L78132 (galectin 8)  LGALSB L78134 (mpt.in receptor gene-related protein  LDC1 AB019527 (leutine rich repeat (in FLII) interacting 14  LLDC1 AB019527 (leutine-rich PPR-motif containing 14  LLAIR1 AF013249 (leukocyte-associated lg-like receptor 1  LDXN AF062075 (leu	1422	37906 at	LTBP2	237976	binding protein 2	LTBP-2 precursor.
LGALS1 Al535946 (galectin 1)  LGALS3 AB006780 (galectin 3)  LGALS3 AB006780 (galectin 3)  LGALS3BP L13210 binding protein  LGALS3BP L13210 binding protein  LGALS3BP L13210 binding protein  LGALS3BP L1322 (galectin 8)  at LEPR U50748 leptin receptor gene-related protein  t HSOBRGRP AW026535 leptin receptor gene-related protein  t HSOBRGRP Y12670 leptin receptor gene-related protein  t HSOBRGRP Y12670 leptin receptor gene-related protein  t HSOBRGRP AW026535 leptin receptor gene-related protein  t HSOBRGRP Y12670 leptin receptor gene-related protein  t LEPROTL1 AF063605 leptin receptor gene-related protein  t LDOC1 AB019527 leucine rich repeat (in FLII) interacting  tr LAIR1 AF013249 leucine-rich PPR-motif containing  tr LPXN AF062075 leucine-rich PPR-motif containing  tr LPXN AF062075 leucknewassociated ig-like receptor 1  libiest16-A02.r bvnorm Homo sapiens  tr RPS29 AI541542 cDNA 5', mRNA sequence.					lectin, galactoside-binding, soluble, 1	•
LGALS3 AB006780 (galectin 3)  LGALS3BP L13210 binding protein  LGALS3BP L13210 binding protein  LGALS3BP L13210 binding protein  LGALS8 L78132 (galectin 8)  AW026535 leptin receptor gene-related protein  t HSOBRGRP Y12670 leptin receptor gene-related protein  t HSOBRGRP Y12670 leptin receptor gene-related protein  t LEPROTL1 AF063605 leptin receptor overlapping transcript-like 1  LDOC1 AB019527 leucine rich repeat (in FLII) interacting  t LAIR1 AF013249 leucine-rich PPR-motif containing  tr LAIR1 AF013249 leucine-rich PPR-motif containing  tr LAIR1 AF062075 leupaxin  libitest16.A02.r bvnorm Homo sapiens  c DNA 5; mRNA sequence.	1423	33412_at	LGALS1	AI535946	(galectin 1)	
LGALS3 AB006780 (galectin 3) lectin, galactoside-binding, soluble, 3 LGALS3BP L13210 binding protein LGALS8 L78132 (galectin 8) LGALS8 L78132 (galectin 8) HSOBRGRP AW026535 leptin receptor gene-related protein HSOBRGRP Y12670 leptin receptor gene-related protein HSOBRGRP Y12670 leptin receptor gene-related protein HSOBRGRP Y12670 leptin receptor gene-related protein LEPROTL1 AF063605 leptin receptor overlapping transcript-like 1 leucine rich repeat (in FLII) interacting t LLDC1 AB019527 leucine zipper, down-regulated in cancer 1 LAIR1 AF013249 leucine-rich PPR-motif containing t LTA4H J03459 leucine-rich PPR-motif containing t LPXN AF062075 leukotriene A4 hydrolase					lectin, galactoside-binding, soluble, 3	
LGALS3BP L13210 binding protein LGALS3BP L13210 binding protein LGALS8 L78132 (galactin 8) at LEPR U50748 leptin receptor gene-related protein HSOBRGRP Y12670 leptin receptor gene-related protein HSOBRGRP Y12670 leptin receptor gene-related protein HSOBRGRP Y12670 leptin receptor gene-related protein at LEPROTL1 AF063605 leptin receptor gene-related protein leucine rich repeat (in FLII) interacting protein 1  LDOC1 AB019527 leucine zipper, down-regulated in cancer 1 LAIR1 AF013249 leucine-rich PPR-motif containing t LAIR1 AF013249 leukocyte-associated lg-like receptor 1 LAIR1 AF062075 leukocyte-associated lg-like receptor 1 LDXN AF062075 leupaxin libtest16.A02.r bynorm Homo sapiens cDNA 5', mRNA sequence.	1424	35367 at	LGALS3	AB006780	(galectin 3)	galectin-3
LGALS3BP L13210 binding protein  LGALS8 L78132 (galactin 8)  LGALS8 L78132 (galactin 8)  LGALS8 L78132 (galactin 8)  LGALS8 L78132 (galactin 8)  HSOBRGRP AW026535 leptin receptor gene-related protein  HSOBRGRP Y12670 leptin receptor gene-related protein  LEPROTL1 AF063605 leptin receptor gene-related protein  at LEPROTL1 AF063605 leptin receptor overlapping transcript-like 1  leptin receptor gene-related protein  leucine rich repeat (in FLII) interacting  to LDOC1 AB019527 leucine rich PPR-motif containing  to LARFIP AF013249 leucine-rich PPR-motif containing  to LTA4H J03459 leucine-rich PPR-motif containing  to LA661 AF013249 leucine-rich PPR-motif containing  to RA661 AF013249 leucine-rich PPR-motif receptor 1					lectin, galactoside-binding, soluble, 3	
LGALS8	1425	37754 at	LGALS3BP	L13210	binding protein	Mac-2 binding protein
at         LGALS8         L78132         (galectin 8)           at         LEPR         U50748         leptin receptor           HSOBRGRP         AW026535         leptin receptor gene-related protein         I           HSOBRGRP         Y12670         leptin receptor gene-related protein         I           LEPROTL1         AF063605         leptin receptor overlapping transcript-like 1         I           at         LRRFIP1         U69609         protein 1           LOC1         AB019527         leucine rich repeat (in FLII) interacting           LAIR1         AF013249         protein 1           LAIR1         AF013249         leucine-rich PPR-motif containing           LAIR1         AF013249         leukocyte-associated Ig-like receptor 1           LTA4H         J03459         leukotriene A4 hydrolase           LPXN         AF062075         leupaxin           RPS29         AI541542         CDNA 5; mRNA sequence.           E46L         AI524873         like mouse brain protein E46					lectin, galactoside-binding, soluble, 8	•
at         LEPR         U50748         leptin receptor           HSOBRGRP         AW026535         leptin receptor gene-related protein           HSOBRGRP         Y12670         leptin receptor gene-related protein           LEPROTL1         AF063605         leptin receptor overlapping transcript-like 1           at         LRRFIP1         U69609         protein 1           LOC1         AB019527         leucine-rich PPR-motif containing           LAIR1         AF013249         leucine-rich PPR-motif containing           LPXN         AF062075         leucine-rich PPR-motif containing           RPS29         AI541542         CDNA 5; mRNA sequence.           CDNA 5; mRNA sequence.         AI524873         like mouse brain protein E46	1426	1846 at	LGALS8	L78132	(galectin 8)	prostate carcinoma tumor antigen
HSOBRGRP AW02635 leptin receptor gene-related protein HSOBRGRP Y12670 leptin receptor gene-related protein LEPROTL1 AF063605 leptin receptor overlapping transcript-like 1 leucine rich repeat (in FLII) interacting protein 1 LDOC1 AB019527 leucine-rich PPR-motif containing LAIR1 AF013249 leucine-rich PPR-motif containing leucine-rich PPR-motif leucine-rich PPR-motif containing leucine-rich PPR-motif leucine-rich PPR-m	1427	34267 r at	LEPR	U50748	leptin receptor	leptin receptor
HSOBRGRP Y12670 leptin receptor gene-related protein  LEPHOTL1 AF063605 leptin receptor overlapping transcript-like 1 leucine rich repeat (in FLII) interacting protein 1  LDOC1 AB019527 leucine-rich PPR-motif containing LAIR1 AF013249 leucine-rich PPR-motif containing leukocyte-associated Ig-like receptor 1  LTA4H J03459 leukocyte-associated Ig-like receptor 1  LTA4H J03459 leukotriene A4 hydrolase leukocyte-associated Ig-like receptor 1  LPXN AF062075 leukocyte-associated Ig-like receptor 1  LPXN AF062075 leukotriene A4 hydrolase containing libitest16.A02.r bynorm Homo sapiens containing libitest16.A02.r bynorm Homo sapiens libites	1428	33830 at	HSOBRGRP	AW026535	leptin receptor gene-related protein	
the PROTL1 AF063605 leptin receptor overlapping transcript-like 1 leucine rich repeat (in FLII) interacting protein 1  LDOC1 AB019527 leucine zipper, down-regulated in cancer 1 LAIR1 AF013249 leucine-rich PPR-motif containing leukocyte-associated Ig-like receptor 1 LAIR1 AF062075 leukocyte-associated Ig-like receptor 1 LPXN AF062075 leukotriene A4 hydrolase libtest 16.A02.r bynorm Homo sapiens cDNA 5; mRNA sequence.	1429	33829_at	HSOBRGRP	Y12670	leptin receptor gene-related protein	leptin receptor gene-related protein
LARFIP1   AB019527   leucine rich repeat (in FLII) interacting protein 1	7	20000	1 EDBOTI 1	A FOR 3605	lentin recentor overlapping transcript-like 1	brain my047 protein
LRRFIP1         U69609         protein 1           LDOC1         AB019527         leucine zipper, down-regulated in cancer 1           LRPPRC         M92439         leucine-rich PPR-motif containing           LAIR1         AF013249         leukocyte-associated Ig-like receptor 1           LTA4H         J03459         leukotrinene A4 hydrolase           LPXN         AF062075         leupaxin           LPXN         AF062075         libtest16.A02.r bvnorm Homo sapiens           RPS29         AI541542         CDNA 5', mRNA sequence.           E46L         AI524873         like mouse brain protein E46	?	30000 - 00000	ייין ווכוריי		leucine rich repeat (in FLII) interacting	
LDOC1 AB019527 leucine zipper, down-regulated in cancer 1 LRPPRC M92439 leucine-rich PPR-motif containing LAIR1 AF013249 leukocyte-associated lg-like receptor 1 LTA4H J03459 leukotriene A4 hydrolase LPXN AF062075 leupaxin Ilbtest16.A02.r bynorm Homo sapiens RPS29 A1541542 cDNA 5; mRNA sequence.	1431	41320_s_at	LRRFIP1	609690	protein 1	transcription repressor
LAPPRC M92439   leucine-rich PPR-motif containing     LAIR1 AF013249   leukocyte-associated lg-like receptor 1     LAIR1 AF062075   leukotriene A4 hydrolase     LPXN AF062075   leupaxin     RPS29 AI541542 CDNA 5; mRNA sequence.     E46  AI524873   like mouse brain protein E46	4 4 3 3	20067 of	1 0001	AR019527	leucine zipper, down-regulated in cancer 1	LDOC1 protein
LAIR1   AF013249   leukocyte-associated lg-like receptor 1     LTA4H	1435	71754 at	I BPPRC	M92439	leucine-rich PPR-motif containing	leucine-rich PPR-motif containing protein
LTA4H	3	27770 of	I AIR1	AE013249	leukocyte-associated lq-like receptor 1	leukocyte-associated Ig-like receptor-1
LPXN AF062075   eupaxin	1435	38081 at	I TA4H	103459	leukotriene A4 hydrolase	leukotriene A4 hydrolase
RPS29 AI5241542 cDNA 5', mRNA sequence. E46L AI524873 like mouse brain protein E46	327	36062 at	I DXN	AF062075	leupaxin	leupaxin
RPS29 AI541542 E46L AI524873	3	20005	i		libtest16.A02.r bvnorm Homo sapiens	
E46L A1524873	1437	35278_at	RPS29	AI541542	cDNA 5', mRNA sequence.	
	1438	39687 at	E46L	A1524873	like mouse brain protein E46	

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1439	1439 39686_g_at	E46L	AL050282	like mouse brain protein E46	hypothetical protein
1440		E46L	AL050282	like mouse brain protein E46	hypothetical protein
				likely homolog of rat kinase D-interacting	
1441	1441 39163_at	KIDINS220	W27233	substance of 220 kDa	
				use suppressors of	
1442	1442 32669_at	SOCS5	AB014571		KIAA0671 protein
443	1443 40555_at	TC10	AL043108	likely ortholog of mouse TC10-alpha	
				likely ortholog of mouse TPR-containing,	
444	1444 40844_at	TSBP	D63875	SH2-binding phosphoprotein	KIAA0155 gene product
1445	1445 41248_at	CSTF2T	AB014589	polyadenylation protein CSTF-64	KIAA0689 protein
				likely ortholog of rat golgi stacking protein	
1446	1446 35805_at	GRASP55	AA447263	homolog GRASP55	
				cell antigen-like	
1447	1447 39232 at	LIMS1	U09284		PINCH protein
1448	1448 36181 at	LASP1	X82456	LIM and SH3 protein 1	LIM and SH3 domain protein
1449	1449 38617_at	LIMK2	D45906	LIM domain kinase 2	LIMK-2
1450	1450 1452 at	LM04	U24576	LIM domain only 4	breast tumor autoantigen
1451	1451 31936 s. at	LKAP	AB007890	limkain b1	KIAA0430 protein
L				olesterol	
1452	1452 38745_at	LIPA	X76488	esterase (Wolman disease)	lysosomal acid lipase
145		LPIN1	D80010	lipin 1	
1454	1454 37542_at	LHFPL2	D86961	lipoma HMGIC fusion partner-like 2	
145	1455 41209 at	LPL	M15856	lipoprotein lipase	lipoprotein lipase precursor
145	1456 1798 at	LIV:1	U41060	LIV-1 protein, estrogen regulated	estrogen regulated LIV-1 protein
				liver form; Homo sapiens glycogen	
				phosphorylase (PYGL) gene, exon 20 and	
145	1457 37215 at	PYGL	AF046798	complete cds.	glycogen phosphorylase

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				long tailed isoform; individual exons 6-14	
•				are alternative exons any of which can be	
				spliced out of the mHNA.; putative; long	
				tailed isoform; putative; long tailed	
				isoform; hemopoietic variant; putative;	
				long tailed isoform; epithelial form;	
				putative; Human cell surface glycoprotein	
1458	1458 40493 at	CD44	L05424		cell surface glycoprotein CD44
				low density lipoprotein-related protein-	
				associated protein 1 (alpha-2-	
				macroglobulin receptor-associated protein	macroglobulin receptor-associated protein alpha-2-macroglobulin receptor-associated
1459	1459 36194_at	LRPAP1	M63959	(1)	protein
				low molecular mass ubiquinone-binding	
1460	1460 34400_at	QP-C	AI540957	protein (9.5kD)	
1461	37025_at	PIG7	AL120815	LPS-induced TNF-alpha factor	
1462	39017_at	LSM1	AJ238094	Lsm1 protein	Lsm1 protein
1463	38038_at	LUM	U21128	lumican	lumican
1464	1464 38115 at	FUS1	AF055479	lung cancer candidate	lung cancer candidate FUS1
1465	1465 39428_at	LNK	AF055581	lymphocyte adaptor protein	adaptor protein Lnk
1466	1466 39396 at	LYPLA1	AF081281	lysophospholipase I	lysophospholipase
1467	1467 33788_at	LYSAL1	AB002390	lysosomal apyrase-like 1	lysosomal apyrase-like 1
1468	1468 39758 f at	I AMP1	.104182	Nsosomal-associated membrane protein 1   Nsosomal membrane glycoprotein-1	Nsosomal membrane glycoprotein-1
7460	1460 28403 et	I AMPO	X77196	lysosomal-associated membrane protein 2	hsosomal-associated membrane protein 2 hsosome-associated membrane protein-2
	4470 28400 et	I AMD	1136336	lysosomal-associated membrane protein 2	Nsosoma-associated membrane protein 2 Nsosome-associated membrane protein-2b
	JOHN THE			Ivsosomal-associated protein	lysosomal-associated protein
1471	39019_at	LAPTM4A	D14696	transmembrane 4 alpha	transmembrane 4 alpha
1472	33127_at	LOXL2	U89942	lysyl oxidase-like 2	lysyl oxidase-related protein
1473	1473 34336_at	KARS	D32053	lysyl-tRNA synthetase	Lysyl tRNA Synthetase
1474	1474 32832_at	MAEA	AF084928	macrophage enythroblast attacher	erythroblast macrophage protein EMP
1 4 7 5	147E 3617A of	MACMABCKS	X70326	macrophage myristoylated alanine-rich C kinase substrate	macrophage mynstoylated alanine-rich C
4	301/4_at	MACINIANCING	1710350	אוונמס ממסטומים	

	A	æ	3	Q	ш
Γ				MAD, mothers against decapentaplegic	
1476	1476 1453_at	MADH2	U68018	homolog 2 (Drosophila)	mad protein homolog
				decapentaplegic	
1477	1477 38944_at	MADH3	U68019		mad protein homolog
	-			decapentaplegic	
1478	1478 1433_g_at	MADH3	U68019	homolog 3 (Drosophila)	mad protein homolog
				MAD, mothers against decapentaplegic	
1479	1479 36953_at	MADH4	U44378	homolog 4 (Drosophila)	Dpc4
				MAD, mothers against decapentaplegic	
1480	1480 1013_at	MADHS	U59913	homolog 5 (Drosophila)	Smad5
				MAD, mothers against decapentaplegic	
1481	1481 1955_s_at	MADH6	AF035528	homolog 6 (Drosophila)	Smad6
				MAD, mothers against decapentaplegic	
1482	1482 1857_at	MADH7	AF010193	homolog 7 (Drosophila)	MAD-related gene SMAD7
				major histocompatibility complex, class I,	
1483	1483 41237_at	HLA-A	D32129	<b>A</b>	HLA-A26
				major histocompatibility complex, class II,	
1484	1484 41609_at	HLA-DMB	U15085	DM beta	HLA-DMB
				major histocompatibility complex, class II,	
1485	1485 38096_f_at	HLA-DPB1	M83664	DP beta 1	HLA-DPB1
				major histocompatibility complex, class II,	
1486	1486 38095_i_at	HLA-DPB1	M83664	DP beta 1	HLA-DPB1
				major histocompatibility complex, class II,	major histocompatibility complex, class II,
1487	1487 37039_at	HLA-DRA	J00194	DR alpha	DR alpha precursor
L				major histocompatibility complex, class II,	
1488	1488 33261_at	HLA-DRB1	M16941	DR beta 1	
L.,				major histocompatibility complex, class I-	
1489	1489 34425_at	HLALS	AF031469	like sequence	MHC class I-related protein 1 isoform D
				major receptor for HIV-1; member of	
_				immunoglobulin supergene family; T cell	
1490	1490 34003_at	CD4	U47924	surface glycoprotein T4	protein 'A', isoform 1
1491	1491 36608 at	MDH1	D55654	malate dehydrogenase 1. NAD (soluble)	cytosolic malate dehydrogenase
				malic enzyme 1, NADP(+)-dependent,	
1492	1492 837_s_at	ME1	U43944	cytosolic	cytosolic NADP(+)-dependent malic enzyme

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ME2         M55905         malic enzyme 2, NAD(+)-dependent, ninochondrial         milochondrial           MPI         X76057         MAP kinase-interacting serine/threonine         PMAP kinase-interacting serine/threonine           MKNK1         AB000409         MAP kinase-interacting serine/threonine         MAP kinase-interacting serine/threonine           MARK3         M80359         3           MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase gene, kinase activated protein kinase gene, complete cds.         FR           MAPKAPK5; PRA AF032437         Complete cds.         FR           MAPKAPK5; PRA AF032437         Complete cds.         FR           Sw.P24270 Tr.062839 Sw.P04362         Sw.P04040 Sw.P0432         FR           Sw.P34270 Tr.062839 Sw.P04387         Sw.P7782         Sw.P7782           Sw.P34280 Tr.P09682 Tr.077229         Tr.027710 Sw.P30265 Sw.P7782         Tr.027782           Tr.027710 Sw.P30265 Sw.P7782         Sw.P7782         Sw.P7782           Sw.P34138         Tr.035929 Tr.0359170         Sw.P31389           Tr.027710 Sw.P30265 Sw.P91138         Sw.P07820 Sw.P30265 Sw.P91138           AL035079         match ESTs W94164 N28621           MUGSC:H RG04AC005053         Tr.027792 Sw.P302631           MUGSC:H RG04AC005053         Tq21, complete sequence.		٨	8	ပ	O	יי
ME2         M55905         mitochondrial           MPI         X76057         mannose phosphate isomerase           MKNK1         AB000409         kinase interacting serine/threonine           MAPK3         M80359         3           MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase gene, complete cds.         FK; Homo sapiens mitogen activated protein kinase gene, complete cds.           MAPKAPK5; PRA AF032437         complete cds.         FK; Homo sapiens mitogen activated protein kinase gene, complete cds.           MAPKAPK5; PRA AF032437         complete cds.         FK; PA270 Tr.O62839 Swr.P044040 Swr.P04762           Swr.P24270 Tr.O62839 Swr.P04040 Swr.P04762         Swr.P24270 Tr.O62839 Swr.P0430           Swr.P338 Tr.O18193 Tr.O77229         Tr.C49133 Swr.P2691 Swr.P5306           Tr.C49133 Swr.P06802 Tr.O18193 Tr.O77229         Tr.C49133 Swr.P07872           Tr.C25902 Tr.C59296 Tr.O59296 Swr.P77872         Tr.C59802 Tr.P77924 Swr.O59170           Swr.P07820 Swr.P07826 Swr.P77872         Tr.C598296 Tr.P77924 Swr.O59170           Swr.P07820 Swr.P07826 Swr.P07812         Tr.C598296 Tr.P77924 Swr.O59170           Swr.P07820 Swr.P07820 Swr.P078138         Swr.P078221           KUD:g3165211, AA032221         (NID:g3165211), AA032221           KUD:g3701112); H.MG041D11.1; Homo sapiens BAC clene CTB-41D11 from           MDACCH TR.D1111; H.MG041D11.1; H.MC041D11.1					2, NAD(+)-dependent,	nitochondrial NAD(P)+ -dependent malic
MKNK1	1493	36599 at		M55905		anzyme
MARNK1   AB000409   kinase-interacting serine/threonine   MAP/microtubule affinity-regulating kinase   PRK;   Homo sapiens mitogen activated protein kinase gene, kinase activated protein kinase gene, complete cds.   Complete cds.   Complete cds.   Complete cds.   MAPKAPK5; PRA AF032437   Complete cds.   Complete serior complete serior complete cds.   Complet	1494	36673 at		X76057		shosphomannose isomerase
MKNK1         AB000409         kinase 1           MARK3         M80359         3           MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase gene, complete cds.         Indept of the complete cds.           MAPKAPK5; PRA AF032437         Complete cds.         Indept of the complete cds.           MAPKAPK5; PRA AF032437         Complete cds.         Indept of the complete cds.           MAPKAPK5; PRA AF032437         Complete cds.         Indept of the complete cds.           Sw.P24270 Tr.O62839 Sw.P04040 Sw.P0432         Sw.P04336 Tr.O17229         Indept of the complete cds.           Sw.P14336 Tr.O18193 Tr.O17229         Tr.C49133 Sw.P26901 Sw.P55306         Sw.P4330           Tr.C49133 Sw.P26901 Sw.P55306         Tr.C49133 Sw.P44390         Tr.C49132 Sw.P4390           Tr.C49133 Sw.P26901 Sw.P55306         Tr.C42910 Sw.P53025 Sw.P1389         Sw.P15202 Tr.C95928 Tr.C33813           Sw.P15202 Tr.C409658 Sw.P1381         Sw.P15202 Tr.C95928 Tr.C33813         Sw.C915204 Sw.P36181           MUGSCH RG04AC005053         Tq21, complete sequence.         Tq21, complete sequence.						, :
MAPKAPKS         MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase gene, complete cds.         MAPKAPKS; PRA AF032437         MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase gene, complete cds.         MAPKAPKS; PRA AF032437         MAPKAPKS; PRA AF032487         MAPKAPKS; PRA AF032241         MAPKAPKS; PRA AF03221         MAPKAPKS; PRA AFOXES         MAPKAPKS; PRA AFOXES <td>1495</td> <td>35299 at</td> <td></td> <td>AB000409</td> <td></td> <td>MNK1</td>	1495	35299 at		AB000409		MNK1
MARK3   M80359   3   MAPK-activated protein kinase; PRK; Homo sapiens mitogen activated protein kinase gene, Homo sapiens mitogen activated protein kinase gene, It is a sapiens mitogen activated protein kinase gene, It is a sapiens mitogen activated protein kinase gene, It is a sapiens surpoded Sw:P04762   Sw:P24270 Tr.O62839 Sw:P0432 Sw:P24270 Tr.O62839 Sw:P0432 Sw:P44390 Tr.O27710 Sw:Q95628 Tr.O77229 Tr.O27710 Sw:Q95628 Sw:C13289 Sw:P07820 Sw:P77872 Tr.O27710 Sw:Q95628 Sw:C13289 Sw:P1388 Tr.O27710 Sw:Q95628 Tr.O73613 Sw:C95602 Tr.O77824 Sw:C69170 Sw:P1388 Tr.O63603 Sw:P1388 Tr.O63603 Sw:P1388 Tr.O63603 Sw:P1388 Tr.O63603 Sw:P1388 Tr.O63603 Sw:P1388 Tr.O63603 Tr.P77924 Sw:C992402 Tr.O63603 Sw:P1388 Tr.O63603 Tr.P77924 Sw:C992402 Tr.O63603 Sw:P1388 Tr.O63603 Tr.P77924 Sw:C992402 Tr.O63603 Tr.P77924 Sw:C992402 Tr.O63603 Tr.P77924 Sw:C992402 Tr.O63603 Tr.P77924 Sw:C992402 Tr.O63603 Sw:C992402 Sw:C992402 Tr.O63603 Tr.P77924 Sw:C99203 Tr.O63603 Tr.O63603 Tr.P77924 Sw:C99203 Tr.O63603 Tr.P77924 Sw:C99203 Tr.O63603 Tr.P77924 Sw:C99203 Tr.O63603 Tr.P77924 Sw:C99203 Tr.O63603 Sw:C992402 Sw:C99203 Tr.O63603 Tr.O63603 Tr.D77924 Sw:C99203 Tr.O63603 Tr.O63603 Tr.O63603 Tr.O63603 Tr.D77924 Sw:C99203 Tr.O63603 Tr.O6360						
MAPK-activated protein kinase; PRK;	1496	40826_at	MARK3	M80359		protein p78
Homo sapiens mitogen activated protein kinase gene, kinase activated protein kinase gene, kinase activated protein kinase gene, complete cds.   Edinase activated protein kinase gene, kinase activated protein kinase gene, complete cds.   Edinase gene, complete cds.   Edinase gene, complete cds.   Edinase gene, complete sequence.   Edinase gene, complete complet					MAPK-activated protein kinase; PRK;	
MAPKAPK5; PRA   AF032437   complete cds.   range activated protein kinase gene,   range   protein kinase gene,   range   proteins: Sw:P04040 Sw:P04762   Sw:P24270 Tr:O62839 Sw:P04322   Sw:P17336 Tr:P90682 Tr:O27487   Sw:D61235 Tr:O18193 Tr:O77229   Tr:O49133 Sw:P26901 Sw:P55306   Sw:P30263 Tr:P95631 Sw:P4390   Tr:O27710 Sw:D95631 Sw:P4390   Tr:O27710 Sw:D95631 Sw:P4390   Tr:O27710 Sw:D95638 Sw:O13289   Sw:P07820 Sw:P30265 Sw:D917872   Tr:O29602 Tr:P77924 Sw:O59170   Sw:P138   match ESTs: W94164 N28621   match to ESTs AA316181   (NID:g3165221), AA032221   (NID:g3165221), AA032221   (NID:g3165221), AA032221   (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.						
MAPKAPK5; PRA AF032437 complete cds.  match proteins: Sw:P04040 Sw:P04762 Sw:P24270 Tr:O62839 Sw:P0432 Sw:P47336 Tr:P90682 Tr:027487 Sw:O61235 Tr:O18193 Tr:O77229 Tr:O49133 Sw:P26901 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:O27710 Sw:O96528 Sw:O13289 Sw:P77710 Sw:O96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:O59602 Tr:P77924 Sw:O59170 Sw:P15202 Tr:O59296 Tr:O33613 Sw:O92405 Sw:O59296 Tr:O33611 (NID:g3165218), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from cTB-						mitogen activated protein kinase activated
match proteins: Sw:P04040 Sw:P04762 Sw:P24270 Tr:O62839 Sw:P00432 Sw:P17336 Tr:P90682 Tr:O27487 Sw:O61235 Tr:O18193 Tr:O77229 Tr:O49133 Sw:P26901 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:O27710 Sw:O96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:O59602 Tr:P77924 Sw:O59170 Sw:P15202 Tr:O59296 Tr:O33613 Sw:C92405 Sw:O59635 Sw:P81138 match to ESTs W94164 N28621 (NID:g3165221), AA032221 (NID:g31652213), and Al167942 (NID:g31652183), and Al167942	1497	41506_at	_	AF032437		protein kinase
Sw.P24270 Tr:O62839 Sw.P0432 Sw.P17336 Tr:P90682 Tr:O27487 Sw.O61235 Tr:O18193 Tr:O77229 Tr:O49133 Sw.P26901 Sw.P55306 Sw.P30263 Tr:P95631 Sw.P44390 Tr:O27710 Sw.C96528 Sw.O13289 Sw.P07820 Sw.P30265 Sw.P77872 Tr:O59602 Tr:P77924 Sw.O59170 Sw.P15202 Tr:O59296 Tr:O33613 Sw.C92405 Sw.O59635 Sw.P81138 match to ESTs W94164 N28621 (NID:g3165221), AA032221 (NID:g3165221), AA032221 (NID:g3165218), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7421, complete sequence.					metrh proteins: Sw.P04040 Sw.P04762	
Sw.P24270 1r.062839 Sw.P00432 Sw.P17336 Tr.P90682 Tr.027487 Sw.O61235 Tr.O18193 Tr.077229 Tr.C49133 Sw.P26901 Sw.P55306 Sw.P30263 Tr.P95631 Sw.P44390 Tr.C27710 Sw.C96528 Sw.O13289 Sw.P07820 Sw.P30265 Sw.P77822 Tr.C49133 Sw.P07820 Sw.C99528 Sw.C913289 Sw.P07820 Sw.C995296 Tr.C33613 Sw.C492405 Sw.C458296 Tr.C33613 Sw.C492405 Sw.C498221 (NID:3162213), AA032221 (NID:31602183), and Al167942 (NID:31602183), and Al167942 (NID:33001112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from sapiens BAC clone CTB-41D11 from 7421, complete sequence.						
Sw.P17336 Tr:P90682 Tr:Q27487 Sw.O61235 Tr:O18193 Tr:O77229 Tr:Q49133 Sw:P26901 Sw.P55306 Sw.P30263 Tr:P95631 Sw.P44390 Tr:Q27710 Sw:Q96528 Sw:O13289 Sw.P07820 Sw:P30265 Sw.P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:P15202 Tr:Q59296 Tr:O33613 Sw:Q92405 Sw:Q59235 Sw.P81138 CAT AL035079 match ESTs: W94164 N28621 (NID:g3165221), AA032221 (NID:g31652219), and Al167942 (NID:g316522183), and Al167942 (NID:g316522183), and Al167942 (NID:g316522183), and Al167942 (NID:g316522183), and Al167942 (NID:g3165183), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.					Sw:P24270 1r:062839 Sw:P00432	
Sw:O61235 Tr:O18193 Tr:O77229 Tr:O49133 Sw:P26901 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:O27710 Sw:O96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:O59602 Tr:P77924 Sw:O59170 Sw:P07820 Sw:P30265 Sw:P77872 Tr:O59602 Tr:P77924 Sw:O59170 Sw:C92405 Sw:O59635 Sw:P81138 Sw:C92405 Sw:O59635 Sw:P81138 Match to ESTs: W94164 N28621 (NID:g3165221), AA032221 (NID:g31652213), and Al167942 (NID:g316522183), and Al167942 (NID:g31652183), and Al167942 (NID:g31652183), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7021, complete sequence.					Sw:P17336 Tr:P90682 Tr:Q27487	
Tr:Q49133 Sw:P26901 Sw:P55306 Sw:P30263 Tr:P95631 Sw:P44390 Tr:Q27710 Sw:Q96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:P15202 Tr:Q59296 Tr:O33613 Sw:Q92405 Sw:Q59235 Sw:P81138 CAT AL035079 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g31652213), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7021, complete sequence.					Sw:O61235 Tr:O18193 Tr:O77229	
Sw:P30263 Tr:P95631 Sw:P44390 Tr:O27710 Sw:Q96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:P15202 Tr:Q59296 Tr:O33613 Sw:Q92405 Sw:Q59235 Sw:P81138 CAT AL035079 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g31652213), and Al167942 (NID:g31652213), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7021, complete sequence.					Tr:Q49133 Sw:P26901 Sw:P55306	
Tr:Q27710 Sw:Q96528 Sw:O13289 Sw:P07820 Sw:P30265 Sw:P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:P15202 Tr:G59296 Tr:O33613 Sw:Q92405 Sw:Q59635 Sw:P81138 CAT AL035079 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g31652213), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.					Sw:P30263 Tr:P95631 Sw:P44390	
Sw:P07820 Sw:P30265 Sw:P77872 Tr:Q59602 Tr:P77924 Sw:Q59170 Sw:P15202 Tr:G59296 Tr:O33613 Sw:Q92405 Sw:Q59635 Sw:P81138 CAT AL035079 match to ESTs: W94164 N28621 match to ESTs: W94164 N28621 (NID:g3165221), AA032221 (NID:g31652213), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.					Tr:Q27710 Sw:Q96528 Sw:O13289	
CAT AL035079 Tr:Q59602 Tr:D59296 Tr:O33613 Sw:Q92405 Sw:Q59635 Sw:P81138 CAT AL035079 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g3165213), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.					Sw:P07820 Sw:P30265 Sw:P77872	
CAT AL035079 match ESTs: W94164 N28621 match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g3165221), AA032221 (NID:g3165211), H. RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.					Tr:Q59602 Tr:P77924 Sw:Q59170	
CAT AL035079 match ESTs: W94164 N28621 match to ESTs A4316181 (NID:33165221), A4032221 (NID:3165221), A4032221 (NID:33701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.					Sw:P15202 Tr:Q59296 Tr:O33613	
CAT AL035079 match ESTs; W94164 N28621 match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g3165221), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from YQ21, complete sequence.				-	Sw:Q92405 Sw:Q59635 Sw:P81138	
match to ESTs AA316181 (NID:g3165221), AA032221 (NID:g1502183), and A1167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.	149	8 37009 at	CAT	AL035079	match ESTs: W94164 N28621	ර <u>්</u> ව3C18.1 (Catalase)
(NID:g3165221), AA032221 (NID:g1502183), and AI167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.					match to ESTs AA316181	
(NID:g1502183), and Al167942 (NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from WUGSC:H RG04/AC005053 7q21, complete sequence.					(NID:g3165221), AA032221	
(NID:g3701112); H_RG041D11.1; Homo sapiens BAC clone CTB-41D11 from 7q21, complete sequence.	_				(NID:g1502183), and Al167942	
Sapiens BAC clone CTB-41D11 from VUGSC:H RG04AC005053 7q21, complete sequence.					(NID:g3701112); H_RG041D11.1; Homo	•
WUGSC:H RG04/AC005053 7q21, complete sequence.					sapiens BAC clone CTB-41D11 from	six transmembrane epithelial antigen of the
	149	9 40297 at		AC005053	7q21, complete sequence.	prostate

	A	8	0	O	П
15003	1500 34860 q. at	BCG1	Z98046	match: cDNAs X67055 X14690 D89287 X70393 S82800 X16260 M18192 Y11283 D38535 D38595 match: proteins Q06033 P97280 O54882 O35802 Q61704 Q14624 P79263 Q63416 O42141 P19823 O02668 Q61703 P97279 Q29052	match: cDNAs X67055 X14690 D89287 X70393 S82800 X16260 M18192 Y11283 D38535 D38595 match: proteins Q06033 P97280 O54882 O35802 Q61704 Q14624 P79263 Q63416 Q42141 P19823 O02668 hepatocellular carcinoma associated protein; D197263 Q63416 Q42141 P19823 O02668 hepatocellular carcinoma associated protein;
				match: cDNAs: Em:Al.050345 match: ESTs: Em:AA304885 Em:AA447346 Em:AA314213 Em:AA209368 Em:AA209372 Em:T84723 Em:H23039	
1501	1501 35336_at	HS508115A	AL021707	Em:AA542125 Em:W41686 Em:AA384854 Em:AA492678	chromosome 22 open reading frame 2
1502	32658_at	dJ1033B10.1	AL031228	match: protein O15214	BING4
1503	1503 31545_at	dJ1033B10.1	AL031228	match: protein O15214	BING4
1504 :	36986_at	dJ886K2.1	AL031295	match: protein SPTREMBL; Q14241	UDY-galactose-4-epimerase
1505	1505 38072 at	dJ465N24.1	AL031432	match: proteins CE02000 O59733 CE01999; supported by FGENES and GENSCAN	hypothetical protein dJ465N24.2.1
				match: proteins O15037 CE16881 supported by GENSCAN possibly this partial gene and dJ281H8.1 are part of	dJ281H8.2 (PUTATIVE novel protein similar
1506	1506 32478_f_at	dJ281H8.1	AL031133	one gene	to KIAA0323 and worm C30F12.1)

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	A	8	၁	Q	W.
1507	1507 39759_at	dJ51J12.1	AL031781	match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 Cterminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the atternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.	dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-7 (isoform 3))
1508	508 39760_at	dJ51J12.1	AL031781	match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110, Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.	dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-77 (isoform 3))
1505	1509 32573_at	COX6A	AL021546	match: proteins P13182 P12074 P10818 P43024 Q02221 P07471 P10817 P43023 P13182 O13085 O13082	cytochrome c oxidase subunit VIa polypeptide 1



	A	80	ပ	۵	ш
1510	1510 33443 et	HSES	709120	match: proteins P38533 Q03933 P38530 P41154 Q00613 P38529 P38531 Q63717 P38532 Q99472	heat shock transcription factor 2
	13-01-01		F301E0		
				match: proteins Q14189 P15924 Q03001	
				P97395 P97396 P97394; Human DNA	
				sequence from clone 512B11 on	
				chromosome 6p24-25. Contains the	
				Desmoplakin I (DPI) gene, ESTs, STSs	
1511	1511 36133_at	dJ512B11.1	AL031058	and GSSs, complete sequence.	dJ512B11.1 (Desmoplakin I (DPI))
				match: proteins Q14209 Q16254 O35261	
				O00716 Q61501 Q90977 Q01094	
1512	1512 37043_at	E2F-2	AL021154	Q27368	E2F transcription factor 2
				match: proteins Q15774; match: protein	
				Q01968 P32019; Homo sapiens DNA	
				sequence from PAC 454M7 on	
				chromosome Xq25-26.3. Contains the	
				OCRL1 gene for Lowe Oculocerebrorenal  d/454M7.1.2 (Lowe Oculocerebrorenal	dJ454M7.1.2 (Lowe Oculocerebrorenal
				Syndrome protein OCRL-1. Contains	Syndrome protein OCRL-1) (isoform 2);
				ESTs, STSs and GSSs, complete	dJ454M7.1.1 (Lowe Oculocerebrorenal
151	1513 41227_at	OCRL1	AL022162	sequence.	Syndrome protein OCRL-1) (isoform 1)
					dJ341E18.1 (Serine/Threonine Protein
				match: proteins Q62726 P20793 Q04859 Kinase (presumptive isolog of Rat protein	Kinase (presumptive isolog of Rat protein
151	1514 38990_at	dJ341E18.1	AL031178	Q39423 P43294 O49669	(062726)
151	138990_at	dJ341E18.1	AL031178		Q39423 P43294 O49669

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ш	dJ232K4.1 (hypothetical 141.7 kD protein JUMONJI)	dJ889N15.1 (novel protein similar to X. laevis Cortical Thymocyte Marker CTX)	dJ747H23.1 (malic enzyme 1, soluble (NADP-dependent malic enzyme, malate oxidoreductase, EC 1.1.1.40))	non-histone chromosome protein 2 (S. cerevisiae)-like 1	
D	match: proteins Q92833 Q62315; protein Q92833 has a different stop codon 19 as further downstream because it jumps frame twice, circumventing the stopcodon in this entry. This could be due to a sequence error in the cDNA sequence; Homo sapiens DNA sequence from PAC 232K4 on chromosome 6p22.3. Contains the JUMONJI gene for a hypothetical 141.7 kD protein. Contains ESTs, STSs, a CA repeat polymorphism and genomic marker D6S260', complete sequence.	match: proteins Q99795 Q91665 Q91664 C09052 P78310 P97792 Q91667 O60939 P54900 Q62861 Q61148 O00426 P06907 P25189 Q92677 P20938 P27573 P10522 P37301 match: patented sequence I80040 dJ889N15.1 (novel protein similar to X. surported by GENSCAN and FGENES laevis Cortical Thymocyte Marker CTX)	match: proteins: Sw:P06801 Sw:P28227 Sw:Q29558 Sw:P13697 Sw:P40927 Sw:Q16798 Tr:Q16797 Sw:P48163	match: proteins: Sw:P12956	match: proteins: Sw:P17861 Tr:O35426; Human DNA sequence from clone CTA- 292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete
ပ	AL021938	77	Z62215 AL049699		
В	ICMOMUL	dJ889N15.1	APOLZ ME1	OTK27 SSFA1	XRP
4	1515 34782_at	1516 37350_at	1517 39738 at 1518 31824 at	151932766 at	1500 30756 n at
	1515	1516	151	15	7.50

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1521	1521 39755_at	XBP1	293930	B)	bK292E10.1 (X-box binding protein 1 (TREB5))
				match: proteins: Sw:P26038 Tr:O35763 Sw:P26041 Sw:P26042 Sw:P26044 Sw:P35241 Sw:P26043 Sw:P15311 Sw:P31976 Sw:P26040 Tr:Q26520 Tr:Q24788 Tr:Q24796 Tr:O94815; Human	
1522	1522 40771 at	ZSX	Z98946		dJ376D21.1 (Moesin (Membrane-organizing Extension Spike protein))
1523	1523 31722 at	RPL3	AL022326	match: proteins: Sw:P39023 Sw:O16797 Sw:P21531 Sw:P39872 Sw:P27659 Sw:Q92901 Sw:P49149 Sw:P22738 Sw:P35684 Sw:P17094 Wp:CE05598	ribosomal protein L3
152	22138 94	i BE21	AI 031714	match: proteins: Sw:P50550 Sw:O09181 Tr:O62622 Sw:P40984 Sw:P50623 Tr:Q42551 Tr:O24240 Tr:Q42973 Sw:P52478 Sw:Q02159 Sw:P15732 Sw:O00102 Tr:O76542 Sw:P27949 Sw:P52490	C358B7.1 (ubiquitin-conjugating enzyme E21 (homologous to veast UBC9))
1525	1525 36607_at	bK250D10.3	299716	match: proteins: Sw:Q12772 Sw:Q60429 Sw:P36956 Sw:Q60416 Tr:O15352	septin 3
1526	1526 38399_at	SNRPB2	AL034428	match; proteins; Sw:Q28038 Sw:Q16674 Tr:P97591 Sw:Q61865	small nuclear ribonucleoprotein polypeptide B"

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-	A	8	3	Q	U
$\dagger$				match: proteins: Tr:O54791 Sw:Q90595	
				Sw:Q61827 Sw:Q90596 Tr:O54790	
				Tr.O15525 Sw:Q90889 Tr.O73679	
507	1E07 26711 of	HSSOGA DKF7P5 AL021977	AL021977	1	chromosome 22 open reading Iranie 3
5007		DIAN A	AI 008583	23 82	chromobox homolog 6
200					
-					dJ738P15.2 (CD39-like 2 (a nucleoside
- 003	0076 01	4 1738P15 1	AL 035252		phosphatase))
252	1329 39070 at			798	
					dJ347H13.1 (aconitase 2, mitochondrial
					(Aconitate Hydratase, EC 4.2.1.3, Citrate
- 001	4E90/37480 at	ACO2	AL 023553		Hydrolyase))
3	1103_at	7000		match: proteins: Tr:P70386 Sw:Q02527	
	1005	TAYDEBET TYPE	XPE A1 022312		activating transcription factor 4
	1531 41235 at		Organia de la composição de la composiçã		dJ117516.1 (Ras inhibitor JC265 (Ras
				match: proteins: Tr:Q00425 Sw:Q13671	association (RaIGDS/AF-6) domain
1001	1000	A 1447516 4	A) 049538	Tr.O15010 Tr.P97680	containing protein))
12861	1532 36550 at	1.000	2000	match: proteins: Tr:Q14621 Tr:Q64012	
				Sw:P07910 Sw:P19600 Tr:O60812	RNA-binding protein (autoantigenic) long
200	10000000	DEAD	Ai 031668	Sw:Q14011 Sw:P26686	isoform
2	33000_at	275		match: proteins: Tr:Q9Y3M0 Tr:Q9WU14	
	20004	4 1483K16 1	AI 034374	Sw.P39540 Tr:Q9Y396	dJ483K16.1.1 (novel protein (isoform 1))
200	1534 33021 at	G10	111861	maternal G10 transcript	maternal G10 transcript
200	1333 39029 at	MANT	X96401	MAX binding protein	ROX protein
200	33143_at	I A II A			MAX interacting protein 1, isoform a; MAX
1	4000	P4V14	1 07648	MAX interacting protein 1	interacting protein 1, isoform b
25	1537 39072 81	INVA	200		MAX interacting protein 1, isoform a; MAX
4520	40 A H	MXII	107648	MAX interacting protein 1	interacting protein 1, isoform b
3	1330 004 - at			MCM2 minichromosome maintenance	
1620	1E20 2E310 at	MCM2	D21063	deficient 2, mitotin (S. cerevisiae)	
2	2000			MCM3 minichromosome maintenance	
				deficient 3 (S. cerevisiae) associated	
1540	1540 40469 at	MCM3AP	AB011144	protein	KIAA0572 protein

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				MCM6 minichromosome maintenance	
				deficient 6 (MIS5 homolog, S. pombe) (S.	
1541	1541 40117_at	MCM6	D84557		HsMcm6
				Meis1, myeloid ecotropic viral integration	
1542	1542 41388_at	MEIS2	AF017418	site 1 homolog 2 (mouse)	homeobox protein MEIS2
Γ				Meis1, myeloid ecotropic viral integration	
1543	543 37486 f at	MEIS3	U68385	site 1 homolog 3 (mouse)	Meis1-related protein 2
				mel transforming oncogene (derived from	
1544	1544 35340 at	MEL	AI819948	cell line NK14)- RAB8 homolog	
				melanoma antigen, family A, 2, copy a;	
				similar to GenBank Accession Number	
1545	1545 36500_at	MAGEAZA	AF027974	L18920	melanoma antigen family A2a
1546	1546 41139_at	MAGED1	W26633	melanoma antigen, family D, 1	
1547	39327 at	D2S448	D86983	Melanoma associated gene	
				membrane cofactor protein (CD46,	membrane cofactor protein (CD46,
				trophoblast-lymphocyte cross-reactive	trophoblast-lymphocyte cross-reactive
1548	1548 38441_s_at	MCP	X59408	antigen)	antigen)
				membrane component, chromosome 11,	
1549	1549 39471 at	M11S1	<b>Z</b> 48042	surface marker 1	GPI-anchored protein p137
				membrane component, chromosome 17,	
				surface marker 2 (ovarian carcinoma	membrane component, chromosome 17,
1550	1550 33444 at	M17S2	D30756	antigen CA125)	surface marker 2
				membrane metallo-endopeptidase	
				(neutral endopeptidase, enkephalinase,	
1551	1551 1389 at	MME	J03779	CALLA, CD10)	membrane metallo-endopeptidase
				mesenchyme homeo box 2 (growth arrest-	
1552	1552 40399 r_at	MEOX2	AI743406	specific homeo box)	
				Met at bp 326 also used as initiation	
				codon in vitro; Met at bp 248 also used as	
				initiation codon in vitro; Homo sapiens	
				porin (por) mRNA, complete cds and	
155	1553 37697_s_at	bot	708666	truncated cds.	porin
155	1554 40244 s at	MPPE1	AI743654	metallo phosphoesterase	

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				and the second of the second o	
				metallothionein (MT)-like gene, n.saprens pseudogene for metallothionein and	
555	1555 31975 at		X55503		metallothionein
556	1556 39081 at	MT2A	AI547258		
1557	1557 38945 at	MTF1	X78710	metal-regulatory transcription factor 1	metal-regulatory transcription factor
1558	1558 1643 q at	MTA1	U35113		metastasis associated protein
1559	1559 35642_at	MTX2	AF053551	metaxin 2	metaxin 2
1560	1560 39342 at	MABS	X94754	methionine-tRNA synthetase	yeast methionyl-tRNA synthetase homolog
1561	1561 37619 at	METAP1	D42084		
1562	1562 41828 at	MBD1	Y10746		methyl-CpG binding protein
1563	1563 33905 at	MBD2	AF072242		methyl-CpG binding protein MBD2
1564	1564 34386_at	MBD4	AF072250		methyt-CpG binding protein MBU4
100	7.004	·		methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyletrehydrofase	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase, precursor
1262	1565 400/4_at	MINFUZ	V10030	illeurelly neurally declared cycles is a constant	
			<del> </del>	methylenetetrahydrofolate dehydrogenase	methylenetetrahydrofolate dehydrogenase methylenetetrahydrofolate dehydrogenase
		-		(NADP+ dependent),	(NADP+ dependent),
				methenyltetrahydrofolate cyclohydrolase,	methenyttetrahydrofolate cyclohydrolase,
1566	1566 674_g_at	MTHFD1	J04031	Tormynetranydrotolate synthetase	Mindigue de la
1567	1567 40105_at	MUT	M65131	methylmalonyl Coenzyme A mutase	metnyimaionyi-con mutase
L				MHC class I chain related gene B; cDNA	
				sequence deposited under GenBank	
				Accession Number X91625; Human MHC	
				class i molecule (MICB) gene, complete	
1568	1568 35937 at	MICB	U65416	cds.	MHC class I molecule
1569	1569 36535 at	MFAP1	U04209	microfibrillar-associated protein 1	associated microfibrillar protein
				microphthalmia-associated transcription	A-type microphthalmia associated
1570	1570 38228 g at	MITF	AB006909	factor	transcription factor
157	820 at	MGST2	U77604	microsomal glutathione S-transferase 2	microsomal glutathione S-transferase 2
1572	1572 38704 at	MACF1	AB007934	microtubule-actin crosslinking factor 1	KIAA0465 protein
157	335917 at	MAP1A	W26631	microtubule-associated protein 1A	
157,	1 33850 at	MAP4	W28892	microtubule-associated protein 4	

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T				ciated protein, RP/EB	
1575	1575 33456_at	MAPRE1	U24166		EB1
				microtubule-associated proteins 1A/1B	
1576	1576 39370_at	MAP1A/1BLC3	W28807		
1577	1577 34296_at	MID1	AF041210		midline 1 fetal kidney isotorm 3
1578	1578 34403_at	MFGE8	U58516		BA46
				mitochondrial ATP synthase regulatory	
1579	1579 40027 at	ATPW	W52999		
1580	1580 37174 at	MRPL19	D14660	mal protein L19	mitochondrial ribosomal protein L19
1581	37726 at	MRPL3	X06323		mitochondrial ribosomal protein L3
1582	1582 39717 g at	MRPL33	AI597616		
1583	1583 32221_at	MRPS18B	AL050361	mitochondrial ribosomal protein S18B	mitochondrial ribosomal protein S18B
1584	1584 38899 s at	MFN1	U95822		putative transmembrane GTPase
1585	1585 34369 at	MFN2	D86987		KIAA0214 protein
1586	1586 36577 at	MIG2	Z24725	mitogen inducible 2	mitogen inducible gene mig-2
1587	1587 37733 at	MAPK14	L35263	rotein kinase 14	CSaids binding protein
1588	1588 36926 at	MAPK6	X80692		p97mapk
1589	1589 38431_at	MAPK9	U09759	6	protein kinase
1590	1590 1238_at	MAPK9	U09759		protein kinase
1591	1591 1130_at	MAP2K1	L11284	-	mitogen-activated protein kinase kinase 1
L				mitogen-activated protein kinase kinase	
1592	1592 1327_s_at	MAP3K5	U67156	kinase 5	mitogen-activated kinase kinase sinase 5
				mitogen-activated protein kinase kinase	
1593	1593 36905_at	MAP3K7	AB009356	kinase 7	I GF-beta activated Kinase 1a
				mitogen-activated protein kinase kinase	
1594	1594 38980_at	MAP3K7IP2	AB018276	kinase 7 interacting protein 2	KIAA0733 protein
				mitogen-activated protein kinase kinase	•
1595	1595 35694_at	MAP4K4	AB014587	kinase kinase 4	KIAA0687 protein
				mitogen-activated protein kinase-activated	
1596	1596 36179_at	MAPKAPK2	U12779	protein kinase 2	MAP kinase activated protein kinase 2
				mitogen-activated protein kinase-activated	
1597	1597 1637_at	<b>MAPKAPK3</b>	U09578	protein kinase 3	MAPKAP kinase
1598	1598 41220_at	MSF	AB023208	MLL septin-like fusion	KIAA0991 protein
1599	1599 38437 at	MLN51	X80199	MLN51 protein	MLN51 protein

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	A	В	C	U	
				MMS19-like (MET18 homolog, S.	
1600	1600 35273_at	MMS19L	AF007151	cerevisiae)	MMS19 (MET18 S. cerevisiae)-like
<u>6</u>	1601 34767_at	MAP-1	Al670788	modulator of apoptosis 1	
1602	1602 41771 g_at	MAOA	AA420624	monoamine oxidase A	
1603	1603 41772_at	MAOA	M68840	monoamine oxidase A	monoamine oxidase A
1604	1604 41770 at	MAOA	AA420624	monoamine oxidase A	
160	1605 37628 at	MAOB	M69177		monoamine oxidase B
				ige differentiation-	monocyte to macrophage differentiation-
1606	1606 37565 at	MMD	X85750		associated, precursor
160	1607 40861 at	MRGX	D14812	MORF-related gene X	MORF-related gene X
				M-phase phosphoprotein 10 (U3 small	
1608	1608 33797 at	MPHOSPH10	X98494	nucleolar ribonucleoprotein)	M phase phosphoprotein 10
600	1609 34306_at	MBNL	AB007888	muscleblind-like (Drosophila)	muscleblind (Drosophila)-like
1610	1610 35992 at	MSC	AF087036	musculin (activated B-cell factor-1)	musculin
1611	1611 31884 at	MLH3	L40399	mutt. homolog 3 (E. coli)	mutL homolog 3
				mutS homolog 2, colon cancer,	
1612	1612 860 at	MSH2	U03911	nonpolyposis type 1 (E. coli)	mutS homolog 2
1613	1613 2003 s at	MSH6	U28946	mutS homolog 6 (E. coli)	G/T mismatch binding protein
1614	1614 33769 at	MPZL1	AF087020	myelin protein zero-like 1	protein zero related protein
				myeloid cell leukemia sequence 1 (BCL2-	myeloid cell leukemia sequence 1 (BCL2-
1615	1615 33146 at	MCL1	L08246	related)	related)
				myeloid cell leukemia sequence 1 (BCL2-	myeloid cell leukemia sequence 1 (BCL2-
1616	1616 277 at	MCL1	L08246	related)	related)
				myeloid/lymphoid or mixed-lineage	myeloid/lymphoid or mixed-lineage leukemia
				leukemia (trithorax homolog, Drosophila);	(trithorax homolog, Drosophila); translocated
1617	1617 39037_at	MLLT2	L13773	translocated to, 2	to, 2
1618	1618 41637_at	MYLE	AF108145	MYLE protein	DEXI
1619	1619 41439 at	MYO1B	AJ001381	myosin IB	myh-1c
1620	1620 35729_at	MYO1D	AB018270	myosin ID	KIAA0727 protein
1621	1621 37631_at	MYO1E	U14391	myosin IE	myosin-IC
1622	38251 at	MLC1SA	AI127424	myosin light chain 1 slow a	
1623	1623 41187_at	MLC-B	U26162	myosin regulatory light chain	myosin regulatory light chain
1624	1624 35362_at	MYO10	AB018342	myosin X	KIAA0799 protein
1625	1625 33447 at	MICB	X54304	myosin, light polypeptide, regulatory, non- sarcomeric (20kD)	myosin, light polypeptide, regulatory, non- Imyosin, light polypeptide, regulatory, non- sarcomeric (20kD)
162	1626 35739 at	MTMR3	AB002369	myotubularin related protein 3	myotubularin related protein 3
3		2	200200		

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1627	39707_at	MTMR4	AB014547		KIAA0647 protein
1628	1628 38035 at	MTMR6	AF072928		myotubularin related protein 6
1629	1629 39607 at	MTMR8	AL080178		hypothetical protein
88	1630 36692 at	MTMR8	AF052099	myotubularin related protein 8	
				myristoylated alanine-rich protein kinase C	
1631	1631 32434_at	MARCKS	D10522	substrate	80K-L protein
1632	1632 39267 at	AGM1	AF102265	N-acety/glucosamine-phosphate mutase	N-acetylglucosamine-phosphate mutase
				N-acylsphingosine amidohydrolase (acid	
1633	1633 36938_at	ASAH	U70063	ceramidase)	acid ceramidase
				N-acylsphingosine amidohydrolase (acid	
1634	1634 461_at	ASAH	U70063	ceramidase)	acid ceralindase
1635	1635 36169 at	NDUFA1	N47307	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (7.5kD, MWFE)	
				NADH dehydrogenase (ubiquinone) 1	NADH-ubiquinone oxidoreductase subunit Cl
1636	1636 40546_s_at	NDUFA2	AF047185	alpha subcomplex, 2 (8kD, B8)	B8
				NADH dehydrogenase (ubiquinone) 1	NADPH:ubiquinone oxidoreductase subunit
1637	1637 38462_at	NDUFAS	U64028	aípha subcomplex, 5 (13kD, B13)	B13
				NADH dehydrogenase (ubiquinone) 1	
1638	1638 32752_at	NDUFA7	W72440	alpha subcomplex, 7 (14.5kD, B14.5a)	
				NADH dehydrogenase (ubiquinone) 1 beta	
1639	1639 38605_at	NDUFB1	AI345944	subcomplex, 1 (7kU, MNLL)	
				NADH dehydrogenase (ubiquinone) 1 beta	
1640	1640 38981_at	NDUFB3	AA203354	subcomplex, 3 (12kD, B12)	
				NADH dehydrogenase (ubiquinone) 1 beta	NADH dehydrogenase (ubiquinone) 1 beta NADH-ubiquinone oxidoreductase subunit Ci
1641	1641 32232_at	NDUFBS	AF047181	subcomplex, 5 (16kD, SGDH)	SGDH
				NADH dehydrogenase (ubiquinone) 1 beta	
1642	1642 32774_at	NDUFB8	AI541050	subcomplex, 8 (19kD, ASHI)	
				NADH dehydrogenase (ubiquinone) 1,	
<b>5</b> 8	1643 38485_at	NDUFC1	AA760866	subcomplex unknown, 1 (6kD, KFYI)	
				NADH dehydrogenase (ubiquinone) Fe-S	
				protein 1 (75kD) (NADH-coenzyme Q	75 kDa subunit NADH dehydrogenase
<u>\$</u>	1644 38395_at	NDUFS1	X61100	reductase)	precursor
				NADH dehydrogenase (ubiquinone) Fe-S	
1645	1645 38695 at	NDUES4	AA203303	protein 4 (10kD) (NADIT-COBILEYING CA	
3	30000 at	5 500	20000		

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Γ				NADH dehydrogenase (ubiquinone) Fe-S	
				protein 5 (15kD) (NADH-coenzyme Q	
1646	1646 38060_at	NDUFS5	AI541336	reductase)	
				NADH dehydrogenase (ubiquinone)	
1647	1647 34893_at	NDUFV2	AI557064	flavoprotein 2 (24kD)	
				natriuretic peptide receptor C/guanylate	
				cyclase C (atrionatriuretic peptide receptor	
1648	1648 34519_at	NPR3	M59305	-	atrial natriuretic peptide clearance receptor
				3	
1649	1649 34234_f_at	NKTR	A1688640	cognition sequence	
1650	1650 41795_at	NCK1	X17576		NCK adaptor protein 1
1651	1651 33357 at	NCKAP1	AB011159	NCK-associated protein 1	KIAA0587 protein
1652	1652 36073 at	NON	U35139	necdin homolog (mouse)	NECDIN related protein
1653	1653 34202 at	DKFZP566B0846	846 AL050071		hypothetical protein
1654	1654 34264 at	NESCA	AB026894	nesca protein	NESCA
1655	38719 at	NSF	U03985	N-ethylmaleimide-sensitive factor	N-ethylmaleimide-sensitive factor
				neural precursor cell expressed,	
1656	1656 39356 at	NEDD4	AB007899	developmentally down-regulated 4-like	ubiquitin-protein ligase NEDD4-like
				neural precursor cell expressed,	neural precursor cell expressed,
1657	1657 40281 at	NEDDS	D63878	developmentally down-regulated 5	developmentally down-regulated 5
	1			neural precursor cell expressed,	
1658	1658 1695 at	NEDD8	D23662	developmentally down-regulated 8	ubiquitin-like protein
				neuroblastoma, suppression of	neuroblastoma, suppression of
1659	1659 37005 at	NBL1	D28124	tumorigenicity 1	tumorigenicity 1
168	1660 31896 at	NAG	AL050281	neuroblastoma-amplified protein	hypothetical protein
166	1661 37286 at	NRCAM	AB002341	neuronal cell adhesion molecule	neuronal cell adhesion molecule
				neutral sphingomyelinase (N-SMase)	
166	1662 37673 at	NSMAF	X96586	activation associated factor	FAN protein
				NGFI-A binding protein 1 (EGR1 binding	
	1663 38692 at	NAB1	AF045451	protein 1)	transcriptional regulatory protein p54
<u>&amp;</u>	1664 34835 at	NCSTN	D87442	nicastrin	
166		NNMT	U08021	nicotinamide N-methyltransferase	nicotinamide N-methyltransferase
100	44700 04	FNN	1140490	nicotinamida nucleotida transhydrogenase	nicotinamida nucleotida transhydrogenase nicotinamide nucleotide transhydrogenase
3 9	1000 71122 at		Managa	nidoden (enactin)	nidoaen
8 6	75300 at		DBEASE	nidonen 9	osteonidogen
ğ	1668 / 53_8t	NIUZ	D00463	illudgail 2	
				(	

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1669	1669 37047_at	NPC1		Niemann-Pick disease, type C1	Niemann-Pick C disease protein
1670 980	980_at	NPC1	AF002020	Niemann-Pick disease, type C1	Niemann-Pick C disease protein
1671	1671 39345_at	NPC2	AI525834	Niemann-Pick disease, type C2	
1672	1672 35153_at	NBS1	AF058696	Nijmegen breakage syndrome 1 (nibrin)	cell cycle regulatory protein p95
				NIMA (never in mitosis gene a)-related	
1673	1673 36047_at	NEK1	AL050385	kinase 1	
1674	1674 35843_at	Nek8	L40402	NIMA-related kinase Nek8	
1675	1675 40866_at	NIPSNAP1	AJ001258	nipsnap homolog 1 (C. elegans)	NIPSNAP1 protein
1676	1676 33916_at	NISCH	AB023192	nischarin	KIAA0975 protein
1677	39165_at	NFU	U47101	nitrogen fixation cluster-like	NitU-like protein
1678	1678 36472_at	IMN	U32849	N-myc (and STAT) interactor	Nmi
1679	1679 36933_at	NDRG1	D87953	N-myc downstream regulated gene 1	RTP
1680	1680 41656_at	NMT2	AF043325	N-myristoyftransferase 2	N-myristoyltransferase 2
				non-canonical ubquitin conjugating	
1681	1681 39040_at	NCUBE1	W28360	enzyme 1	
				non-canonical ubquitin conjugating	
1682	1682 39039_s_at	NCUBE1	A1557497	enzyme 1	
				non-metastatic cells 1, protein (NM23A)	
1683	1683 1521_at	NME	X17620	expressed in	Nm23 protein
				non-metastatic cells 2, protein (NM23B)	
1684	1684 33415_at	NME2	X58965	expressed in	NM23-H2 protein
				non-metastatic cells 2, protein (NM23B)	
1685	1685 1980_s_at	NME2	X58965	expressed in	NM23-H2 protein
				non-POU domain containing, octamer-	
1686	1686 38527_at	ONON	U02493	binding	54 kDa protein
1687	1687 38750_at	NOTCH3	N97669	Notch homolog 3 (Drosophila)	Notch3
1688	1688 34781_at	WS-3	D84145	novel RGD-containing protein	novel RGD-containing protein
1689	1689 40122_at	NSAP1	AF037448	NS1-associated protein 1	<b>Gry-rb</b> p
1690	1690 33752_at	NS1-BP	AB020657	NS1-binding protein	KIAA0850 protein
_				N-sulfoglucosamine sulfohydrolase	
1691	1691 35626_at	SGSH	U30894	(sulfamidase)	N-sulphoglucosamine sulphohydrolase
1692	1692 37352_at	SP100	M60618	nuclear antigen Sp100	nuclear autoantigen
1693	1693 37353_g_at	SP100	M60618	nuclear antigen Sp100	nuclear autoantigen
1694	1694 40901_at	GS2NA	U17989	nuclear autoantigen	GS2NA
1695	1695 32789_at	NCBP2	AA149428	nuclear cap binding protein subunit 2, 20kD	
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1696 35836_at h 1697 39782_at C			I	· · · · · · · · · · · · · · · · · · ·
		40,0,004	nuclear distribution gene C homolog (A. In	nuclear distribution gene C (A.nidulans) homolog
	3		NA binding protein	C1D protein
-	NDP52	U22897	nuclear domain 10 protein	NUPSZ
	NEE 21 2	S74017	nuclear factor (erythroid-derived 2)-like 2	Nrt2
				CCAAT/enhancer binding protein (C/EBP),
	CEBPB; LAP; CRI	CRIX52560		beta
			lls,	nuclear factor of activated 1-cells,
-=	NFATC3	L41067		cytoplasmic, calcineurin-dependent 3
	i	00001	nuclear factor of kappa light polypeptide	niclear factor kappa-B DNA binding subunit
1	NFKBI	MOOOLS	genie entratice in promo jak pokopatide	
	NFKB1	M58603	nuclear factor of kappa light polypopulor gene enhancer in B-cells 1 (p105)	nuclear factor kappa-B DNA binding subunit
			nuclear factor of kappa light polypeptide	nuclear factor of kappa light polypeptide
	NFKBIA	M69043	gene enhancer in B-cells inhibitor, alpha	gene enhancer in B-cells inhibitor, alpha
		X64318	nuclear factor, interleukin 3 regulated	nuclear factor, interleukin 3 regulated
		U80760	nuclear matrix transcription factor 4	CAGH1 alternate open reading frame
			nuclear phosphoprotein similar to S.	
	PWP1	L07758	cerevisiae PWP1	IEF SSP 9502
	NCOA2	AI040324	nuclear receptor coactivator 2	
	NCOA3	AF012108	nuclear receptor coactivator 3	Amplified in Breast Cancer
	NCOA4	X77548	nuclear receptor coactivator 4	Ret fused gene
	NRIP1	X84373	nuclear receptor interacting protein 1	nuclear factor RIP140
			nuclear receptor subfamily 2, group F,	
	NR2F2	M64497	member 2	apolipoprotein Al regulatory protein-1
			nuclear receptor subfamily 3, group C,	nuclear receptor subfamily 3, group C,
1713 36690 at	NR3C1	M10901	member 1	member 1
	NXF1	AJ132712	nuclear RNA export factor 1	nuclear RNA export factor 1
171537928 at	NFYB	AA621555	nuclear transcription factor Y, beta	
1716 34667 at	NFX1	U15306	nuclear transcription factor, X-box binding	NFX1
			nuclear; Homo sapiens tyrosine	
1717 33413_at	PRL-1	AF051160	phosphatase (PRL-1) gene, complete cds. lyrosine phosphatase	Infrosine prospriatase

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T				nuclease sensitive element binding protein	
718	1718 32340_s_at	NSEP1	M85234		nuclease sensitive element binding protein-
17198		NUCB2	X76732	nucleobindin 2	NEFA protein
1720	1720 36597_at	NOLCI		Spriplotein	5
1721	1721 37520 at	HSA6591	AJ006591	rich protein	cysteine-rich protein
1722	1722 36930_at	HUMAUANTIG	L05425	nucleolar GTPase	nucleolar GTPase
1723	1723 39390_at	NUP133	AF052123	nucleoporin 133kD	
1724	1724 32850_at	NUP153	Z25535	nucleoporin 153kD	nuclear pore complex protein hnup153
1725	1725 39024 at	NUP98	AF042357	nucleoporin 98kD	
1726	1726 571 at	NAP1L1	M86667	nucleosome assembly protein 1-like 1	nucleosome assembly protein 1-like 1
1727	1727 743 at	NAP1L3	D50370	nucleosome assembly protein 1-like 3	nucleosome assembly protein
1728	1728 32575 at	NAP1L4	U77456	nucleosome assembly protein 1-like 4	nucleosome assembly protein 2
1729	1729 36127 g at	NBP	U18919	nucleotide binding protein	nucleotide binding protein
				nudix (nucleoside diphosphate linked	diphosphoinositol polyphosphate
1730	1730 41584_at	NUDT3	AF062529	moiety X)-type motif 3	phosphohydrolase
1731	1731 37693 at	NUMB	L40393	numb homolog (Drosophila)	numb homolog
				ob15e02.s1 NCI_CGAP_Kid3 Homo	
				sapiens cDNA clone IMAGE:1323770 3'	
				similar to SW:ROA3_HUMAN P51991	-
				HETEROGENEOUS NUCLEAR	
				RIBONUCLEOPROTEIN A3; mRNA	
1732	35916_s_at	INHBC	AA877215	sequence.	
1733	1733 34169 s at	OCRL	U57627	oculocerebrorenal syndrome of Lowe	ocr11
				offactory receptor; Human offactory	Č C
1734	1734 31921_at	OLF3	U56421	receptor (OLTS) gene, complete cus.	
				O-linked N-acetylglucosamine (GICNAC)	
				Itansi erase (OOF-14*	
100	0000		A1 050366	acetyglucosarimie.polypoprocess	hypothetical protein
2 / S	1736 Anago at	OGER	AF109134	opioid growth factor receptor	09-Inf
1737	1737 39745 at	OPA1	AB011139	optic atrophy 1 (autosomal dominant)	KIAA0567 protein
138	1738 41744 at	OPTN	AF070533	optineurin	optineurin
				OR11-3; offactory receptor; Homo sapiens	
				OR7E12P pseudogene, complete	
1739	1739 34539 at	OR7E12P	AF065854	sequence.	

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-					7,8-diamino-pelargonic acid
1740	1740[AFFX-BioC-3_at bioA	bioA	J04423	ORF 1	aminotraristerase
					7,8-diamino-pelargonic acid
1741	1741 AFFX-BioB-M atbioA	PioA	J04423	ORF 1	aminotransferase
					7,8-diamino-pelargonic acid
1742	1742 AFEX-BioDn-5 a bioA		J04423	ORF 1	aminotransferase
					7,8-diamino-pelargonic acid
1743	1743 AFEX.BioDn.3 abioA	ApioA	J04423	ORF 1	aminotransferase
-	-2 112212 11 12				7,8-diamino-pelargonic acid
1744	1744 AFFX-BioC-5 at bioA	bioA	J04423	ORF 1	aminotransferase
				ORF; putative; Human ribosomal protein	
1745	1745 32412 at	RPS14	M13934 °	S14 gene, complete cds.	unknown protein; ribosomal protein S14
				ORF1; ORF 2; no start codon; Human	
				mRNA for ornithine decarboxylase	•
1746	1746 1315 at	OAZ1	D78361	antizyme, ORF 1 and ORF 2.	ornithine decarboxylase antizyme 1
_				ORF-2; OHF-3; Human retinoid A receptor	
1747	1747 32800_at	RXRA; NR2B1	U66306	alpha mRNA, 3' UTR, partial sequence.	retinoid X receptor, aipna
				origin recognition complex, subunit 5-like	origin recognition complex subunit 5
1748	1748 38155_at	ORCSL	U92538	(yeast)	homolog
				omithine aminotransferase (gyrate	•
1749	1749 36636_at	OAT	M12267	atrophy)	ornithine aminotransferase
		1112	00004	antitudes antitume inhibitor antitume inhibitor	entizyme inhibitor
1750	1750 1959_at	OAZIN	D886/4	סנוווווווווווווווווווווווווווווווווווו	
1751	1751 33367 s at	OAZIN	D88674	omithine decarboxylase antizyme inhibitor	antizyme inhibitor
1750	1750 1081 21	500	M33764	decarboxylase dene complete cds.	ornithine decarboxylase 1
	1001	122	15 150	omhan G protein-coupled receptor, Homo	
				sapiens G protein-coupled receptor	
175	1753 31700_at	GPR35	AF027957	(GPR35) gene, complete cds.	G protein-coupled receptor
175,	1754 1451 s at	OSF-2	D13666	osteoblast specific factor 2 (fasciclin I-like) osteoblast specific factor 2	osteoblast specific factor 2
175	1755 39774_at	OXA1L	X80695	oxidase (cytochrome c) assembly 1-like	oxidase (cytochrome c) assembly 1-like

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1756	756 39136_at	OSR1	AB017642	oxidative-stress responsive 1	oxidative-stress responsive 1
1757	1757 41438_at	L8	AL049923		oxysterol-binding protein-like protein 8
1758			N25547	9.2	
1759			U30521		P311 HUM
1760			AF010315	protein	Pig11
1761	1761 40441_g_at	BP1	AL080119	PAI-1 mRNA-binding protein	hypothetical protein
1762	1762 40440_at	1			hypothetical protein
1763	1763 32001 s at		M80482	paired basic amino acid cleaving system 4 subtilisin-like protease	subtilisin-like protease
					paired box gene 8, isoform PAX8A; paired
					box gene 8, isoform PAX8B; paired box
					gene 8, isoform PAX8C; paired box gene 8,
					isoform PAX8D; paired box gene 8, isoform
1764 121	121_at	PAX8	66969X	paired box gene 8	PAX8E
1765	1765 40127_at		M95929	paired mesoderm homeo box 1	homeobox protein
1766	1766 41191_at	992	AB023209	palladin	KIAA0992 protein
1767	1767 40504 at		AF001601	paraoxonase 2	paraoxonase
				ted by FGENES and	
1768	1768 36032_at	dJ167A19.1	AL031427		hypothetical protein
1769	1769 39243_s_at	PSIP2	U94319	PC4 and SFRS1 interacting protein 2	DFS70
1770	1770 41665_at		AB020631	PCF11p homolog	KIAA0824 protein
1771	1771 38758 at	PDAP1	R98910	PDGFA associated protein 1	
1772	1772 36937 s at	PDLIM1	U90878	PDZ and LIM domain 1 (elfin)	carboxyl terminal LIM domain protein
				PDZ domain containing guanine	PDZ domain containing guanine nucleotide
1773	1773 32026_s_at	PDZ-GEF1	AB002311	nucleotide excharige factor(GEF)1	exchange factor(GEF)1
				PDZ domain containing guanine	
1774	1774 34745_at	PDZ-GEF1	AF070570	nucleotide exchange factor(GEF)1	
				PEDF; Human pigment epithelium-derived	
1775	1775 40856_at	SERPINF1; PEDF	EDF U29953	factor gene, complete cds.	pigment epithelium-derived factor
	,,,,,	SA L		pentaxin-related gene, rapidly induced by	action of order of a contract
	1//6 1491_at	PIX3	M31186	IL-1 Deta	ותווות וופכוספוט ושכנסו
1777	1777 38465 at	PAM	M37721	peptidylglycine alpha-amidating monooxygenase	peptidylglycine alpha-amidating monooxygenase
				i i	
1778	1778 35823_at	PPIB	M63573	peptidylprolyl isomerase B (cyclophilin B)	secreted cyclophilin-like protein

K3.2

<	<b>1</b> 0	ပ	O	
1779 37422 at	DIA	S71018	peptidyprolyl isomerase C (cyclophilin C)	cyclophilin C
1780 37385 at	PPIG	U40763	clophilin G)	CARS-Cyp
1781 36829 at	PER1	AF022991	period homolog 1 (Drosophila)	Rigui
1782 35835 at	PDL-108	AB019409	protein	
				peripheral benzodiazapine receptor;
			Human peripheral benzodiazepine	peripheral benzodiazapine receptor short
1783 32806 at	BZRP: MBR: PBR	PBR M36035	ds.	form
1784 38653 at	PMP22	D11428		PMP-22(PAS-II/SR13/Gas-3)
1785 41213 at	PRDX1	X67951		peroxiredoxin 1
				Aop1_Human, MER5(Aop1_Mouse)-like
1786 36631 at	PRDX3	D49396	peroxiredoxin 3	protein
1787 38435 at	PRDX4	U25182	peroxiredoxin 4	antioxidant enzyme AOE37-2
1788 37900 at	PEX118	AF093670	peroxisomal biogenesis factor 11B	peroxisomal biogenesis factor
1789 36864 at	PEX3	AJ001625	peroxisomal biogenesis factor 3	Pex3 protein
			peroxisomal long-chain acyl-coA	peroxisomal long-chain acyl-coA
1790 36625 at	ZAP128	L40401	thioesterase	thioesterase
			peroxisomal membrane protein 3 (35kD,	,
1791 33265_at	PXMP3	M86852	Zellweger syndrome)	peroxisome assembly factor-1
1792 36502 at	PFTK1	AB020641	PFTAIRE protein kinase 1	KIAA0834 protein
1793 37694 at	PHF3	D87685	PHD finger protein 3	PHD finger protein 3
				PHD zinc linger protein XAP135, isoform a;
1794 39381_at	XAP135	AF055030	PHD zinc finger protein XAP135	PHD zinc finger protein XAP135, isoform b
	į		phosphatase and tensin homolog	COMM
1795 1434_at	T EN	082436	(mualed in muliple advanced cancers 1)	hme.2 phosphatidic acid phosphatase alpha-
1796 34797 at	PPAP2A	AF014402	phosphatidic acid phosphatase type 2A	lype-z prospriation acid prospriataso cipria
				phosphatidic acid phosphohydrolase
1797 33862_at	PPAP2B	AF017786	phosphatidic acid phosphatase type 2B	homolog
4700 40703 c ot	PIKACA	1 36151	phosphatidylinositol 4-kinase, catalytic, alpha polymentide	phosphatidylinositol 4-kinase
8 0 2			phosphaticklinositol binding clathrin	
1799 37685 at	PICALM	U45976	assembly protein	CALM

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PIGA D11466 (paroxysmal noctumal hemoglobinuria) FIGB D42138 phosphatidylinositol glycan, class B FIGB D13435 phosphatidylinositol glycan, class FIGG D13435 phosphatidylinositol glycan, class FIGH L19783 phosphatidylinositol glycan, class FIGH L20971 phosphatidylinositol glycan, class FIGH PTDSS1 D14694 phosphodiesterase E4 dunce homolog, phosphodiesterase E4 dunce homolog, phosphodiesterase B4 class phosphodiesterase B4 class PEKP D25328 phosphodiesterase B4 class PEKRP D25328 phosphodiesterase B4 class B4 class PEKRP D25328 phosphodiesterase B4 class		4	ď	ပ	O	'n
PIGA         D11466         (paroxysmal noctumal hemoglobinuria)           PIGB         D42138         phosphatidylinositol glycan, class B           PIGF         D13435         phosphatidylinositol glycan, class F           PIGF         D13435         phosphatidylinositol glycan, class F           PIGH         L19783         phosphatidylinositol glycan, class F           PIGH         L19783         phosphatidylinositol glycan, class F           PICH         D14694         phosphatidylinositol glycan, class F           PPESA         membrane-associated Phosphate 5-phosphate 6-phosphate 5-phosphate 5-phosphate 6-phosphate 5-phosphate 5-phosphate 6-phosphate 6-phospha	1					
PIGB         D42138         phosphatidylinositol glycan, class B           PIGC         D85418         phosphatidylinositol glycan, class F           PIGF         D13435         phosphatidylinositol glycan, class F           PIGF         D13435         phosphatidylinositol glycan, class F           PIGH         L19783         phosphatidylinositol glycan, class F           PIGH         L19783         phosphatidylinositol glycan, class F           PIGH         L19783         phosphatidylinositol glycan, class F           PIGH         U85245         phosphatidylinositol-4-phosphate 5-           PIDEST         D14694         phosphatidylinositol-4-phosphate 5-           PPDEST         D14694         phosphatidylinositol-4-phosphate 5-           PDEADIP         D14694         phosphatidylinositol-4-phosphate 5-           PDEADIP         AB007923         phosphodiesterase B4 clurce homolog, choosphate 6- phosphodiesterase B4 clurce homolog, choosphate 6- phosphodiesterase B4 clurce homolog, choosphate 6- phosphodiesterase B4 clurce carboxykinase 2           R         PCKZ         X92720         (mitochondrial)           R         PGM1         W83088         phosphodiesterase B4 clurce homolog, choosphate 6- phosphodiesterase B4 clurce carboxykinase 6- phosphodiesterase B4 clurce choosphate 6- phosphodiesterase B4 clurce choosphate 6- phosphodiesterase B4 clurce choosphate 6- phosphodiesterase B4 cl	1800	39993 at	PIGA			PIG-A protein
PIGC D85418 phosphatidylinositol glycan, class C PIGF D19435 phosphatidylinositol glycan, class F PIGH L19783 phosphatidylinositol glycan, class F Phosphatidylinositol glycan gl	Ē	314 at	PIGB			PIG-B
at PIGC D13435 phosphatidylinositol glycan, class F PIGH L19783 phosphatidylinositol glycan, class F PIGH D14694 phosphatidylinositol glycan, class F Rivase, type II, beta PIGH D14694 phosphatidylinositol glycan, class F Rivase, type II, beta PIGH PIGH POEAB L20971 phosphodiesterase E4 dunce homolog, phosphodiesterase E4 du						phosphatidylinositol-alycan-class C (PIG-C)
PiGF   D13435   Phosphatidylinositol gycan, class   PiGH   L19783   Phosphatidylinositol gycan, class   Phosphatidylinositol gycan   Phosphatidylinositol gycan   Phosphatidylian gycan	1802	/51_aī	Pigo			1 30
29_at         PIGH         L19783         phosphatidylinositol glycan, class H           97_at         PITDM         X9854         membrane-associated           41_at         PITDNS         U85245         membrane-associated           41_at         PIDSS1         U14694         phosphatidylinositol 4-phosphate 5-phosphatidylisenine synthase 1           20_at         PTDSS1         D14694         phosphatidylisenine synthase 1           20_at         PTDSS1         D14694         phosphatidylsenine synthase 1           20_at         PDE4B         L20971         Drosophila)           05_at         PDE4B         L20971         Drosophila)           77_at         PDE4DIP         AF056490         phosphodiesterase 4B interacting protein           75_at         PDE4DIP         AF056490         phosphodiesterase 4B interacting protein           75_at         PCKZ         X92720         (mitochondrial)           75_at         PCKZ         X92720         phospholiusterase 8A           10_at         PCKZ         X92720         (mitochondrial)           75_at         PCKZ         X92720         (mitochondrial)           88_at         PCKZ         X92720         (mitochondrial)           865_at         PIKST <td>1803</td> <td></td> <td>PIGF</td> <td></td> <td></td> <td></td>	1803		PIGF			
PITPNIM X98654 membrane-associated phosphatidylinositol transfer protein, membrane-associated phosphatidylinositol-4-phosphate 5- PTDSS1 D14694 phosphatidylserine synthase 1 PTDSS1 D14694 phosphodiesterase E4 dunce homolog, phosphodiesterase E4 dunce homolog, Drosophila) phosphodiesterase E4 dunce homolog, Drosophila) phosphodiesterase E4 dunce homolog, phosphodiesterase E4 dunce homolog, phosphodiesterase E4 dunce homolog, CMC DDE8A AF056490 phosphodiesterase BA phosphodiesterase BA phosphodiesterase BA phosphodiosterase BA pho	1804	40629 at	PIGH	L19783		phosphatidylinositol glycan, class n
PITPNIM X98654 membrane-associated phosphatidylinositol-4-phosphate 5- phosphatidylinositol-4-phosphate 5- kinase, type II, beta PTDSS1 D14694 phosphodiesterase 4B, cAMP-specific phosphodiesterase E4 dunce homolog, phosphodiesterase E4 dunce homolog, Drosophila) phosphodiesterase E4 dunce homolog, CMMP-specific Drosophila) Dro						homologue of Drosphila retinal degeneration
PIP5K2B U85245 kinase, type II, beta phosphatidylinositol-4-phosphate 5- kinase, type II, beta phosphatidylserine synthase 1 phosphatidylserine synthase 2 phosphatidylserines E4 dunce homolog, (phosphatiesterase E4 dunce homolog, (phosphatiase  E4 phosphatiase E4 dunce homolog, (phosphatiase) E4 phosphatiase Homology, (phosphatiase) E4 phosphatiase E4 phosphatiase Homology, (phosphatiase) E4 phosphatiase Homology, (phosphatiase) E4 phosphatiase Homology, (phosphatiase) E4 phosphatiase E4 phosphatiase) E4 phosphatiase Homology, (phosphatiase) E4 phosphatiase E4 phosphatiase) E4 phosphatiase E4 dunce homology, (phosphatiase) E4 phosphatiase E4 dunce homology, (phosphatiase) E4 dunce homology, (phosphatiase) E4 dunce homology, (phosphatiase) E4 dunce homology, (phosphatiase) E4 dunc	1805	38297 at	PITPNM	X98654		B gene
PIP5K2B U85245 kinase, type II, beta phosphatidylserine synthase 1 phosphatidylserine synthase 2 phosphatidylserine synthase 2 phosphatidylserine synthase 2 phosphatidylserine set 4 dunce homolog, phosphatidisterase E4 dunce homolog, phosphatide Strainse I phosphatidisterase E4 dunce homolog, phosphatidise I (prair) phosph						phosphatidylinositol-4-phosphate 5-kinase
PTDSS1 D14694 phosphatidylserine synthase 1 phosphodiesterase 4B, cAMP-specific phosphodiesterase E4 dunce homolog, pDE4B L20971 Drosophila) phosphodiesterase AD interacting protein phosphodiesterase 4B, cAMP-specific phosphodiesterase 4B, cAMP-specific phosphodiesterase AD interacting protein phosphodiesterase 8A phosphodiesterase 8A phosphodiesterase 8A phosphodiesterase 8A phosphodiesterase 8A phosphodiecterase 8A phosphodicomutase 1 pGM1 M83088 phosphodirocomutase 1 pGM2 V2025 phosphodirocomutase 1 pGAM1 J04173 phosphodicomate dehydrogenase phosphodirocomitase 1 (brain) phosphomiositide-3-kinase, regulatory phosphomiositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha) phosphomiositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma) at PLSCR1 AB006746 phosphoriosin enriched in astrocytes 15 phosphoribosyl pyrophosphate synthetase phosphoribosyl pyrophosphate synthetase	1806	35741 at	PIP5K2B	U85245	kinase, type II, beta	type II beta
PDE4B L20971 Drosophials) PDE4B L20971 Drosophials) PDE4DIP AB007923 (myomegalin) PDE8A AF056490 phosphodiesterase 8A phosphodiesterase 1 phosphodiesteramblase 1 phosphodiest	1807	37320 at	PTDSS1	D14694	phosphatidylserine synthase 1	phosphatidylserine synthase 1
PDE4B   L20971   Drosophila					phosphodiesterase 4B, cAMP-specific	
PDE4B       L20971       Drosophila)         PDE4DIP       AB007923       (myomegalin)         PDE8A       AF056490       phosphodiesterase 8A         PDE8A       AF056490       phosphodiesterase 8A         PCK2       X92720       (mitochondrial)         PCK2       X92720       (mitochondrial)         PGM1       M83088       phosphofiructokinase 1 platelet         PGM1       M83088       phosphofiructokinase 1 platelet         PGM1       V00572       phosphofiructokinase 1 platelet         PGAM1       J04173       phosphoglycerate kinase 1         PRAM1       J04173       phosphoglycerate kinase 1         PIK3R1       M61906       subunit, polypeptide 1 (p85 alpha)         PRSR1       AB006746       phosphoinositide-3-kinase, regulatory         PLSCR1       AB006746       phosphoinositide-3-kinase, regulatory         R       PLSCR1       AB006746       phosphoinositide-sulation enriched in astrocytes 15         Phosphoriositide					(phosphodiesterase E4 dunce homolog,	
PDE4DIP AB007923 (myomegalin) PDE8A AF056490 phosphodiesterase 8A phosphodiesterase 8A phosphodiesterase 8A phosphodiesterase 8A phosphoenolpyruvate carboxykinase 2 phosphoenolpyruvate carboxykinase 2 phosphoenolpyruvate carboxykinase 2 phosphofurctokinase 1 phosphofurctokinase 1 phosphofurctokinase 1 phosphoglucomutase 1 phosphoglucomate dehydrogenase platelet phosphoglucomate dehydrogenase 1 phosphoinositide-3-kinase 1 (pass 3 phosphoinositide-3-kinase, regulatory phosphoinositide-3-kinase, regulatory phosphoinositide-3-kinase, regulatory phosphoinositide-3-kinase, regulatory phosphoinositide-3-kinase, regulatory phosphoinositide 3 (p55, gamma) phosphoinositide 3 (p55, gamma) phosphoinositide 3 (p55, gamma) phosphoprotein enriched in astrocytes 15 phosphoribosyl pyrophosphate synthetase phosphoribosyl pyrophosphate synthetase 1 phosphoribosyl pyrophosphate synthetase	1808	33705 at	PDE4B	170971	Drosophila)	phosphodiesterase
PDE4DIP     AB007923     (myomegalin)       PDE8A     AF056490     phosphodiesterase 8A       PDE8A     AF056490     phosphodiesterase 8A       PCK2     X92720     (mitochondrial)       PCK2     X92720     (mitochondrial)       PGM1     M83088     phosphoglucomutase 1       PGM1     U30255     phosphoglycerate kinase 1       PGM1     J04173     phosphoglycerate kinase 1       PGAM1     J04173     phosphoglycerate mutase 1 (brain)       PIK3R1     M61906     phosphoinositide-3-kinase, regulatory       PIK3R1     M61906     subunit, polypeptide 1 (p85 alpha)       PPK3R3     U90907     subunit, polypeptide 3 (p55, gamma)       at     PLSCR1     AB006746     phosphoinositide-3-kinase, regulatory       phosphoinositide-3-kinase, regulatory     phosphoinositide-3-kinase, regulatory       pthosphoinositide-3-kinase, regulatory     phosphoinositide-3-kinase, regulatory       pthosphoinositide-3-kinase, regulatory     phosphoinositide-3-kinase, regulatory       pthosphoinositide-3-kinase, regulatory     phosphoinositide-3-kinase, regulatory       pthosphoinositide-3-kinase, regulatory     phosphoinositide-3-kinase, regulatory       pthosphorotein enriched in astrocytes 15     phosphorotein enriched in astrocytes 15       phosphorotein enriched in astrocytes 15     phosphorotein enriched in as					phosphodiesterase 4D interacting protein	
PDE8A AF056490 phosphodiesterase 8A phosphoenolpyruvate carboxykinase 2 phosphofuctokinase, platelet pGM1 D25328 phosphoglucomate dehydrogenase phosphoglucomate dehydrogenase phosphoglycerate kinase 1 phosphoglycerate mutase 1 (brain) phosphoinositide-3-kinase, regulatory plik3R1 M61906 subunit, polypeptide 1 (p85 alpha) phosphoinositide-3-kinase, regulatory plik3R3 U90907 subunit, polypeptide 3 (p55, gamma) phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma) phosphoinositide-3-kinase, regulatory plik3R3 AB006746 phosphoinositide-3-kinase, regulatory phosphoinositide-3-kinase, regulatory phospholipid scramblase 1 phosphoribosyl pyrophosphate synthetase phosphoribosyl pyrophosphate synthetase 1 phosphoribosyl pyrophosphate synthetase 1 phosphoribosyl pyrophosphate synthetase 1 phosphoribosyl pyrophosphate synthetase	1809	39422 at	PDE4DIP	AB007923	(myomegalin)	KIAA0454 protein
PCK2 X92720 (mitochondrial) PFKP D25328 phosphofructokinase, platelet PGM1 M83088 phosphoglucomutase 1 PGM1 M83088 phosphoglucomutase 1 PGM1 V00572 phosphoglucomate dehydrogenase PGAM1 J04173 phosphoglycerate kinase 1 PGAM1 J04173 phosphoglycerate mutase 1 (brain) PIK3R1 M61906 phosphoinositide-3-kinase, regulatory physphoinositide-3-kinase, regulatory phosphoinositide-3-kinase, regulatory	181	37676 at	PDE8A	AF056490	phosphodiesterase 8A	cAMP-specific phosphodiesterase 8A
PCK2       X92720       (mitochondrial)         PFKP       D25328       phosphofructokinase, platelet         PGM1       M83088       phosphoglucomutase 1         PGD       U30255       phosphoglucomate dehydrogenase         PGAN       V00572       phosphoglycerate kinase 1         PGAM1       J04173       phosphoglycerate kinase 1         PGAM1       J04173       phosphoglycerate kinase 1         PIK3C3       Z46973       phosphoinositide-3-kinase, regulatory         PIK3R1       M61906       subunit, polypeptide 3-kinase, regulatory         PIK3R3       U90907       subunit, polypeptide 3 (p55, gamma)         phosphoinositide-3-kinase, regulatory       subunit, polypeptide 3 (p55, gamma)         phosphoinositide-3-kinase, regulatory       phosphoinositide-3-kinase, regulatory         phosphoinositide-3-kinase, regulatory       phosphoinositide-3-kinase, reg		2000			phosphoenolpyruvate carboxykinase 2	
PFKP   D25328   PGM1   M83088   PGM1   U30255   PGD   U30255   PGK1   V00572   PGAM1   J04173   PIK3R3   Z46973   PIK3R1   M61906   PIK3R1   M61906   PLSCR1   AB006746   PLSCR1   X86809   PRPS1   D00860   PRPS1   D00860   PGM1	1811	37188 at	PCK2	X92720	(mitochondrial)	phosphoenolpyruvate carboxykinase (GTP)
PGM1   M83088   PGD   U30255   PGK1   V00572   PGAM1   J04173   PIK3C3   Z46973   PIK3R1   M61906   PIK3R1   M61906   PLSCR1   AB006746   PLSCR1   X86809   PRPS1   D00860	1812	39175 at	PFKP	D25328	phosphofructokinase, platelet	platelet-type phosphofructokinase
PGD         U30255           PGK1         V00572           PGAM1         J04173           PIK3C3         Z46973           PIK3R1         M61906           R         PIK3R3         U90907           R         PLSCR1         AB006746           R         PEA15         X86809           R         PRPS1         D00860	1813	32210 at	PGM1	M83088	phosphoglucomutase 1	phosphoglucomutase 1
PGK1         V00572           PGAM1         J04173           PIK3C3         Z46973           PIK3R1         M61906           R         PIK3R3         U90907           R         PLSCR1         AB006746           R         PEA15         X86809           R         PRPS1         D00860	1814	36963 at	PGD	U30255	phosphogluconate dehydrogenase	phosphogluconate dehydrogenase
PGAM1         J04173           PIK3C3         Z46973           PIK3R1         M61906           at         PLSCR1         AB006746           r         PEA15         X86809           r         PRPS1         D00860	1815	37677 at	PGK1	V00572	phosphoglycerate kinase 1	phosphoglycerate kinase 1
PIK3R3   Z46973   PIK3R1   M61906	1816	41221 at	PGAM1	J04173	phosphoglycerate/mutase 1 (brain)	phosphoglycerate mutase 2
PIK3R1 M61906	1817	35665 at	PIK3C3	Z46973	phosphoinositide-3-kinase, class 3	phosphatidylinositol 3-kinase
at PRPS1 N61906  at PLSCR1 AB006746  at PEA15 X86809  at PRPS1 D00860					phosphoinositide-3-kinase, regulatory	
PIK3R3 U90907 PLSCR1 AB006746 PEA15 X86809 PRPS1 D00860	1818	1269_at	PIK3R1	M61906	Subunit, polypeptide I (pos aipila)	
PLSCR1					phosphoinositide-3-kinase, regulatory	
PLSCR1 AB006746 PEA15 X86809 PRPS1 D00860	1819	37961_at	PIK3R3	U90907	subunit, polypeptide 3 (p55, gamma)	
PEA15 X86809 PRPS1 D00860	182	32775_r_at	PLSCR1	AB006746	phospholipid scramblase 1	phospholipid scramblase I
PRPS1 D00860	5	1200CC	PEA15	X86809	phosphoprotein enriched in astrocytes 15	
PRPS1 D00860	3				phosphoribosyl pyrophosphate synthetase	phosphoribosyl pyrophosphate synthetase
	182	2 36489_at	PRPS1	D00860		subunit I

Fig. &

phosphoribosyl pyrophosphate synthetase- phosphoribosyl pyrophosphate synthetase- associated protein 1 phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole X84908 phosphorylase, glycogen; brain phylanoyl-CoA hydroxylase (Refsum disease) U77718 phylanoyl-CoA hydroxylase (Refsum disease) phosphorylase, glycogen; brain phylanoyl-CoA hydroxylase (Refsum disease) D177718 phylanoyl-CoA hydroxylase (Refsum disease) protein phultary tumor-transforming 1 interacting protein phylanoyl-CoA hydroxylase (Refsum disease) platelet-activating factor acetylhydrolase, platelet-activating factor acetylhydrolase, platelet-activating factor receptor, alpha polypeptide pleckstrin homology, Sec7 and coiled/coil domains 1 (cytohesin 1) pleckstrin homology, Sec7 and coiled/coil domains 2 (cytohesin 2) AR002313 pleixin C1 AR00339 plexin C1 AR00339 plexin C1 AR005043 poly(ADP-ribose) glycohydrolase AJ005698 (deadenylation nuclease) AL005698 (deadenylation nuclease) X78136 poly(C) binding protein 2 X78136 poly(C) binding protein 2 AL046394 poly(C) binding protein 3	ŀ					
PRPSAP1 D61391 phosphoribosyl pyrophosphate synthetase- associated protein 1 phosphoribosylaminoimidazole carboxylase, PHKB X84908 phosphoribosylaminoimidazole pPKGB U47025 phosphoribosylaminoimidazole pPKGB U47025 phosphoribosylaminoimidazole pPKGB U47025 phosphoribosylaminoimidazole pPKGB U47025 phosphoribosylaminoimidazole at PLS3 M22299 pinin, desmosome associated protein plytanoyl-CoA hydroxylase (Refsum plytanoylase))  to PAFAH1B1 L13385 isoform ib, alpha subunit (45kD)  to PAFAH1B1 L13385 isoform ib, alpha		∢	œ	ပ		<b>u</b>
PRPSAP1 D61391 associated protein 1  Carboxylases phosphoribosylaminolimidazole phosphoribase kinase, beta phosphoribase kinase kinase, beta phosphoribase kinase phosphoribase kinase, beta phosphoribase kinase,	T				phosphoribosyl pyrophosphate synthetase-	phosphoribosypyrophosphate synthetase-
PAICS X53793 succinocarboxamide synthetase carboxylase, phosphoribosylaminoimidazole carboxylase, phosphorylase kinase, beta phosphorylase, glycogen; brain phytanoyl-CoA hydroxylase (Relsum disease)  PHYH AF023462 phosphorylase, glycogen; brain at PLS3 M22299 plastin 3 (T isoform)  PAFAH1B1 L13385 plotein apha subunit (45kD) platelet-activating factor acetylhydrolase, isoform ib, alpha subunit (45kD) platelet-activating factor acetylhydrolase, isoform ib, alpha subunit (45kD) platelet-activating factor acetylhydrolase, isoform ib, alpha subunit (45kD) alpha phosphorylase, isoform ib, alpha subunit (45kD) platelet-activating factor acetylhydrolase, isoform ib, alpha subunit (45kD) at alpha phosphorylase, isoform ib, alpha subunit (45kD) and coiled/coil domains 2 (cytohesin-2) at PABPC1 V00345 poly(A) binding protein, cytoplasmic 1 poly(A), specific ribonuclease poly(C) binding protein 2 at PCBP2 X78136 poly(C) binding protein 3 at PCBP2 A78136 poly(C) binding protein 3 at PCBP2 A78138 poly(C) binding protein 3 at PCBP2 A78138 poly(C) binding protein 3	1823	37338_at	PRPSAP1	D61391		associated protein 39
PAICS X53793 succinocarboxamide synthetase PHKB X84908 phosphorybase kirase, beta PHKB X84908 phosphorybase kirase, beta PHKB UA7025 phosphorybase kirase, beta PHKB UA7025 phosphorybase kirase, beta PHKB UA7025 phosphorybase glycogen; brain PHYH AP023462 disease)  at PLS3 M22299 pintin, desmosome associated protein phytanoyl-CoA hydroxylase (Relsum dividence of the phosphorybase glycogen; brain phytanoyl-CoA hydroxylase (Relsum dividence of the protein phytanoyl-CoA hydroxylase (Relsum dividence of the phytanoyl-CoA hydroxylase) dividence of the phytanoyl-CoA hydroxylase (Relsum domains 1 (cytohesin-2) dividence of the phytanoyle adenoma gene-like 1 deadenylation nuclease) deadenylation nuclease) deadenylation nuclease) deadenylation nuclease) deadenylation nuclease) deadenylation nuclease deadenylation nuclease deadenylation nuclease deadenylation protein 2 deadenylation protein 3 deadenylation protein 3 deadenylation protein 3 deadenylation protein 3	T				phosphoribosylaminoimidazole	•
PAICS X53793 succinocarboxamide synthetisse PHKB X84908 phosphorylase kinase, beta PHKB X84908 phosphorylase kinase, beta PHKB V84908 phosphorylase kinase, beta PHYH AF023462 disease) at PNN U77718 pinin, desmosome associated protein phytanoyl-CoA hydroxylase (Relsum disease) at PLK3 M22299 pinin, desmosome associated protein phytanoyl-CoA hydroxylase (Relsum phytanoyl-CoA hydroxylase (Relsum disease) plutiary tumor-transforming 1 interacting pituitary tumor-transforming 1 interacting plastin 3 (T isoform) plastin 3 (T isoform) the PAFAH1B1 L13385 isoform ib, alpha subunit (45kD) plackstrin homology, Sec7 and coiled/coil domains 1 (cytohesin-2) at PLAGL1 U81992 pleiomorphic adenoma gene-like 1 at PLAGL1 U81992 pleiomorphic adenoma gene-like 1 at PABPC1 AF030339 plexin B2 at PABPC1 A65013 poly (ADP-ribose) glycohydrolase at PABPC1 Y00345 poly (ADP-ribose) glycohydrolase at PCBP1 Z29505 poly(C) binding protein 1 at PCBP2 X78136 poly(C) binding protein 2 at PCBP2 A78136 poly(C) binding protein 3 at PCBP2 A78136 poly(C) binding protein 3 at PCBP2 A78136 poly(C) binding protein 3 at PCBP2 A78136						phosphoribosylaminoimidazole carboxylase,
PAICS X53793 succinocarboxamide synthetase PHKB X84908 phosphorylase kinase, beta PYGB U47025 phosphorylase, glycogen; brain PYGB U47025 phosphorylase, glycogen; brain PHYH AF023462 disease)  at PLK3 M22299 pituin, desmosome associated protein pituitary tumor-transforming 1 interacting protein PTG1IP Z50022 protein  at PLK3 M22299 plastin 3 (T isoform)  PDGFRA M21574 alpha subunit (45kD)  t PSCD1 M85169 plestin homology, Sec7 and coiled/coil pleckstrin homology, Sec7 and coiled/coil domains 1 (cytohesin 1)  PECD2 U70728 domains 2 (cytohesin 1)  PLKNB2 AB002313 pleckstrin homology, Sec7 and coiled/coil domains 2 (cytohesin 2)  at PLKNB2 AB002313 pleckstrin homology, Sec7 and coiled/coil domains 2 (cytohesin 2)  at PARRG AF005043 poly (ADP-ribose) glycohydrolase  the PABPC1 X48501 poly(A) binding protein, cytoplasmic 1  PARR AJ005698 (deadenylation nuclease)  at PCBP2 X78136 poly(C) binding protein 2  at PCBP2 X78136 poly(C) binding protein 2  at PCBP2 X78136 poly(C) binding protein 3  at PCBP3 AL04534 poly(C) binding protein 3	-					phosphoribosylaminoribosylaminoimidazole
PHKB         X84908         phosphorylase kinase, beta           PYGB         U47025         phosphorylase glycogen; brain           PHYH         AF023462         disease)           at         PHYH         AF023462         disease)           phytanoyl-CoA hydroxylase (Relsum of Interacting protein         phrint, desmosome associated protein           ptt         PTG1IP         Z50022         pinin, desmosome associated protein           ptt         PLS3         M22299         pinin, desmosome associated protein           ptt         PLS3         M22299         platelet-activating factor acetylhydrolase, protein           ptt         PLS3         M22299         platelet-derived growth factor receptor, apha subunit (45kD)           ptt         PLS3         M21574         platelet-derived growth factor receptor, apha subunit (45kD)           ptt         PCD4         M21574         platelet-derived growth factor receptor, apha subunit (45kD)           ptt         PCD5         U70728         platelet-derived growth factor receptor, apha subunit (45kD)           ptt         PLXMD2         M85169         pleckstrin homology, Sec7 and coiled/coil           ptt         PLXMD2         AB002333         pleckstrin homology, Sec7 and coiled/coil           ptt         PLXNC1         AF005043	1824	39056 at	PAICS	X53793	•	succinocarboxamide synthetase
PYGB U47025 phosphorylase, glycogen; brain phytanoyl-CoA hydroxylase (Refsum phytanoyl-CoA hydroxylase (Refsum phytanoyl-CoA hydroxylase (Refsum phytanoyl-CoA hydroxylase (Refsum D17718 pinin, desmosome associated protein prutiary tumor-transforming 1 interacting platelet-activating factor acetylhydrolase, isoform lb, alpha subunit (45kD) platelet-activating factor acetylhydrolase, isoform lb, alpha subunit (45kD) platelet-derived growth factor receptor, alpha polypeptide platelet-derived growth factor receptor, alpha polyces in the platelet activating factor acetylhydrolase, at PCBPC AF030339 plexin C1	1825	37392 at	PHKB	X84908		phosphorylase kinase
at PHYH AF023462 disease)  at PNN U77718 pinin, desmosome associated protein pitutiary tumor-transforming 1 interacting pitutiary tumor-transforming 1 interaction pitutiary tumor-transforming pitutiary tumor-transforming 1 interaction pitutiary tumor-transforming pitutiary tumor-transforming pitutiary tumor-transforming protein, cytoplasmic 1 poly(A) binding protein 1 poly(A) binding protein 2 z29505 poly(C) binding protein 3 at PCBP2 x78136 poly(C) binding protein 3 at PCBP3 AL046394 poly(C) binding protein 3	1826	36667 at	PYGB	U47025	phosphorylase, glycogen; brain	glycogen phosphorylase B
PHYH AF023462 disease)  PHYH DY7718 pinin, desmosome associated protein pituitary tumor-transforming 1 interacting protein pro					phytanoyl-CoA hydroxylase (Refsum	peroxisomal phytanoyl-CoA alpha-
PTG1IP Dituitary tumor-transforming 1 interacting protein prot	1827	32724 at	РНҮН	AF023462	disease)	hydroxylase
PTTG1IP Z50022 protein priuitary tumor-transforming 1 interacting protein PLS3 M22299 plastin 3 (T isoform)  PLS3 M22299 plastin 3 (T isoform)  PAFAH1B1 L13385 isoform lb, alpha subunit (45kD)  platelet-activating factor acetyfhydrolase, isoform lb, alpha subunit (45kD)  platelet-derived growth factor receptor, alpha polypeptide pleckstrin homology, Sec7 and coiled/coil domains 1 (cytohesin 1)  PCD2 U70728 domains 2 (cytohesin 1)  PLAGL1 U81992 pleiomorphic adenoma gene-like 1  PLXNB2 AF030339 plexin B2 ' PABPC1 AF030339 plexin	1828	33543 s at	PNN	U777718	pinin, desmosome associated protein	pinin
PTTG1IP         Z50022         protein           PLS3         M22299         plastin 3 (T isoform)           PLS3         M22299         platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit (45kD)           PAFAH1B1         L13385         isoform Ib, alpha subunit (45kD)           PDGFRA         M21574         alpha polypeptide           PCD1         M85169         domains 1(cytohesin 1)           PCD2         U70728         domains 2 (cytohesin 2)           PLAGL1         U81992         pleickstrin homology, Sec7 and coiled/coil           PLAGL1         U81992         pleickstrin homology, Sec7 and coiled/coil           PLAGL1         U81992         pleickstrin homology, Sec7 and coiled/coil           PLXNB2         AB002313         pleickstrin homology, Sec7 and coiled/coil           PLXNB2         AB002313         pleickstrin homology, Sec7 and coiled/coil           PLXNB2         AB002313         pleicmorphic adenoma gene-like 1           PLXNC1         AF030339         pleicmorphic adenoma gene-like 1           PABPC1         AF030339         pleixin C1           PABPC1         Y00345         poly (ADP-ribose) glycohydrolase           PCBP1         X78136         poly(A) binding protein 2           PCBP2         X78136					pituitary tumor-transforming 1 interacting	
PLS3 M22299 plastin 3 (T isoform)  PAFAH1B1 L13385 isoform lb, alpha subunit (45kD)  PDGFRA M21574 alpha pohyaptide  PDGFRA M21574 alpha pohyaptide  PCD1 M85169 domains 1(cytohesin 1)  PCD2 U70728 domains 2 (cytohesin 2)  PLAGL1 U81992 pleiomorphic adenoma gene-like 1  PLXNC1 AR002313 plexin B2 '  PLXNC1 AF030339 plexin C1  PABC1 Z48501 pohy(A) binding protein, cytoplasmic 1  PABR AJ005698 (deadenylation nuclease)  PCBP1 Z29505 pohy(C) binding protein 1  PCBP2 X78136 pohy(C) binding protein 2  PCBP3 AL046394 pohy(C) binding protein 3	1829	39003 at	PTTG11P	Z50022	protein	putative surface glycoprotein
PAFAH1B1 L13385 isoform lb, alpha subunit (45kD) PDGFRA M21574 alpha pohypeptide PSCD1 M85169 pleckstrin homology, Sec7 and coiled/coil PSCD2 U70728 domains 1 (cytohesin 1) PLXNB2 AB002313 pleckstrin homology, Sec7 and coiled/coil PLXNC1 AF030339 plexin C1 PLXNC1 AF030339 plexin C1 PABPC1 Z48501 pohy(A) binding protein, cytoplasmic 1 PABPC1 Z29505 pohy(C) binding protein 1 PCBP1 Z29505 pohy(C) binding protein 1 PCBP2 X78136 pohy(C) binding protein 2 PCBP3 AL046394 pohy(C) binding protein 3	1830 30	34793 s at	PLS3	M22299	plastin 3 (T isoform)	T-plastin polypeptide
PAFAH1B1 L133B5 isoform lb, alpha subunit (45kD)  PDGFRA M21574 alpha pohypeptide  PCD1 M85169 domains 1 (cytohesin 1)  PSCD1 M85169 domains 2 (cytohesin 1)  PSCD2 U7072B domains 2 (cytohesin-2)  PLXNB2 AB002313 plexin homology, Sec7 and coiled/coil  PLXNC1 AF030339 plexin C1  PLXNC1 AF030339 plexin C1  PABPC1 Z48501 pohy(A) binding protein, cytoplasmic 1  PABPC1 Y00345 pohy(A) binding protein, cytoplasmic 1  PABPC1 Y00345 pohy(A) binding protein, cytoplasmic 1  PABPC1 Z29505 pohy(C) binding protein 1  PCBP1 Z29505 pohy(C) binding protein 2  at PCBP2 X78136 pohy(C) binding protein 2  at PCBP3 AL046394 pohy(C) binding protein 3						
PAFAH1B1 L13385 isoform lb, alpha subunit (45kD)  PDGFRA M21574 alpha polypeptide PDGFRA M21574 alpha polypeptide PSCD1 M85169 domains 1 (cytohesin 1) PSCD2 U70728 domains 2 (cytohesin-2) PSCD2 U70728 domains 2 (cytohesin-2) PLXNB2 AB002313 plexin B2 ' PLXNB2 AB002313 plexin B2 ' PLXNC1 AF030339 plexin C1 PABPC1 Z48501 poly(A) binding protein, cytoplasmic 1 PABPC1 Z48501 poly(A) binding protein, cytoplasmic 1 PABPC1 Z29505 poly(C) binding protein 1 PCBP1 Z29505 poly(C) binding protein 1 PCBP2 X78136 poly(C) binding protein 2 at PCBP2 X78136 poly(C) binding protein 2 at PCBP3 AL046394 poly(C) binding protein 3					platelet-activating factor acetylhydrolase,	
PDGFRA M21574 alpha polypeptide PSCD1 M85169 domains 1 (cytohesin 1) PSCD2 U70728 domains 2 (cytohesin-2) PSCD2 U70728 domains 2 (cytohesin-2) PLXNB2 AB002313 plexin B2 ' PLXNB2 AB002313 plexin B2 ' PLXNC1 AF030339 plexin B2 ' PLXNC1 AF030339 plexin C1 PABPC1 Z48501 poly(A) binding protein, cytoplasmic 1 PABPC1 Z48501 poly(A) binding protein, cytoplasmic 1 PABPC1 Z29505 poly(C) binding protein 1 PCBP1 Z29505 poly(C) binding protein 1  R PCBP2 X78136 poly(C) binding protein 2 at PCBP2 X78136 poly(C) binding protein 2 at PCBP3 AL046394 poly(C) binding protein 3	1831	32569_at	PAFAH1B1	L13385	isoform lb, alpha subunit (45kD)	Miller-Dieker lissencephaly protein
PDGFRA   M21574   alpha polypeptide					platelet-derived growth factor receptor,	platelet-derived growth factor receptor A
PSCD1   M85169   pleckstrin homology, Sec7 and coiled/coil at PSCD2   U70728   domains 1(cytohesin 1)	1832	1731 at	PDGFRA	M21574	alpha polypeptide	chain
PSCD1   M85169   domains 1 (cytohesin 1)					pleckstrin homology, Sec7 and coiled/coil	cytohesin 1, isoform 1; cytohesin 1, isoform
at         PSCD2         U70728         domains 2 (cytohesin-2)         ofference of the control	1833	38666 at	PSCD1	M85169	domains 1(cytohesin 1)	2
at         PSCD2         U70728         domains 2 (cytohesin-2)           at         PLAGL1         U81992         pleiomorphic adenoma gene-like 1           PLXNB2         AB002313         plexin B2         '           PLXNC1         AF030339         plexin C1           PLXNC1         AF005043         poly (ADP-ribose) glycohydrolase           at         PABPC1         Z48501         poly(A) binding protein, cytoplasmic 1           PABPC1         Y00345         poly(A) binding protein, cytoplasmic 1           PARN         AJ005698         (deadenylation nuclease)           PCBP1         Z29505         poly(C) binding protein 1           at         PCBP2         X78136         poly(C) binding protein 2           pCBP3         AL046394         poly(C) binding protein 3		3			pleckstrin homology, Sec7 and coiled/coil	
at         PLAGL1         U81992         pleiomorphic adenoma gene-like 1           PLXNB2         AB002313         plexin B2         '           PLXNC1         AF030339         plexin C1           PARG         AF005043         poly (ADP-ribose) glycohydrolase           at         PABPC1         Z48501         poly(A) binding protein, cytoplasmic 1           PABPC1         Y00345         poly(A) binding protein, cytoplasmic 1           PARN         AJ005698         (deadenylation nuclease)           PCBP1         Z29505         poly(rC) binding protein 1           at         PCBP2         X78136         poly(rC) binding protein 2           at         PCBP3         AL046394         poly(rC) binding protein 3	1834	38741 at	PSCD2	U70728	domains 2 (cytohesin-2)	cytohesin-2
PLXNB2	1835	36943 r at	PLAGL1	U81992	pleiomorphic adenoma gene-like 1	C2H2 zinc finger protein PLAGL1
PLXNC1   AF030339   plexin C1	1836	34780_at	PLXNB2	AB002313	plexin B2 '	plexin B2
at         PARG         AF005043         poly (ADP-ribose) glycohydrolase           at         PABPC1         Z48501         poly(A) binding protein, cytoplasmic 1           PABPC1         Y00345         poly(A) binding protein, cytoplasmic 1           PABPC1         Y00345         poly(A)-specific ribonuclease           PARN         AJ005698         (deadenylation nuclease)           PCBP1         Z29505         poly(C) binding protein 1           at         PCBP2         X78136         poly(C) binding protein 2           at         PCBP2         X78136         poly(C) binding protein 2           PCBP3         AL046394         poly(C) binding protein 3	1837	32193 at	PLXNC1	AF030339	plexin C1	VESPR
at         PABPC1         Z48501         poly(A) binding protein, cytoplasmic 1           PABPC1         Y00345         poly(A) binding protein, cytoplasmic 1           PABN         AJ005698         (deadenylation nuclease)           PCBP1         Z29505         poly(C) binding protein 1           at         PCBP2         X78136         poly(C) binding protein 2           at         PCBP2         X78136         poly(C) binding protein 2           PCBP3         AL046394         poly(C) binding protein 3	1838	38270 at	PARG	AF005043	poly (ADP-ribose) glycohydrolase	poly(ADP-ribose) glycohydrolase
PABPC1         Y00345         poly(A) binding protein, cytoplasmic 1           PARN         AJ005698         (deadenylation nuclease)           PCBP1         Z29505         poly(C) binding protein 1           at         PCBP2         X78136         poly(C) binding protein 2           at         PCBP2         X78136         poly(C) binding protein 2           PCBP3         AL046394         poly(C) binding protein 3	1839		PABPC1	Z48501	poly(A) binding protein, cytoplasmic 1	polyadenylate binding protein II
PARN         AJ005698         (deadenylation nuclease)           PCBP1         Z29505         poly(rC) binding protein 1           at         PCBP2         X78136         poly(rC) binding protein 2           at         PCBP2         X78136         poly(rC) binding protein 2           at         PCBP2         X78136         poly(rC) binding protein 2           PCBP3         AL046394         poly(rC) binding protein 3	18 8	ă	PABPC1	Y00345	poly(A) binding protein, cytoplasmic 1	poly(A) binding protein, cytoplasmic 1
PARN         AJ005698         (deadenylation nuclease)           PCBP1         Z29505         poly(rC) binding protein 1           at         PCBP2         X78136         poly(rC) binding protein 2           at         PCBP2         X78136         poly(rC) binding protein 2           PCBP3         AL046394         poly(rC) binding protein 3					poly(A)-specific ribonuclease	:
at PCBP2 X78136 poly(rC) binding protein 1 at PCBP2 X78136 poly(rC) binding protein 2 at PCBP2 X78136 poly(rC) binding protein 2 PCBP3 AL046394 poly(rC) binding protein 3	1841	36003 at	PARN	AJ005698	(deadenyfation nuclease)	poly(A)-specific ribonuclease
at PCBP2 X78136 poly(rC) binding protein 2 at PCBP2 X78136 poly(rC) binding protein 2 PCBP3 AL046394 poly(rC) binding protein 3	1842	34305 at	PCBP1	229505	poly(rC) binding protein 1	sub2.3
at PCBP2 X78136 poly(rC) binding protein 2 PCBP3 AL046394 poly(rC) binding protein 3	85	35746 r at	PCBP2	X78136	poly(rC) binding protein 2	hnRNP-E2
PCBP3 AL046394	\$	35745_f_at	PCBP2	X78136	poly(rC) binding protein 2	hnRNP-E2
	1845	39868 at	PCBP3	AL046394	poly(rC) binding protein 3	

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	A	В	ပ	Q	Э
10/6	1046 20120 01	2070	1150038	połycystic kidney disease 2 (autosomal	polycystin 2
2		LINDS			
1847	1847 33380_at	POLS	AB005754		LAK-I
				DNA directed), epsilon 3	polymerase (DNA directed), epsilon 3 (p17
1848	1848 38702_at	POLE3	AF0/0640		Suburity
				polymerase (RNA) II (DNA directed)	
1849	1849 40791_at	POLR2A	X63564	polypeptide A (220kD)	RNA polymerase II largest subunit
				polymerase (RNA) II (DNA directed)	
1850	1850 39746_at	POLR2B	X63563	polypeptide B (140kD)	RNA polymerase II 140 kDa subunit
				polymerase (RNA) II (DNA directed)	
1851	1851 36027_at	POLR2F	AA418779	polypeptide F	
				polymerase (RNA) II (DNA directed)	
1852	1852 35631_at	POLRZH	U37689	polypeptide H	RNA polymerase II subunit
				polymerase (RNA) II (DNA directed)	
1853	1853 1248_at	POLR2H	U37689	polypeptide H	RNA polymerase II subunit
				polymerase (RNA) II (DNA directed)	
1854	1854 503_at	POLR2L	U37690	polypeptide L (7.6kD)	RNA polymerase II subunit
L				polymerase (RNA) II (DNA directed)	
1855	1855 35841_at	POLR2L	N24355	polypeptide L (7.6kD)	
		1			
1856		PIRF	AL050224	polymerase I and transcript release factor	
1857		PIGR	X73079	polymeric immunoglobulin receptor	Polymeric immunoglobulin receptor
1858	1858 40593_at	PTBP1	X66975	polypyrimidine tract binding protein 1	nuclear ribonucleoprotein
1850	1850 31600 c at	PMC214	N38435	Prostmaintic segrenation increased 2-like 1	
	, - , - , - , - , - , - , - , - , - , -			201 JOE 1 /20 1 79). OBE9 mit ore	
		-		protein (aa 1-343); Bacteriophage P1 cre	
1860	1860 AFFX-CreX-5 at		X03453	gene for recombinase protein.	
				pot. ORF1 (aa 1-73); ORF2, put. cre	
				protein (aa 1-343); Bacteriophage P1 cre	
186	1861 AFFX-CreX-3_at		X03453	gene for recombinase protein.	
186,	1862 315 at	PRDM2	D45132	PR domain containing 2, with ZNF domain zinc-finger DNA-binding protein	zinc-finger DNA-binding protein
186	1863 32696_at	PBX3	X59841	pre-B-cell leukemia transcription factor 3	homeobox protein

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	∢	80	ပ	O	
				precursor; Human prolyl 4-hydroxylase	
				beta-subunit and disulfide isomerase	
				(P4HB) gene, exon 11, clones 6B-	
1864	1864 36666 at	P4HB	M22806	(1,3,5,6).	prolyl 4-hydroxylase beta-subunit
1865	1865 34321 i at	GS3786	D87120	d osteoblast protein	GS3786
1866	1866 41003 at	PFDN4	U41816	prefoldin 4	C-1
1867	1867 38698 at	PREI3	AL080070	ation protein 3	hypothetical protein
1868	1868 40269 at	PRP18	U51990	ctor 18	hPrp18
				ephalin	
1869	1869 38291 at	PENK	J00123	gene: exon 3 and 3 lank.	proenkephalin
1870	1870 641 at	PSEN1	L76517	sease 3)	presenilin 1
1871	1871 40621 at	PAWR	U63809		prostate apoptosis response protein par-4
1872	1872 41773 at	PCOLN3	U58048	procollagen (type III) N-endopeptidase	PRSM1
1873	1873 31609 s at	PCOLCE	L33799	ī	procollagen C-proteinase enhancer protein
1874	1874 34795 at	PLOD2	U84573		lysyl hydroxylase isoform 2
				procollagen-lysine, 2-oxoglutarate 5-	
				dioxygenase (lysine hydroxylase, Ehlers-	
1875	1875 36184 at	PLOD	L06419	Danlos syndrome type VI)	lysyl hydroxylase
				procollagen-proline, 2-oxoglutarate 4-	procollagen-proline, 2-oxoglutarate 4-
				dioxygenase (proline 4-hydroxylase),	dioxygenase (proline 4-hydroxylase), alpha
1876	1876 37037 at	P4HA1	M24486	alpha polypeptide I	polypeptide l
				procollagen-proline, 2-oxoglutarate 4-	
				dioxygenase (proline 4-hydroxylase),	
1877	1877 34390_at	P4HA2	U90441	alpha polypeptide II	prolyl 4-hydroxylase alpha (II) subunit
_		-		procollagen-proline, 2-oxoglutarate 4-	procollagen-proline, z-oxogiutarate 4-
				dioxygenase (proline 4-hydroxylase), beta	dioxygenase (proline 4-hydroxylase), beta
				bolypeptide (protein disulfide isomerase;	polypeptide (protein disulfide isomerase;
1878	1878 691 a at	P4HB	J02783	(thyroid hormone binding protein p55)	thyroid hormone binding protein p55)
1870	1879 38840 c at	PENS	110678	profilin 2	profilin II
1880	1880 38839 at	PFN2	AL096719	profilin 2	profilin 2 isoform b; profilin 2 isoform a
				progesterone receptor membrane	
1881	1881 38802 at	PGRMC1	Y12711	component 1	putative progesterone binding protein
		2011	000000	progesterone receptor membrane	prograstarona binding protein
1882	1882 38821_at	PGRMC2	AJUNZUSU	component z	moral Supring proposed Social

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	A	8		O	ij
1883	39035_at	DDS			progestin induced protein
1884	1884 39036 g at	005	AF006010	progestin induced protein	progestin induced protein
1885	1885 35218_at	PDCD10	AF022385	programmed cell death 10	TFAR15
1886	1886 37569 at	PDCD6	AF035606	programmed cell death 6	calcium binding protein
				(apoptosis-	
1887	1887 32212_at	PDCD8	AL049703		hypothetical protein
1888	1888 36592_at	PHB	S85655		prohibitin
1889	1889 1884_s_at	PCNA	M15796	proliferating cell nuclear antigen	proliferating cell nuclear antigen
1890	1890 41600_at	PA2G4	U59435	proliferation-associated 2G4, 38kD	cell cycle protein p38-2G4 homolog
				proline-rich Gla (G-carboxyglutamic acid)	
1891	1891 35978_at	PRRG1	AF009242	polypeptide 1	proline-rich Gla protein 1
1892	1892 36023_at	PRH1	A1864120	proline-rich protein Haelll subfamily 1	
				pro-oncosis receptor inducing membrane	pro-oncosis receptor inducing membrane
1893	1893 40803_at	PORIMIN	AL050161		injury gene
				senzyme A carboxylase, alpha	Propionyl-Coenzyme A carboxylase, alpha
1894	1894 1348_s_at	PCCA	S79219	polypeptide	polypeptide precursor
				propionyl Coenzyme A carboxylase, beta	
1895	1895 36561_at	PCCB	X73424	polypeptide	propionyl-CoA carboxylase
				proprotein convertase subtilisin/kexin type	
1896	1896 41032_at	PCSK5	U56387	5	protease PC6 isotorm A
					and the same of th
1807	1807 3E70E at	DCAD	103077	prosaposin (variant daucijej disease and	variant metachromatic leukodystrophy)
		50	1,000		
1898	1898 38406_f_at	PTGDS	AI207842	prostaglandin D2 synthase (21kD, brain)	
				prostaglandin E receptor 2 (subtype EP2),	
1895	1899 828_at	PTGER2	U19487	53KD	prostaglandin E2 receptor
1900	1900 1890_at	PLAB	AB000584	prostate differentiation factor	TGF-beta superfamily protein
1901	32611_at	PBP	X75252	prostatic binding protein	phosphatidylethanolamine binding protein
1902	719 g at	PRSS11	D87258	protease, serine, 11 (IGF binding)	serin protease with IGF-binding motif
190	1903 718_at	PRSS11	D87258	protease, serine, 11 (IGF binding)	serin protease with IGF-binding motif
190	1904 33368_at	PRSS15	X76040	protease, serine, 15	Lon protease-like protein
<u>-</u>	1905 40078_at	SPUVE	AF015287	protease, serine, 23	serine protease
98	1906 39845_at	PRSS25	AF020760	protease, serine, 25	serine protease
190	1907 688 at	PSMC1	1.02426	proteasome (prosome, macropain) 26S subunit. ATPase. 1	26S protease (S4) regulatory subunit
	13.000	1. Cirilo	22. 22.		



	A	В	၁	۵	u)
				proteasome (prosome, macropain) 26S	
1908	1908 35353_at	PSMC2	D11094	1	MSS I protein
				ne, macropain) 265	proteasome (prosome, macropain) zos
1909	1909 592_at	PSMC3	M34079	subunit, ATPase, 3	subunit, Al Pase, 3
				proteasome (prosome, macropain) 26S	
1910	1910 37766_s_at	PSMC5	AF035309	subunit, ATPase, 5	
				proteasome (prosome, macropain) 26S	:
1911	1911 949 s at	PSMC6	D78275	subunit, ATPase, 6	proteasome subunit p42
				proteasome (prosome, macropain) 26S	
1912	1912 1314_at	PSMD1	D44466	subunit, non-ATPase, 1	proteasome subunit p112
				proteasome (prosome, macropain) 26S	
1913	1913 1192_at	PSMD12	AB003103	subunit, non-ATPase, 12	26S proteasome subunit p55
				proteasome (prosome, macropain) 26S	proteasome (prosome, macropain) 265
1914	1914 32240_at	PSMD5	D31889	subunit, non-ATPase, 5	subunit, non-ATPase, 5
		•	·	300 (1)	
104	1015 045 04	DCM07	ווייים	proteasome (prosome, macropain) 203 subunit non-ATPase 7 (Mov34 homolog) proteasome subunit p40 / Mov34 protein	proteasome subunit p40 / Mov34 protein
2	340 at		2000		
				proteasome (prosome, macropain) 26S	
1916	1916 40276_at	PSMD7	D50063	subunit, non-ATPase, 7 (Mov34 homolog) proteasome subunit p40 / Mov34 protein	proteasome subunit p40 / Mov34 protein
				proteasome (prosome, macropain) 26S	
1917	1917 32584_at	PSMD8	D38047	subunit, non-ATPase, 8	26S proteasome subunit p31
				proteasome (prosome, macropain) 26S	
1918	1918 36492_at	PSMD9	Al347155	subunit, non-ATPase, 9	
				proteasome (prosome, macropain)	
1919	1919 41171_at	PSME2	D45248	activator subunit 2 (PA28 beta)	proteasome activator nPAZ8 suunit peta
				proteasome (prosome, macropain)	
1920	1920 1184_at	PSME2	D45248	activator subunit 2 (PA28 beta)	proteasome activator nPAZ6 suumi peta
			<del></del>	proteasome (prosome, macropain)	
1921	1921 36974_at	PSMF1	D88378	inhibitor subunit 1 (PI31)	proteasome inhibitor hPI31 subunit
				proteasome (prosome, macropain)	
1922	1922 38371_at	PSMA1	M64992	subunit, alpha type, 1	prosomal protein P30-33K
				proteasome (prosome, macropain)	proteasome (prosome, macropain) subunit,
1923	1923 1446_at	PSMA2	D00760	subunit, alpha type, 2	alpha type, 2
				proteasome (prosome, macropain)	proteasome (prosome, macropain) subunit,
1924	1924 1448 at	PSMA3	D00762	subunit, alpha type, 3	laipna type, 3



	Α	В	၁		n
				s, macropain)	proteasome (prosome, macropain) subunit,
1925	1925 1450_g_at	PSMA4	D00763		alpha type, 4
				e, macropain)	proteasome (prosome, macropain) subunit,
1926	1926 1449_at	PSMA4	D00763		alpha type, 4
				proteasome (prosome, macropain)	
1927	1927 37046_at	PSMA5	AI246726	subunit, alpha type, 5	
				proteasome (prosome, macropain)	
1928	1928 36122_at	PSMA6	X59417		prosomal P27K protein
				e, macropain)	proteasome (prosome, macropain) subunit,
1929	1447_at	PSMB1	D00761	subunit, beta type, 1	beta type, 1
				ne, macropain)	
1930	1930 1310_at	PSMB2	D26599		proteasome subunit HsC7-1
				ю, macropain)	
1931	931 33154_at	PSMB4	D26600	subunit, beta type, 4	proteasome subunit HsN3
				proteasome (prosome, macropain)	
1932	932 1311_at	PSMB4	D26600	subunit, beta type, 4	proteasome subunit HsN3
				ie, macropain)	
1933	37666_at	PSMB5	D29011	subunit, beta type, 5	proteasome subunit X
				proteasome (prosome, macropain)	
1934	934 941_at	PSMB6	D29012	subunit, beta type, 6	proteasome subunit Y
				proteasome (prosome, macropain)	
1935	1935 39060_at	PSMB7	D38048	subunit, beta type, 7	proteasome subunit z
				proteasome (prosome, macropain)	
1936	1936 1313_at	PSMB7	D38048	subunit, beta type, 7	proteasome subunit z
				proteasome (prosome, macropain)	
				subunit, beta type, 9 (large multifunctional	
1937	1937 38287_at	PSMB9	AA808961	protease 2)	
					! !
1938	1938 41750_at	P5	D49489	protein disulfide isomerase-related protein human P5	human P5
1939	1939 32558_at	PIAS3	AB021868	protein inhibitor of activated STAT3	protein inhibitor of activatied STAT3
				protein kinase (cAMP-dependent,	
1940	1940 34376_at	PKIG	AB019517	catalytic) inhibitor gamma	protein kinase inhibitor gamma
1941	1941 36957_at	PRKCBP1	W22296	protein kinase C binding protein 1	
1942	1942 1602_at	PRKCI	L33881	protein kinase C, iota	protein kinase C iota
1943	1943 1603_g_at	PRKCI	L33881	protein kinase C, iota	protein kinase C iota
1944	1944 36835_at	PRKCL2	U33052	protein kinase C-like 2	PRK2

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_	A	8	ပ	a	L L
1945	1945 41768 at	PRKAR1A	98288W	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific oxtinguisher 1)	cAMP-dependent protein kinase type I-alpha subunit
	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	A + 0 4 7 0 0	00000	, cAMP-dependent, e I, alpha (tissue specific	cAMP-dependent protein kinase type I-alpha
2	1340 CZ/_9_81	אושאשו	Missesso	profein kingse, cAMP-dependent,	
1947	1947 226_at	PRKAR1A	M33336	secific .	cAMP-dependent protein kinase type I-alpha subunit
				protein kinase, interferon-inducible double protein activator of the interferon-induced	protein activator of the interferon-induced
1948	1948 32205_at	PRKRA	AF072860	stranded RNA dependent activator	protein kinase
				itase 1, catalytic subunit,	serine /threonine specific protein .
1949	1949[37725_at	PPP1CC	X74008		pnospnatase
1050	1050 40438 at	PPP1B12A	D87930	protein phosphatase 1, regulatory (inhibitor) subunit 12A	myosin phosphatase target subunit 1
				, regulatory	
1951	1951 39366_at	PPP1R3C	N36638	(inhibitor) subunit 3C	
				protein phosphatase 1, regulatory subunit	
1952	1952 41540_at	PPP1R7	Z50749		yeast sds22 homolog
4059	0E7 of	DDM1A	S87759	protein phosphatase 1A (formerly 2C),	profein phosphatase 2C alpha
222	1333 037 _at		201100		
1954	1954 36501 at	PPM1A	S87759		protein phosphatase 2C alpha
				protein phosphatase 1D magnesium-	
1955	1955 37107_at	PPM1D	U78305	dependent, delta isoform	LdiW
		-		protein phosphatase 2 (formerly 2A),	
1956	1956 924_s_at	PPP2CB	J03805	catalytic subunit, beta isotorm	
				protein phosphatase 2 (formerly 2A),	
				regulatory subunit B (PH 52), alpha	
1957	1957 41167_at	PPP2R2A	M64929	isoform	protein phosphatase-zA subutiit-aipita
				protein phosphatase 2 (formerty 2A), regulatory subunit B (PR 52), alpha	•
1958	1958 1383_at	PPP2R2A	M64929	isoform	protein phosphatase-2A subunit-alpha
5	1- 7000	730000	00637.1	protein phosphatase 2, regulatory subunit	nrotein phosphatase R56-epsilon
808L	1959/32/34_at	rrrzkae	L/0/03	D (DOO), epsilon isototini	promit productions are observed.



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1				regulatory subunit	protein phosphatase 2A B'alpha1 regulatory
1960	1960 40786 at	PPP2R5C	U37352		subunit
	1			agulatory subunit	protein phosphatase 2A B'alpha1 regulatory
1961	1961 176_at	PPP2R5C	U37352		subunit
				protein phosphatase 2A, regulatory	
1962	1962 39127_f_at	PPP2R4	X73478		phosphotyrosyl phosphatase activator
				protein phosphatase 3 (formerly 2B),	protein phosphatase 3 (formerly 2B),
-				eurin	catalytic subunit, beta isoform (calcineurin A
1963	1963 38277_at	PPP3CB	M29550		beta)
				protein phosphatase 3 (formerly 2B),	
				catalytic subunit, gamma isoform	
1964	1964 32541_at	PPP3CC	S46622	(calcineurin A gamma)	calcineurin A catalytic subunit
				protein phosphatase 4, regulatory subunit	
1965	1965 34371_at	PPP4R1	U79267		
		0			a cooperate ricecon
1966	1966 37581_at	PPP6C	X929/2	protein priospitatase o, catalytic suburill	piotein priospriatase o
1967	s_at	PROS1	M15036	protein S (alpha)	protein S (alpha)
1968		SEC61B	AA083129	protein translocation complex beta	
1969	# H	PTK9	U02680	protein tyrosine kinase 9	protein tyrosine kinase
				protein tyrosine phosphatase type IVA,	
1970	1970 843 at	PTP4A1	U48296	member 1	protein tyrosine phosphatase PTPCAAX1
				protein tyrosine phosphatase type IVA,	
1971	1971 38415_at	PTP4A2	U14603	member 2	protein-tyrosine phosphatase
				protein tyrosine phosphatase type IVA,	
1972	1972 1241_at	PTP4A2	U14603	member 2	protein-tyrosine phosphatase
L				protein tyrosine phosphatase, non-	protein tyrosine phosphatase, non-receptor
1973	1973 40137_at	PTPN1	M31724	receptor type 1	type 1
				protein tyrosine phosphatase, non-	
1974	1974 1463_at	PTPN12	M93425	receptor type 12	protein tyrosine phosphatase
				protein tyrosine phosphatase, non- recentor type 13 (APO-1/CD95 (Fas)-	
1975	1975 34198 at	PTPN13	U12128	associated phosphatase)	protein tyrosine phosphatase 1E
					protein tyrosine phosphatase, receptor type,
					A, isoform 1 precursor; protein tyrosine
				protein tyrosine phosphatase, receptor	phosphatase, receptor type, A, isoform 2
1976	1976 1496_at	PTPRA	M34668	type, A	precursor

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1977   36204_at   PTPRF   Y00815   Protein tyrosine phosphatase, receptor Protein flipfin), abilta 1						
PTPRF   Y00815   P   P   P   P   P   P   P   P   P		¥	89	ပ	O	U
PTPRF   Y00815   Y0	$\vdash$				protein tyrosine phosphatase, receptor	000
PPFIA1   U22816   PPFIA1   U22816   PPFIA1   U22816   PPFIA1   U22818   PPFIA1   U22818   PPFIA1   U22818   PPFIA1   U22818   PPFIA1   U22818   PPFIA1   U22828   PPFIA1   U225547   PPGIA1   U225547   PPGIA1   UA4630   PPFIA2   PPFIA4   UA4630   PPFIA2   PPFIA4   UA4630   PPFIA2   UA4630   PPFIA3   PPFIA3   PPFIA3   PPFIA3   PPFIA3   UA4630   PPFIA3	7	1204 at		Y00815		put. LAH preprotein (AA - 16 to 1661)
PPFIA1   U22816   PPFIA1   U22816   PPFIA1   U22816   PPFIA1   U22818   PPFIA1   U22818   PPFIA1   U22818   PPFIA1   U22818   PPFIA1   U22547   PPGIA   UA4630   PPGIA   UA4630   PPGIA   UAA4630   PPGIA   UA4630   PPGIA   UA4630   PPGIA   UAA630   PPGIA   UA4630   PPGIA   PPGIA   UA4630   PPGIA	+				protein tyrosine phosphatase, receptor	
PPFIA1   U22816   PPFIA1   U22816   PPFIA1   U22816   PPFIA1   U22818   PPFIA1   U22818   PPFIA1   U22818   PPFIA1   U22818   PPFIA1   U22547   PPGIA1   UA4630   PPGIA   UA4630   PPGIA   UA4630   PPGIA   UA4630   PPFIAA   PPFIAA   UA4630   PPFIAA   PPFIAA   UA4630   PPFIAA   PPFI					_	•
PTPRK   L77886   PTPRK   L77886   PTPRK   L77886   PTPRK   K58288   PTPRK   AL049970   PTPRK   A1049970   PTPRK   A1049970   PTPRG   A1049970   PTPRG   A104630   PTRK   A104630   PTRK   A1049970   PTRK   A104630   PTRK   A104630   PTRK   A104755   PTRK   A104755   PTRK   A104755   PTRK   A104755   PTRK   A104755   PTRK   A104756   PTRK   A104	78 41	780 at	PPFIA1	U22816	$\neg$	LAR-interacting protein 1b
1488_at PTPRK L77886 htm	-				hatase, receptor	
995_g_at PTPRM X58288 the 31892_at PTPRM X58288 the 31141_at PRKRIR AL049970 representation of the 37737_at PCMT1 D25547 representation of the 37736_at PCMT1 D13892 representation of the 37899_i_at PTMA M14630 representation of the 37936_at	79 14	IAR at	PTPRK			protein tyrosine phosphatase
995_g_at PTPRM X58288 pt 18192_at PTPRM X58288 pt 181141_at PRKRIR AL049970 pt 182227_at PCMT1 D13892 pt 18589_i_at PRG1 X17042 pt 18589_i_at PTMA M14630 pt 18589_at PUM1 pt 18699_at 18589_at PUM2 pt 18699_at 18589_at PUMA M14690_at 18699_at	-	in=004			yrosine phosphatase, receptor	•
31892_at PTPRM X58288 P  41141_at PRKRIR AL049970 F  37736_at PCMT1 D13892 P  32227_at PRG1 X17042 P  38590_r_at PTMA M14630 P  38589_i_at PTMA M14630 P  31697_s_at FTHP1 J04755 P  40048_at PUM1 D43951 D87078 PUM2 D87078 D87078 PUM2 D43951 D87078 PUM2 D87078 PUM3 PUM4 X91648 PUM4 PUM4 X91648 PUM4 X91648 PUM4 PUM4 X91648 PUM4 PUM4 X91648 PUM4 PUM5 PUM4 X91648 PUM4 PUM5 PUM4 PUM5 PUM4 PUM4 PUM4 PUM5 PUM4 PUM4 PUM4 PUM4 PUM4 PUM4 PUM4 PUM4	30	35 g at	PTPRM	X58288		protein-tyrosine phosphatase
1141_at   PTPRM   X58288   PTPRM   PTPRM   AL049970   PT   PT   PT   PT   PT   PT   PT   P	-				protein tyrosine phosphatase, receptor	•
37737_at   PRKRIR   AL049970   F   37736_at   PCMT1   D13892   F   52227_at   PRG1   X17042   F   53227_at   PTMA   M14630   F   53690_r_at   PUM1   D43951   D87078   S5251_at   PUM2   D87078   S5221_at   PUMA   X91648   S5221_at   PUMA   X91648   S5221_at   PUMA   X91648   S5221_at   PUMA   X91648   S5221_at   PUMA   X04526   S33720_at   L0C56902   L48692   S33720_at   L0C56902   L48692   S33720_at   C0C56902   L48692   S33720_at   C0C56902   C	81 31	1892 at	PTPRM	X58288	type, M	protein-tyrosine phosphatase
37737_at         PRKRIR         AL049970         r           37737_at         PCMT1         D25547         r           37736_at         PCMT1         D13892         r           38590_r_at         PTMA         M14630         r           38590_r_at         PTMA         M14630         r           37936_at         PTMA         M14630         r           37936_at         PTMA         M14630         r           36117_at         PTK2         L13616         r           40048_at         PUM1         D43951         r           35259_at         PUM1         D43951         r           35221_at         PUM2         D87078         r           35221_at         PURA         X91648         r           33341_at         GNB1         X04526         r           33720_at         LOC56902         L48692         r	+				protein-kinase, interferon-inducible double	
41141_at         PRKRIR         AL049970         F           37737_at         PCMT1         D25547         F           37736_at         PCMT1         D13892         F           38590_r_at         PTMA         M14630         F           38590_r_at         PTMA         M14630         F           37936_at         PTMA         M14630         F           37936_at         PTMA         M14630         F           37936_at         PTMA         A1184802         F           36117_at         PTK2         L13616         D43951           40048_at         PUM1         D43951         D87078           35251_at         PUM2         D87078         D87078           35221_at         PURA         X91648         X91648           33320_at         LOC56902         L48692					stranded RNA dependent inhibitor,	
37737_at PCMT1 D25547 F T T T T T T T T T T T T T T T T T T	824	1141 at	PRKRIR	AL049970	repressor of (P58 repressor)	hypothetical protein
37737_at         PCMT1         D25547         F           37736_at         PCMT1         D13892         F           32227_at         PRG1         X17042         F           38590_r_at         PTMA         M14630         F           38590_r_at         PTMA         M14630         F           37936_at         PTMA         M184802         F           37936_at         PTK2         L13616         F           40048_at         PUM1         D43951         D87078           35359_at         PUM2         D87078         D87078           35221_at         PURA         X91648         X91648           333341_at         GNB1         X04526         A8520           33720_at         LOC56902         L48692         L48692	+				protein-L-isoaspartate (D-aspartate) O-	
32227_at PCMT1 D13892 I S2227_at PRG1 X17042 I S8590_r_at PTMA M14630 I S1595_at PTMA M14630 I S1595_at PTMA M14630 I S1595_at PTMP M184802 I S1697_s_at PTMP M184802 I S1697_s_at PTMP M184802 I S1697_s_at PUM1 D43951 I S16359_at PUM1 D43951 I S16359_at PUM2 D87078 I S16359_at PUMA X91648 I S16359_at PUMA X04526 I S16359_at PUMA I S16359_	83	7737 at	PCMT1	D25547	methyttransferase	PIMT isozyme I
at PTMA M14630 I ATMA M14630 I ATMA M14630 I ATMA M14630 I ATMA M14630 I ATMA M14630 I ATMA M184802 I ATMA M184802 I ATMA ATMA M184802 I ATMA ATMA I PUM2 D87078 I PUM2 D87078 I ATMA M3648 I ATMA M3648 I ATMA M3648 I ATMA M18692 I ATMA M18692 I ATMA M18692 I ATMA M14630 I ATMA M18692 I ATMA M14630 I ATMA M16630 I					protein-L-isoaspartate (D-aspartate) O-	•
at PTMA M14630 I at PTMA M14630 I HPRP4P A1184802 I A1184802 I A1184802 I A1184802 I A1184802 I A1184802 I A1184802 I A1184802 I A1184802 I A1184802 I A118692 I A118630 I A118692 I A118630 I A1	84	7736 at	PCMT1	D13892	methyttransferase	carboxyl methyltransferase
at PTMA M14630 I ATMA M14630 I ATMA M14630 I A1184802 I A1184802 I A1184802 I A1184802 I A1184802 I A1184802 I A1184802 I A118630 I	75	2227 at	PRG1	X17042	proteoglycan 1, secretory granule	proteoglycan 1, secretory granule
PTMA   M14630	3 6	8590 r at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
t FTHP1 J04755 PUM1 J04755 PUM1 D43951 PUM2 D87078 PUM2 D87078 PURA X91648 GNB1 X04526 LOC56902 L48692	2 2	8589 i at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
at FTHP1 J04755 PTK2 L13616 PUM1 D43951 PUM2 D87078 PURA X91648  1 GNB1 X04526 1 LOC56902 L48692		1000	OVOCOTI.	Alterens	PRPA/STK/WD splicing factor	
FTHP1 J04755 PTK2 L13616 PUM1 D43951 PUM2 D87078 PURA X91648 GNB1 X04526 LOC56902 L48692	2	7936 at	חרתיי	A110#002		
FTHP1 J04755 PTK2 L13616 PUM1 D43951 PUM2 D87078 PURA X91648 GNB1 X04526 LOC56902 L48692					pseudoferritin H protein; Human ferritin H	
PTK2 L13616 PUM1 D43951 PUM2 D87078 PURA X91648 GNB1 X04526 LOC56902 L48692	189	11697 s at	FTHP1	J04755	processed pseudogene, complete cds.	
PUM1 D43951 PUM2 D87078 PURA X91648 GNB1 X04526 LOC56902 L48692	3903	16117 at	PTK2	L13616	PTK2 protein tyrosine kinase 2	focal adhesion kinase
PUM2 DB7078 PURA X91648 GNB1 X04526 LOC56902 L48692	3914	10048 at	PUM1	D43951	pumilio homolog 1 (Drosophila)	KIAA0099 protein
PURA X91648  GNB1 X04526  LOC56902 L48692	3923	15359 at	PUM2	D87078	pumilio homolog 2 (Drosophila)	KIAA0235 protein
at GNB1 X04526 at LOC56902 L48692	393	35221 at	PURA	X91648	purine-rich element binding protein A	
GNB1 X04526 LOC56902 L48692					put. ORFX (AA 1-75); beta subunit (AA 1-	
GNB1 X04526 LOC56902 L48692					340); Human liver mRNA for beta-subunit	
GNB1 X04526 LOC56902 L48692				_	signal transducing proteins Gs/Gi (beta-	guanine nucleotide-binding protein, beta-1
LOC56902 L48692	994		GNB1	X04526	(G).	subunit
	995	33720_at	LOC56902	L48692	putatative 28 kDa protein	
					putative breast adenocarcinoma marker	DC.2 protein
1996 39363_at   BC-2   AF042384   (32KU)	966	39363_at	BC-2	AF042384	(32kU)	loc-z protein

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		20040	A F004070	T	putative dimothyladenocine transferace
1997	39884_g_at	HSA9761	AF0910/8	Т	Julative diffielliyladeflosiffe flatisferase
				e glialblastoma cell differentiation-	putative gliaiblastoma cell differentiation-
1998	1998 38841_at	GDBH1	AF068195		related protein
1999	1999 41188_at	LC27	W28186	putative integral membrane transporter	
				putative L-type neutral amino acid	
2000	2000 38984_at	KIAA0436	AB007896	transporter	
2001	2001 39116_at	LOC54499	AF070626	putative membrane protein	
2002	2002 35286 r at	BY1	X76302	outative nucleic acid binding protein RY-1 Inucleic acid binding protein	nucleic acid binding protein
				Putative prostate cancer tumor	
2003	2003 36852_at	N33	U42349	suppressor	
				ein similar to nessy	
2004	2004 33710_at	C3F	U72515		C3f
2005	2005 40203_at	SUI1	AJ012375	or or	putative translation initiation factor
2006	2006 37678_at	NMA	U23070	putative transmembrane protein	putative transmembrane protein
				putative transmembrane protein; homolog	
				of yeast Golgi membrane protein Yif1p	
2007	2007 35326_at	54TM	AF004876	(Yip1p-interacting factor)	54TMp
				putative; Homo sapiens PTS gene,	
2008	2008 35697_at	PTS	L76259		6-pyruvoyltetrahydropterin synthase
				putative; originaly identified as an	
				oncogene', product renamed by NCBI	
2009	2009 40887_g_at	PTI-1	L41498	cds.	longation factor 1-alpha 1
				putative; originaly identified as an	
				'oncogene', product renamed by NCBI	
				staff; Homo sapiens longation factor 1-	
2010	2010 40886_at	PTI-1	L41498	alpha 1 (PTI-1) mRNA, complete cds.	longation factor 1-alpha 1
				pVHL-interacting deubiquitinating enzyme	
2011	2011 33219_at	VDU1	AB029020		KIAA1097 protein
				Pyruvate dehydrogenase complex, lipoyl-	
				containing component X; E3-binding	pyruvate dehydrogenase complex protein X
2012	36164_at	PDX1	U82328	protein	subunit precursor
2013	2013 32378_at	PKM2	M26252	pyruvate kinase, muscle	pyruvate kinase, muscle
2014	2014 260_at	QDPR	M16447	quinoid dihydropteridine reductase	quinoid dihydropteridine reductase

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			1	e-stranded	::0000 <b>4</b>
2015	2015 36610_at	R3HDM	D21852		KIAAUUZ9 protein
2016	2016 39030_at	RABAC1	AJ133534	Rab acceptor 1 (prenylated)	prenylated Rab acceptor 1 (PRA1)
				Rab geranylgeranyltransferase, beta	•
2017	2017 37703_at	RABGGTB	Y08201	subunit	rab geranylgeranyl transferase
2018	2018 38264_at	RABIF	U74324	RAB interacting factor	guanine nucleotide exchange factor mss4
					, , , , , , , , , , , , , , , , , , ,
2019	2019]36660_at	RAB11A	AF000231		rabila
2020	2020 35325_at	RAB14	AF052113	RAB14, member RAS oncogene family	
2021	2021 34393 r at	RAB1A	AL050268	RAB1A, member RAS oncogene family	hypothetical protein
2022	2022 34392 s at	RAB1A	AL050268	RAB1A, member RAS oncogene family	hypothetical protein
2023	33326_at	RAB21	D42087	RAB21, member RAS oncogene family	RAB21, member RAS oncogene family
2024	2024 809 at	BAB27A	1157094	RAR27A member RAS oncodene family	Bab27a
200	2025 33371 s. at	RAR31	U59877	RAB31 member RAS oncogene family	low-Mr GTP-binding protein Rab31
2026	6	RARSA	M28215	RAB5A, member RAS oncogene family	GTP-binding protein
	2			rabe GTPase activating protein (GAP and	
2027	2027 35289 at	GAPCENA	AJ011679	centrosome-associated)	Rab6 GTPase activating protein, GAPCenA
2028	2028 35304 at	RABGA	AF052130	RAB6A, member RAS oncogene family	
2029	2029 39628 at	RAB9A	AI671547	RAB9A, member RAS oncogene family	
888	2030 41716 at	RC3	AB020663	rabconnectin-3	KIAA0856 protein
				Rac/Cdc42 guanine nucleotide exchange	
2031	2031 37543_at	ARHGEF6	D25304	factor (GEF) 6	
2032	2032 36857_at	RAD1	AF084513	RAD1 homolog (S. pombe)	DNA repair exonuclease
2033	2033 38114 at	RAD21	D38551	RAD21 homolog (S. pombe)	RAD21 homolog
2034	20134 1874 at	RAD23R	D21090	RAD23 homolog B (S. cerevisiae)	XP-C repair complementing protein (p58/HHR23B)
		ŭ d	1104700	DAE1 DNA extend 1 homolog (S. nomba)	mBNA export protein
3	2035 5275/_al	שאנו	004/50	ביבב להיים אלאונים אלים היים	
				RAGE-4 ORF2; one of 2 possible coding regions; RAGE-4 ORF3; one of 2 possible	
				coding regions; Human renal cell	
		•		carcinoma antigen RAGE-4 mRNA,	
2036	2036 1524_at		U46194	complete putative cds.	
2037	2037 36628_at	RALBP1	L42542	ralA binding protein 1	RLIP76 protein
2038	337539_at	RGL	AB023176	RalGDS-like gene	KIAA0959 protein

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2039	41342_at	RANBP1	D38076		Han-br I (Han-Dinging Protein 1)
8	2040 40824_at	RANBP16	AB018288		KIAA0745 protein
¥	2041 41174_at	RANBP2L1	AF012086	ke 1	Ran binding protein 2
242	2042 35255_at	RANBP7	AF098799	RAN binding protein 7	RanBP7/importin 7
843	2043 32602_at	RAP1GDS1	X63465	RAP1, GTP-GDP dissociation stimulator 1 smg GDS	smg GDS
044	2044 1848_at	RAP1A	M22995	RAP1A, member of RAS oncogene family ras-related protein	ras-related protein
045	2045 40146_at	RAP18	AL080212	RAP1B, member of RAS oncogene family hypothetical protein	hypothetical protein
046	2046 39601 at	RASSF1	AF061836	Ras association (RalGDS/AF-6) domain family 1	putative tumor suppressor protein
				Ras association (RalGDS/AF-6) domain	Ras association (RaIGDS/AF-6) domain
8		RASSF2	D79990	family 2	tamily 2
048	2048 1659_s_at	RHEB2	D78132	Ras homolog enriched in brain 2	ras-related GTP-binding protein
949	2049 37309_at	ARHA	L09159	ras homolog gene tamily, member A	Multidrug resistance protein
	2050 1394_at	AHHA	L25080 592240	ras nomolog gene tarmily, member A	Bhoff
<u></u>	2051 35803_at	ARME	282240	Tas Hornoug gene ranny, member E	
2052	2052 36935 at	RASA1	M23379	RAS p21 protein activator (G1 rase activating protein) 1	GTPase-activating protein
				RAS p21 protein activator (GTPase	
2053	2053 1675_at	RASA1	M23379	activating protein) 1	GTPase-activating protein
				Ras-GTPase activating protein SH3	
2054	2054 35793_at	G3BP2	AB014560	domain-binding protein 2	KIAA0660 protein
				ras-related C3 botulinum toxin substrate 1	
	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	Č	7,0300	(rho family, small GTP binding protein	
	2000 40004_al	2	023274	racii) ras-related C3 botulinum toxin substrate 1	ras-related C3 botulinum toxin substrate 1
				(rho family, small GTP binding protein	isoform Rac1; ras-related C3 botulinum toxin
2056	2056 2050 s at	RAC1	M29870	Rac1)	substrate 1 isoform Rac1b
2057	2057 35316 at	RAGA	U41654	Ras-related GTP-binding protein	adenovirus E3-14.7K interacting protein 1
205	2058 33234_at	BCAA	AA887480	RBP1-like protein	
2059	2059 41407_at	RDBP	L03411	RD RNA-binding protein	RD protein
200	2060 34684 at	RECOL	L36140	RecQ protein-like (DNA helicase Q1-like) DNA helicase	DNA helicase

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	A	В	ပ	O	Ш
2061	2061 34685_at	RECOL	AI685944	RecQ protein-like (DNA helicase Q1-like)	
				requisted at the translational level:	
				contains I-mfa domain; untilizes unique	
•				protein isoform p40 and HIC protein	HIC protein isoform p40; HIC protein isoform
2062	2062 37842_at	呈	AF054589		p32
				regulator of G-protein signalling 19	
2063	2063 35756_at	RGS19IP1	AF089816		RGS-GAIP interacting protein GIPC
2064	2064 37701_at	RGS2	L13463	24kD	helix-loop-helix phosphoprotein
2065	2065 35722_at	RENT2	AL080198		hypothetical protein
				related RAS viral (r-ras) oncogene	
2066	2066 32827_at	RRAS2	Al365215	homolog 2	
				remainder of gene in clone 549K18	
2067	2067 34845_at	dJ796117.4	AL035398	(AL023654)	CGI-51 protein
2068	2068 1055 g at	BEC4	M87339	replication factor C (activator 1) 4 (37kD)	replication factor C, 37-kDa subunit
2069	2069 38481 at	RPA1	M63488	Г	replication protein A, 70-kDa subunit
2070	652 q at	RPA3	L07493	replication protein A3 (14kD)	replication protein A 14kDa subunit
2071	2071 37651_at	RCOR	D31888	REST corepressor	REST corepressor
207.0	2070/24250 04	Noo	VEAB3B	restin (Heed-Steinberg cell-expressed intermediate filament-associated protein)	in
2072	2073 31851 at	RFP?	A.1224819	1	tumor suppressor
	-			reticulocalbin 1, EF-hand calcium binding	
2074	2074 40556 at	HCN1	D42073	domain	reticulocalbin
				reticulocalbin 2, EF-hand calcium binding	
2075	2075 37727_i_at	RCN2	X78669	domain	EF-hand protein
				reticulocalbin 2, EF-hand calcium binding	,
2076	37728_r_at	RCN2	X78669	domain	EF-hand protein
2077	2077 31536_at	RTN4	AB020693	reticulon 4	KIAA0886 protein
2078	2078 39964 at	RP2	AJ007590	retinitis pigmentosa 2 (X-linked recessive) XRP2 protein	XRP2 protein
2079	2079 38164_at	RPGR	U57629	retinitis pigmentosa GTPase regulator	retinitis pigmentosa GTPase regulator
		à	144 7 400	retinoblastoma 1 (including	ratinoblactoma 1 (including actaocarroma)
	2080 2044_s_at	HBJ	M15400	osteosarcomaj	Helifobiasionia i (ilicidulity ostaosarconia)



	¥	В	ပ		U .
2081	35227 at	RBBP8	U72066		CtBP interacting protein CtIP
2082	2082 33860 at	RBAF600	AB007931	. 600	KIAA0462 protein
2083	2083 32597 at		X76061		130K protein
8	2084 35848 at		AL049432	retinoic acid induced 17	
				retropseudogene; Human	
			• •	DNA, complete	
2085	2085 31672 q at	RBMS1P; MSSP1	P1 D82351	_	MSSP-1
				REV3-like, catalytic subunit of DNA	
2086	2086 38908 s at	REV3L	AL096744		hypothetical protein
				reversion-inducing-cysteine-rich protein	
2087	2087 35236 q at	RECK	AA099265	with kazal motifs	
				reversion-inducing-cysteine-rich protein	
2088	2088 35235_at	RECK	AA099265	with kazal motifs	
				reversion-inducing-cysteine-rich protein	
2089	2089 35234 at	RECK	D50406	with kazal motifs	RECK protein precursor
2090	2090 553 g at	ARHGAP1	U02570	Rho GTPase activating protein 1	CDC42 GTPase-activating protein
2091	2091 39700 at	ARHGAP1	Al961929	Rho GTPase activating protein 1	
				Rho guanine nucleotide exchange factor	
2092	2092 34180_at	ARHGEF10	AB002292	(GEF) 10	Rho guanine nucleotide exchange factor 10
				Rho guanine nucleotide exchange factor	•
2093	2093 40828 at	ARHGEF7	D63476	(GEF) 7	PAK-interacting exchange factor beta
				rho/rac guanine nucleotide exchange	•
2094	2094 40100_at	ARHGEF2	U72206	factor (GEF) 2	guanine nucleotide regulatory factor
				Rho-specific guanine nucleotide exchange	
2095	2095 36537_at	P114-RHO-GEF	AB011093	factor p114	-
2096	2096 41040 at	RPP38	U77664	ribonuclease P (38kD)	RNaseP protein P38
2097	2097 32664 at	RNASE4	D37931	ribonuclease, RNase A family, 4	RNase 4
2098	2098 36187_at	RNH	X13973	ribonuclease/angiogenin inhibitor	ribonuclease/angiogenin inhibitor
900	20000 34314_at	BBM1	X59543	ribonucleotide reductase M1 polypeptide	M1 subunit of ribonucleotide reductase
2100	2100 2016 s at	RPL10	M64241	ribosomal protein L10	Wilm's tumor-related protein
2101	2101 41178 at	RPL11	X79234	ribosomal protein L11	ribosomal protein L11
2102	2102 33668 at	RPL12	AF037643	ribosomal protein L12	
2103	2103 31509 at	RPL13	X64707	ribosomal protein L13	ribosomal protein L13
210	2104 35119 at	RPL13A	X56932	ribosomal protein L13a	23 kD highly basic protein
2105	2105 31907 at	RPL14	D87735	ribosomal protein L14	ribosomal protein L14

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A         B         C           Lat         RPL15         L25899           at         RPL17         X53777           at         RPL18         L11566           at         RPL19         X63527           at         RPL21         U25789           r_at         RPL21         U25789           r_at         RPL23         X65954           r_at         RPL23         X55954           r_at         RPL23         X55954           r_at         RPL23         X55954           at         RPL23         X55954           at         RPL23         X55954           at         RPL23         X55954           at         RPL27         AA044823           at         RPL27         AA044823           at         RPL27         AA044823           at         RPL34         L36941           at         RPL34         L36941           at         RPL35         L05095           at         RPL35         L05095           at         RPL35         L05095           at         RPL34         L05360           at         RPL34		Ì				
32432_f_at         RPL15         L25899           32440_at         RPL17         X53777           31546_at         RPL18         L11566           32614_at         RPL18         X80822           32435_at         RPL21         V25789           32435_at         RPL21         U25789           32435_at         RPL22         Al526079           32345_s_at         RPL23         X55954           32345_s_at         RPL23         X55954           32344_at         RPL23         X55954           3244_at         RPL23         X55954           3244_at         RPL23         X55954           3256_at         RPL27         A044823           3244_at         RPL27         A044823           3256_at         RPL27         A15868           31708_at         RPL30         L05095           3156_at         RPL34         RPL34           3246_at         RPL35         RPL36 <t< th=""><th>_</th><th></th><th>മ</th><th>ပ</th><th>Q</th><th>J.</th></t<>	_		മ	ပ	Q	J.
RPL17   X53777   RPL18	32432_(		1PL15	L25899	ribosomal protein L15	ribosomal protein L10
RPL18			1PL17	X53777	ribosomal protein L17	ribosomal protein L17
RPL18A   X80822   RPL19   X63527   RPL21   U25789   RPL23   X55954   RPL23   X55954   RPL23   X55954   RPL23   X55954   RPL24   X69392   RPL27   X69392   RPL27   X69392   RPL27   X15940   RPL27   X15940   RPL27   X15940   RPL27   X15940   RPL32   X15941   RPL32   X15941   RPL34   RPL34   X15941   RPL34   X15941   RPL37   X15941   RPL37   X15960   RPL37   RPL37   L06499   RPL37   RPL3   Z26876   RPL3   Z26876   RPL3   X5958   RPL4   RPL4   D23660   RPL4   RPL5   U14966   RPL5   X57958   RPL6   X69391   RPL6   X69391   RPL7   X57958   RPL6   X69391   RPL8   X57958   RPS11   X06617   RPS12   A4977163   RPS12   A49	2108 31546_a		3PL18	L11566	ribosomal protein L18	ribosomal protein L18
RPL19   X63527   RPL21   U25789   RPL21   U25789   RPL23   X55954   RPL23   X55954   RPL23   X55954   RPL23   X55954   RPL24   M94314   RPL27   AA044823   RPL27   AA044823   RPL27   AA044823   RPL27   AA044823   RPL30   L05095   RPL30   L05095   RPL30   L05095   RPL30   L05095   RPL34   L38941   RPL34   L38941   RPL34   L06499   RPL37   L06499   RPL37   L06499   RPL37   L06499   RPL37   L06499   RPPL3   L06499   RPPL3   L04966   RPPL3   L04966   RPPL3   RPPL4   L053660   RPPL4   L053660   RPPL5   RPPL5   L014966   RPPL5   RPPL5   L014966   RPPL5   RPPL5   L014966   RPPL5   RPPL5   L014966   RPPL5   RPPL5   RPPL5   L014966   RPPL5   RPPL	2109 33614_e		PL18A	X80822	ribosomal protein L18a	ribosomal protein L18a
at RPL21 U25789 r at RPL22 AI526079 r at RPL23 X55954 r at RPL23 X55954 r at RPL23 X55954 r RPL24 M94314 r RPL27 AA044823 r R RPL27 AA044823 r R RPL37 AA044823 r R RPL37 L38941 r R RPL37 X03342 r R RPL36 L38941 r R RPL37 X03342 r R RPL37 X03341 r R RPL37 X57958 r R RPL6 X69391 r R RPL6 X69391 r R RPL8 Z28407 r R RPS10 U14966 r R RPL8 Z28407 r R RPS11 X06617 r A4977163 r R RPS13 AA977163 r R RPS14 AA977163 r R RPS15 AA977163 r R RPS1	2110 32435_a		1PL19	X63527	ribosomal protein L19	ribosomal protein L19
at         RPL22         AI526079           at         RPL23         X55954           at         RPL23         X55954           at         RPL23         X55954           at         RPL23         X55954           r         RPL24         M94314           r         RPL26         X69392           r         RPL27         AA044823           r         RPL27         AA044823           r         RPL27         AA044823           r         RPL30         L05095           r         RPL34         L05095           r         RPL34         L06499           r         RPL37A         L06499           r         RPL37A         L06499           r         RPL37         L04966           r         RPL44         Z12962           r         RPL4         D2360           r         RPL4         D2361	2111 32337_a		1PL21	U25789	ribosomal protein L21	ribosomal protein L21
at         RPL23         X55954         r           at         RPL23         X55954         r           at         RPL23         X55954         r           RPL24         M94314         r           RPL26         X69392         r           RPL27         AA044823         r           RPL27         AA044823         r           RPL27         AA044823         r           RPL30         L05095         r           RPL37         X15940         r           RPL36         X15940         r           RPL37         X03342         r           RPL36         X15941         r           RPL37         X03342         r           RPL36         X15961         r           RPL37         D23661         r           RPL37         D23660         r           RPL37         D23660         r           RPL36         X67966         r           RPL4         D23660         r           RPL4         D23660         r           RPL4         D23660         r           RPL4         X67956         r           RPL4 </td <td>2112 33451_s</td> <td>at</td> <td>3PL22</td> <td>AI526079</td> <td>ribosomal protein L22</td> <td></td>	2112 33451_s	at	3PL22	AI526079	ribosomal protein L22	
RPL23	2113 32395_r	at	7PL23	X55954	ribosomal protein L23	HL23 ribosomal protein
RPL234   U37230   FPL24   M94314   FPL24   M94314   FPL26   X69392   FPL27   AA044823   FPL27   U14968   FPL30   L05095   FPL31   EPL31   EPL31   EPL32   EPS32   EPS323   EPS333   EPS3333   EPS	2114 32394_s		7PL23	X55954	ribosomal protein L23	HL23 ribosomal protein
RPL24   M94314   FPL26   X69392   FPL27   AA044823   FPL27   AA044823   FPL27   C C C C C C C C C C C C C C C C C C	2115 32341 1		7PL23A	U37230	ribosomal protein L23a	ribosomal protein L23a
RPL26   X69392   r     RPL27	2116 33677_8		7PL24	M94314	ribosomal protein L24	ribosomal protein L30
RPL27   AA044823   Interpretation   RPL27A   U14968   Interpretation   U14968   Interpretation   U14968   Interpretation   U14968   Interpretation   Interpretation   U14966   Interpretation   U14972	2117 32444_E		APL26	X69392	ribosomal protein L26	ribosomal protein L26
RPL27A   U14968   PEL30   L05095   PEL31   X15940   PEL31   X15940   PEL32   X03342   PEL34   REL34   REL34   REL34   REL34   REL34   REL34   REL34   REL41   REL41   Z12962   PEL41   Z12962   PEL41   Z12962   PEL5   REL5   U14966   PEL5   REL5   U14966   PEL5   REL5   U14966   PEEL5   REL5   REL5   REL5   REL5   REPL5   REPL5   REPL5   REPL5   REPL5   REPL5   REPL5   REPL5   REPS10   U14972   PEES10   REPS11   X06617   REPS12   A4977163   REPS13   REPS14   REPS14   W52024   PEES15   W52024   PEES15   W52024	2118 39830_£		RPL27	AA044823	ribosomal protein L27	
RPL30   L05095   PRL31   X15940   PRL32   X03342   PRL34   L38941   PRL34   L38941   PRL34   L38941   PRL35   A1541285   PRL35   A1541285   PRR37   D23661   PRL37   D23660   PRR41   D23660   PRR41   D23660   PRR51   X67958   PRR51   X67958   PRS10   D14966   PRS11   X06617   PRS11   X06617   PRS11   X06617   PRS12   A4977163   PRS13   C1124   PRS15   W52024   PRS15   W52024	2119 32436_8		RPL27A	U14968	ribosomal protein L27a	ribosomal protein L27a
RPL31   X15940   RPL32   X03342   RPL34   L38941   L39941   L399	2120 31708		RPL30	L05095	ribosomal protein L30	ribosomal protein L30
RPL32   X03342   In the control of	2121 33676		RPL31	X15940	ribosomal protein L31	ribosomal protein L31
RPL34   L38941   L38941   RPL35   Al541285   RPL35   L06499   L26876   RPL37A   L06499   L26876   RPL38   L26876   L26876   RPL41   Z12962   L46876   L46976   L469	2122 32276		RPL32	X03342	ribosomal protein L32	ribosomal protein L32
at RPL35 AI541285 i RPL36A T89651 i RPL37 D23661 i RPL37A L06499 i RPL38 Z26876 i RPL41 Z26876 i RPL41 Z12962 i RPL5 U14966 i RPL5 X69391 i RPL6 X69391 i RPL6 X69391 i RPL7 X57958 i RPL8 Z28407 i RPS10 U14972 i RPS11 X06617 i RPS11	2123 33657_1		RPL34	L38941	ribosomal protein L34	ribosomal protein L34
fat         RPL36A         T89651         I           at         RPL37         D23661         I           at         RPL37A         L06499         I           at         RPL38         Z26876         I           at         RPL4         D23660         I           at         RPL41         Z12962         I           at         RPL5         U14966         I           at         RPL5         X69391         I           at         RPL6         X69391         I           at         RPL8         Z28407         I           at         RPS10         U14972         I           at         RPS11         X06617         I           t at         RPS11         X06617         I           t at         RPS12         AA977163         I           at         RPS13         W52024         I	2124 41765		RPL35	AI541285	ribosomal protein L35	
RPL37   D23661   RPL37A   L06499   RPL38   Z26876   RPL41   D23660   RPL41   Z12962   RPL5   U14966   RPL6   X69391   RPL8   Z28407   RPS10   U14972   RPS10   U14972   RPS11   X06617   RPS11   X06617   RPS12   A4977163   RPS13   L01124   RPS13   L01124   RPS15A   W52024	2125 41152		RPL36A	T89651	ribosomal protein L36a	
RPL37A   L06499   RPL38   Z26876   RPL41   Z12962   RPL41   Z12962   RPL5   U14966   RPL6   X69391   RPL7   X57958   RPL8   Z28407   RPS10   U14972   RPS11   X06617   A4977163   RPS13   L01124   RPS13   L01124   RPS15   W52024	2126 33656_		RPL37	D23661	ribosomal protein L37	ribosomal protein L37
RPL38   Z26876   RPL41   D23660   RPL41   Z12962   RPL5   U14966   RPL6   X69391   RPL7   X57958   RPL8   Z28407   RPS10   U14972   RPS11   X06617   X06617   RPS12   A4977163   RPS13   L01124   RPS15   W52024	2127 31962	at	RPL37A	L06499	ribosomal protein L37a	ribosomal protein L37a
RPL4   D23660   RPL41   Z12962   RPL5   U14966   RPL6   X69391   RPL7   X57958   RPL8   Z28407   RPS10   U14972   RPS11   X06617   RPS12   A4977163   RPS13   L01124   RPS15A   W52024	2128 34085		RPL38	Z26876	ribosomal protein L38	ribosomal protein
RPL41   Z12962   RPL5   U14966   RPL6   X69391   RPL7   X57958   RPL8   Z28407   RPS10   U14972   RPS11   X06617   X06617   RPS12   AA977163   RPS13   L01124   RPS15A   W52024	2129 33485		RPL4	D23660	ribosomal protein L4	ribosomal protein
RPL41   Z12962   RPL5   U14966   RPL6   X69391   RPL7   X57958   RPL7   Z28407   RPS10   U14972   RPS11   X06617   A977163   RPS12   A4977163   RPS13   L01124   at RPS15A   W52024					_	human homologue to yeast ribosomal
RPL5   U14966   RPL6   X69391   RPL6   X69391   RPL7   X57958   RPL8   Z28407   RPS10   U14972   RPS11   X06617   RPS12   AA977163   RPS13   L01124   RPS15A   W52024	2130 32466		RPL41	Z12962	ribosomal protein L41	protein YL41
RPL6   X69391   RPL7   X57958   RPL8   Z28407   RPS10   U14972   RPS11   X06617   A977163   RPS12   A4977163   RPS13   L01124   RPS15A   W52024	2131 33660		RPLS	U14966	ribosomal protein L5	ribosomal protein L5
RPL7   X57958   RPL8   Z28407   RPS10   U14972   RPS11   X06617   RPS12   AA977163   RPS13   L01124   RPS15A   W52024	2132 31952		RPL6	X69391	ribosomal protein L6	ribosomal protein L6
RPL8   Z28407   RPS10   U14972   RPS11   X06617   RPS12   AA977163   RPS13   L01124   RPS15A   W52024	2133 36333		RPL7	X57958	ribosomal protein L7	ribosomal protein L7
APS10 U14972  APS11 X06617  APS12 AA977163  APS13 L01124  ARPS15A W52024	2134 31505	at	RPL8	Z28407	ribosomal protein L8	ribosomal protein L8
at RPS12 AA977163 RPS12 AA977163 RPS13 L01124 at RPS15A W52024.	2135 31568		RPS10	U14972	ribosomal protein S10	ribosomal protein S10
at RPS12 AA977163 RPS13 L01124 at RPS15A W52024	2136 32330		RPS11	X06617	ribosomal protein S11	ribosomal protein S11
at RPS154 L01124	2137 33116	at	RPS12	AA977163	ribosomal protein S12	
at RPS15A W52024	2138 33619	at	RPS13	L01124	ribosomal protein S13	ribosomal protein S13
	2139 34317	g_at	RPS15A	W52024	ribosomal protein S15a	ribosomal protein S15a
_at.   RPS16   Al541256	2140 38061	at	RPS16	AI541256	ribosomal protein S16	

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2141	34593_g_at	RPS17	M13932	ribosomal protein S17	ribosomal protein S17
2142	2142 34592_at			ribosomal protein S17	ribosomal protein S17
2143	2143 31330_at	RPS19	M81757	ribosomal protein S19	S19 ribosomal protein
2144	2144 31527_at		X17206	ribosomal protein S2	ribosomal protein S2
2145	2145 32438_at	RPS20	L06498	ribosomal protein S20	ribosomal protein S20
2146	2146 347_s_at	RPS23	D14530	ribosomal protein S23	ribosomal protein
2147	2147 32315_at	RPS24	M31520	ribosomal protein S24	ribosomal protein S24
2148	2148 31573_at	RPS25	M64716	ribosomal protein S25	ribosomal protein
				ribosomal protein S27 (metallopanstimulin	
2149	2149 32748_at		AI557852	1)	
2150	2150 34570_at	RPS27A	S79522	ribosomal protein S27a	ubiquitin carboxyl extension protein
2151	39798_at	RPS28	R87876	ribosomal protein S28	
2152	34645_at	RPS3	X55715	ribosomal protein S3	ribosomal protein S3
2153	2153 1653_at	RPS3A	M84711	ribosomal protein S3A	v-fos transformation effector protein
2154	34643_at	RPS4X	M58458	ribosomal protein S4, X-linked	ribosomal protein S4X isoform
2155	32437_at	RPSS	U14970	ribosomal protein S5	ribosomal protein S5
2156	31511	RPS9	U14971	ribosomal protein S9	ribosomal protein S9
2157	31538_at	RPLP0	M17885	ribosomal protein, large, P0	ribosomal protein P0
2158	31956_f_at	RPLP1	M17886	ribosomal protein, large, P1	ribosomal protein P1
2159	31957_r_at	RPLP1	M17886	ribosomal protein, large, P1	ribosomal protein P1
				ribosome binding protein 1 homolog	
2160	2160 33213_g_at	RRBP1	AF006751	180kD (dog)	ES/130
				Ric-like, expressed in many tissues	
2161	2161 38331_at	RIT	Y07566	(Drosophila)	Ric-like, expressed in many tissues
2162	2162 35656_at	RNF6	AJ010346	ring finger protein (C3H2C3 type) 6	RING-H2
2163	2163 39150_at	RNF11	U69559	ring finger protein 11	
2164	2164 35811_at	RNF13	AF037204	ring finger protein 13	RING zinc finger protein
2165	2165 33343_at	RNF14	AB022663	ring finger protein 14	ring finger protein 14
2166	2166 33484_at	RNF2	Y10571	ring finger protein 2	ring finger protein 2
2167	2167 37964_at	RNF3	W25793	ring finger protein 3	
2168	35777_at	RNF4	AB000468	ring finger protein 4	zinc finger protein
				ring zinc-finger protein; escapes X	
				chromosome inactivation; Human ring zinc	
				finger protein (ZNF127-Xp) gene and 5'	
2169	2169 37650_at	ZNF127-Xp	U41315	flanking sequence.	ZNF127-Xp
2170	2170 37732_at	RYBP	AL049940	RING1 and YY1 binding protein	

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1713		RNMT	AB007858	RNA (guanine-7-) methyttransferase	RNA (guanine-7-) methyltransferas
1724	2172 41460 at	RBM14		RNA binding motif protein 14	SYT interacting protein SIP
173					RNPL
1743		RBM4			Hlark
2175		RBM5	AF091263		RNA binding motif protein 5
21764	at	RBM6	AF069517		RNA binding protein DEF-3
11/2		RBM9	AL009266		hypothetical protein
2178	2178 39731 at	RBMX	723064	RNA binding motif protein, X chromosome hnRNP G protein	hnRNP G protein
				RNA binding motif, single stranded	RNA binding motif, single stranded
2179	2179 33867_s_at	RBMS1	X77494	interacting protein 1	interacting protein 1, isoform a
				RNA binding protein S1, serine-rich	=
2180	2180 36186_at	RNPS1 ~	L37368	domain	HNA-binding protein
				RNA guanylyttransferase and 5'-	
2181	2181 35202_at	RNGTT	AF025654	phosphatase	mRNA capping enzyme
2182	2182 33237_at	KIAA0801	AB018344	RNA helicase	KIAA0801 protein
2183	2183 36045_at	RNAH	AJ223948	RNA helicase family	RNA helicase
2184	2184 38762 at	RNAHP	AF083255	RNA helicase-related protein	RNA helicase-related protein
				RNA-binding protein gene with multiple	
2185	2185 38049 q at	RBPMS	D84110	splicing	RBP-MS/type 4
				RNA-binding protein gene with multiple	
2186	2186 38047 at	RBPMS	D84109	splicing	RBP-MS/type 3
2187	2187 38974 at	53-1	AF021819	RNA-binding protein regulatory subunit	RNA-binding protein regulatory subunit
				RNA-binding region (RNP1, RRM)	
2188	2188 39725 at	RNPC2	L10910	containing 2	splicing factor
2189	2189 38011 at	RMP	AB006572	RPB5-mediating protein	RPB5 meidating protein
2190	2190 35195_at	RTCD1	Y11651	RTC domain containing 1	phosphate cyclase
				runt-related transcription factor 1 (acute	
2191	2191 943_at	RUNX1	D43968	myeloid leukemia 1; aml1 oncogene)	AML1b protein
		i i	27077		erythrocyte cytosolic protein of 54 kDa, ECP-
2192	2192 40124_at	HOVBLI	10410	Carbellas (C. coll)	Dind like DNIA helience TIDAOh
2193	2193 35758_at	RUVBL2	AB024301	HuvB-like 2 (E. coli)	HUVD-IIKE DIVA HEIICASE HIT 43D
				S100 calcium binding protein A10 (annexin II ligand, calpactin I, light	
2194	2194 39338_at	S100A10	A[201310	polypeptide (p11))	
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1				ntaining inositol	
2195 3	36089_at	SAC2	AB023183		KIAAU966 protein
				ntaining inositol	
196	2196 41101 at	SAC3	D87464	_	KIAA0274 gene product
				SAC1 suppressor of actin mutations 1-like	
197	2197 36511_at	SACM1L	AB020658	(yeast)	KIAA0851 protein
198	2198 34792_at	AHCYL1	AL049954	S-adenosylhomocysteine hydrolase-like 1 hypothetical protein	hypothetical protein
3199	2199 41302 at	AHCYL1	. R59606	S-adenosylhomocysteine hydrolase-like 1	
,     	2200 36685 at	AMD1	_	_	
					S-adenosylmethionine decarboxylase 1
2201	2201 263_g_at	AMD1	M21154	ne decarboxylase 1	precursor
2202	2202 41449 at	SGCE	AJ000534		epsilon-sarcoglycan
2203	2203 36083 at	SAS	U01160		SAS
2204	2204 36536 at	SCHIP1	AF070614	schwannomin interacting protein 1	schwannomin interacting protein 1
2205	2205 33423 g at	SEC13L1	AF052155	SEC13-like 1 (S. cerevisiae)	SEC13 (S. cerevisiae)-like 1
2206	2206 33422 at	SEC13L1	AF052155	SEC13-like 1 (S. cerevisiae)	SEC13 (S. cerevisiae)-like 1
2207	2207 36207 at	SEC14L1	D67029	SEC14-like 1 (S. cerevisiae)	SEC14 (S. cerevisiae)-like 1
2208	2208 39099 at	SEC23A	X97064	Sec23 homolog A (S. cerevisiae)	Sec23 protein
				SEC24 related gene family, member A (S.	
2209	2209 34199 at	SEC24A	AJ131244	cerevisiae)	Sec24A protein
	1			SEC24 related gene family, member B (S.	
2210	2210 35845 at	SEC24B	AJ131245	cerevisiae)	Sec24B protein
				SEC24 related gene family, member D (S.	
2211	2211 32770 at	SEC24D	AB018298	cerevisiae)	KIAA0755 protein
2212	2212 34349 at	SEC63L	AJ011779	SEC63 protein	SEC63 protein
2213	2213 32521 at	SFRP1	AF056087	secreted frizzled-related protein 1	secreted frizzled related protein
				secreted phosphoprotein 1 (osteopontin,	
				bone sialoprotein I, early T-lymphocyte	
2214	2214 34342 s at	SPP1	AF052124	activation 1)	osteopontin
				secreted protein, acidic, cysteine-rich	secreted protein, acidic, cysteine-ncn
2215	2215 671_at	SPARC	J03040	(osteonectin)	(osteonectin)
				secretory granule, neuroendocrine protein	secretory granule, neuroendocrine protein (secretory granule, neuroendocrine protein)
2216	2216 34265_at	SGNE1	Y00757	1 (/BZ protein)	(102 piotein)
2217	2217 37405_at	SELENBP1	U29091	selenium binding protein 1	selenium-binding proteiii



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2218	39078_at	SPS2	U43286	se 2	selenophosphate synthetase 2
2219	at	SEPP1	Z11793		selenoprotein P
T				sema domain, immunoglobulin domain	
				(Ig), short basic domain, secreted,	
2220	2220 377_g_at	SEMA3C	AB000220		semaphorin E
				sema domain, immunoglobulin domain	
2221	2221 376 at	SEMA3C	AB000220		semaphorin E
				sema domain, immunoglobulin domain	
				(Ig), short basic domain, secreted,	
2222	2222 35666_at	SEMA3F	U38276	(semaphorin) 3F	semaphorin III family homolog
2223	2223 38826 at	2	-Sep D50918	septin 6	septin 2
					phosphotyrosine independent ligand for the
2224	2224 40898_at	SOSTM1	U46751	sequestosome 1	Lck SH2 domain p62
				serine (or cysteine) proteinase inhibitor,	
2225	2225 34789_at	SERPINB6	S69272	clade B (ovalbumin), member 6	cytoplasmic antiproteinase
				serine (or cysteine) proteinase inhibitor,	serine (or cysteine) proteinase inhibitor,
				clade E (nexin, plasminogen activator	clade E (nexin, plasminogen activator
2226	2226 38125 at	SERPINE1	M14083	inhibitor type 1), member 1	inhibitor type 1), member 1
				serine (or cysteine) proteinase inhibitor,	
				clade H (heat shock protein 47), member	
2227	2227 39167_r_at	SERPINH2	D83174	2	collagen binding protein 2
				serine palmitoyftransferase, long chain	
2228	2228 38818 at	SPTLC1	Y08685	base subunit 1	serine palmitoyttransferase, subunit l
				serine threonine kinase 39 (STE20/SPS1	
2229	2229 40966_at	STK39	AF099989	homolog, yeast)	Ste-20 related kinase SPAK
2230	2230 41737 at	SRRM1	AF048977	serine/arginine repetitive matrix 1	Ser/Arg-related nuclear matrix protein
2231	2231 36019 at	STK19	126260	serine/threonine kinase 19	RP protein
				serine/threonine kinase 24 (STE20	
2232	2232 40473_at	STK24	AF024636	homolog, yeast)	STE20-like kinase 3
				serine/threonine kinase 3 (STE20	
2233	2233 32142_at	STK3	U26424	homolog, yeast)	MST2
				serine/threonine-protein kinase PRP4	
2234	2234 32784_at	PRP4	AB011108	homolog	KIAA0536 protein

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Γ				serum response factor (c-fos serum	serum response factor (c-tos serum
				response element-binding transcription	response element-binding transcription
2235	2235 40109 at	SRF	J03161	factor)	factor)
				serum response factor (c-fos serum	serum response factor (c-fos serum
		-		response element-binding transcription	response element-binding transcription
2236	2236 1409 at	SRF	J03161	factor)	factor)
2237	2237 41544 at	SNK	AF059617	serum-inducible kinase	serum-inducible kinase
223B		SARS	X91257	servi-tRNA synthetase	seryl-tRNA synthetase
	ii-			SET translocation (myeloid leukemia-	SET translocation (myeloid leukemia-
2239	2239 40189_at	SET	M93651	associated)	associated)
2240	2240 32160 at	SIAH1	U76247	seven in absentia homolog 1 (Drosophila) hSIAH1	hSIAH1
2241	2241 33799 at	SIAH2	U76248	seven in absentia homolog 2 (Drosophila)	hSIAH2
2242	2242 39088 at	NIFIE14	Y18007	seven transmembrane domain protein	seven transmembrane domain protein
				seventh largest subunit; Human RNA polymerase II seventh subunit (rpb-7)	
2243	2243 39747 at	rob-7	U52427	gene, complete cds.	RNA polymerase II seventh subunit
2244		SCML2	Y18004	sex comb on midleg-like 2 (Drosophila)	SCML2 protein
				SH3 domain binding glutamic acid-rich	
2245	2245 36040_at	SH3BGR	AI337192	protein	
				SH3 domain binding glutamic acid-rich	SH3 domain binding glutamic acid-rich-like
2246	2246 39714_at	SH3BGRL	AF042081	protein like	protein
				SH3-domain binding protein 5 (BTK-	
2247	2247 38968_at	SH3BP5	AB005047	associated)	SH3 binding protein
2248	2248 39691_at	SH3GLB1	AB007960	SH3-domain GRB2-like endophilin B1	SH3-containing protein SH3GLB1
				SHC (Src homology 2 domain containing)	
2249	2249 38118_at	SHC1	U73377	transforming protein 1	p66shc
				sialyttransferase 9 (CMP-	
				NeuAc:lactosylceramide alpha-2,3-	
2250	2250 34256_at	SIAT9	AB018356	sialyttransferase; GM3 synthase)	GM3 synthase
2251	2251 39139_at	SPC18	Al357653	signal peptidase complex (18kD)	
				signal recognition particle 14kD	
2252	2252 41194_at	SRP14	AI525652	(homologous Alu RNA binding protein)	3
2253	2253 35231_at	SRP19	X12791	signal recognition particle 19kD	signal recognition particle 19kD
2254	2254/36060_at	SRP54	U51920	signal recognition particle 54kD	signal recognition particle

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255	at at	SRP72	AF069765	signal recognition particle 72kD	signal recognition particle 72
2256		SRP9	AF070649		
				ptor	signal recognition particle receptor (docking
2257	2257 36679_at	SRPR	X06272		protein')
Γ				sactivator of	
2258	2258 AFFX-HUMISGFISTAT1	STAT1	M97935		transcription factor ISGF-3
				d activator of	
2259	2259 32860 q at	STAT1	M97935		transcription factor ISGF-3
				signal transducer and activator of	1
2260	2260 32859 at	STAT1	M97935		transcription factor ISGF-3
				signal transducer and activator of	
2261	2261 33338 at	STAT1	M97936	transcription 1, 91kD	
				signal transducer and activator of	
				transcription 3 (acute-phase response	
2262	2262 39708 at	STAT3	129277	factor)	DNA-binding protein
				signal transducing adaptor molecule (SH3	
2263	2263 160 at	STAM	U43899	domain and ITAM motif) 1	STAM
				similar to Drosophila ash2 gene; Homo	
				sapiens ASH2L gene, complete cds,	
2264	2264 35804_at	ASH2L	AB022785	similar to Drosophila ash2 gene.	
2265	2265 41552 q at	RER1	AW044624	similar to S. cerevisiae RER1	
2266	2266 41551 at	RER1	AW044624	similar to S. cerevisiae RER1	
2267	2267 33632 g at	DIM1	AF023612	similar to S. pombe dim1+	Dim1p homolog
				similar to SW:GOLI_DROME Q06003	
2268	2268 35083_at	G1L	AL031670	GOLIATH PROTEIN	ring finger protein 24
2269	2269 37178 at	na	M74089	similar to TB1	
				similar to Wiskott-Aldrich syndrome	
2270	2270 40787 at	WIRE	110001	protein interacting protein	
2271	2271 34705 at	BET3	AJ224335	similar to yeast BET3 (S. cerevisiae)	hBET3 protein
2272	2272 39131 at	UPF3A	N36842	similar to yeast Upf3, variant A	
2273	2273 41277 at	SAP18	AW021542	sin3-associated polypeptide, 18kD	
2274	2274 33859 at	SAP18	U96915	sin3-associated polypeptide, 18kD	sin3 associated polypeptide p18
2275	2275 40992_s_at	SAP30	AF055993	sin3-associated polypeptide, 30kD	mSin3A associated polypeptide p30
				sine oculis homeobox homolog 1	sine oculis homeobox (Urosophila) nomotog
2276	2276 40004_at	SIX1	X91868	(Drosophila)	

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				fascin homolog, sea urchin)	
2277	2277 39070_at	SNL	U03057		actin bundling protein
2278	2278 39086_g_at	SSBP1	AA768912		
2279		SSBP2		2	hypothetical protein
2280	2280 35294_at	SSA2	M25077	<u>@</u>	60kD Ro/SSA autoantigen
2281	2281 35295_g_at	SSA2	M25077	ribonucleoprotein autoantigen SS-A/Ro)	60kD Ro/SSA autoantigen
		-		gren syndrome antigen B (autoantigen	Sjogren syndrome antigen B (autoantigen
2282	2282 38450_at	SSB		(a.)	La)
2283	2283 37715_at	SNW1	AF045184	SKI-interacting protein	nuclear receptor coactivator NCoA-62
2284	2284 37389_at	IMAGE145052	A1346580	small acidic protein	
				small nuclear ribonucleoprotein 70kD	
2285	2285 40875_s_at	SNRP70	X06815	polypeptide (RNP antigen)	hU1-70K-like protein (216 AA)
				small nuclear ribonucleoprotein	
2286	2286 38679_g_at	SNRPE	AA733050	polypeptide E	
				small nuclear ribonucleoprotein	
2287	2287 37337_at	SNRPG	AI803447	polypeptide G	
				small nuclear ribonucleoprotein	
2288	2288 34842_at	SNRPN	U41303	polypeptide N	small nuclear ribonuleoprotein particle N
				small nuclear RNA activating complex,	
2289	2289 35247_at	SNAPC5	AI557062	polypeptide 5, 19kD	
				SMART/HDAC1 associated repressor	
2290	2290 32172_at	SHARP	AL096858	protein	hypothetical protein
				SMC1 structural maintenance of	
2291	32849_at	SMC1L1	D80000	chromosomes 1-like 1 (yeast)	
				SMT3 suppressor of mif two 3 homolog 1	
2292	2292 38738_at	SMT3H1	X99584	(yeast)	SMT3A protein
				SMT3 suppressor of mif two 3 homolog 2	
2293	2293 41185_f_at	SMT3H2	Al971724	(yeast)	
2294	2294 38288_at	SNAI2	U69196	snail homolog 2 (Drosophila)	
				soc-2 suppressor of clear homolog (C.	
2295	2295 38659_at	SHOC2	AB020669	elegans)	KIAA0862 protein
2296	2296 40928 at	WSB1	W26496	SOCS box-containing WD protein SWiP-1	
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2297	2297 36609_at		D26443	solute carrier family 1 (glial high affinity glutamate transporter), member 3	glutamate transporter
2298	2298 35320_at	SLC11A2	AB004857	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 NRAMP2	NRAMP2
2299	2299 33143_s_at	SLC16A3	U81800	solute carrier family 16 (monocarboxyfic acid transporters), member 3	monocarboxylate transporter
2300	2300 39260_at	SLC16A4	U59185	solute carrier family 16 (monocarboxylic acid transporters), member 4	solute carrier family 16 (monocarboxylic acid transporters), member 4
2301	2301 36979_at	SLC2A3	M20681	solute carrier family 2 (facilitated glucose transporter), member 3	solute carrier family 2 (facilitated glucose transporter), member 3
2302	2302 32084_at	SLC22A5	AF057164	solute carrier family 22 (organic cation transporter), member 5	organic cation transporter OCTN2
2303	2303 38122_at	SLC23A1	D87075	solute carrier family 23 (nucleobase transporters), member 1	
				solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator),	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator),
2304	2304 32822_at	SLC25A4	J02966	member 4	member 4
2000		24 20 10	60000	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator),	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), memher 5
	מין אסין אסין אין אין אין אין אין אין אין אין אין א	OFOSCA C	20220	solute carrier family 25 (mitochondrial carrier: adenine nacleotide translocator),	
2306	2306 40436_g_at	SLC25A6	J03592	member 6	
2307	2307 40435 at	SLC25A6	103592	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	
2308	2308 37675 at	SLC25A3	X60036	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	phosphate carrier protein
2309	2309 33901_at	SLC29A1	U81375	solute carrier family 29 (nucleoside transporters), member 1	equilibrative nucleoside transporter 1
2310	2310 40364_at	SLC31A1	U83460	solute carrier family 31 (copper transporters), member 1	high-affinity copper uptake protein



A B B C   Solute carrier family 31 (copper 2015)   Solute carrier family 31 (copper 2015)   Solute carrier family 31 (copper 2015)   Solute carrier family 32 (CMP-sialic acid CMP-sialic acid transporter 2015   Solute carrier family 32 (CMP-sialic acid copper uptake protein 2015   Solute carrier family 32 (CMP-sialic acid farisporter 2015   Solute carrier family 32 (CMP-sialic acid farisporter 2015   Solute carrier family 32 (CMP-sialic acid farisporter 2015   Solute carrier family 32 (CMP-sialic acid farisporter 2015   Solute carrier family 32 (CMP-sialic acid farisporter 2015   Solute carrier family 32 (CMP-sialic acid farisporter 2015   Solute carrier family 32 (CMP-sialic acid farisporter 2015   Solute carrier family 32 (CMP-sialic acid farisporter 2015   Solute carrier family 32 (caltoric amino acid solute carrier family 32 (caltori						
SLC31A2		¥	8		0	IJ
SLC35A1					copper	urtafiva copper uptake protein
SLC35A1 D87969   1	311	4449_8t			1 1 1 1 1 1 1	diagno coppor aprairo process
SLC35A1 D87969   SLC35A3   AB021981   SLC35A3   AB021981   SLC4A7   SB0071   SLC6A7   SB0071   SLC7A5   M80244   SLC7A6   D87432   SLC7A6   D87432   SCA753   SCA755   SCA75755   SCA757						
SLC35A3	2312 3	37895_at	_			CMP-static acid transporter
SLC35A3 AB021981  SLC4A7 AB012130  SLC6A7 S80071  SLC7A6 D87432  SLC7A6 D87432  SLC9A6 AF030409  SON X63753  AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034545  SNX3 AF03455  SNX3 AF034545  SNX5 AF034545  SNX5 AF034545  SNX5 AF034545  SNX5 AF034545  SNX5 AF034545  SNX5 AF034545  SNX5 AF034545  SNX5 AF034545  SNX5 AF034545  SNX5 AF034545  SNX5 AF034545  SNX5 AF034545  SNX5 AF034545  SNX5 AF034545  SNX5 AF034545  SNX5	$\vdash$				solute carrier family 35 (UDP-N-	
SLC36A3 AB021981  SLC4A7 AB012130  SLC6A7 S80071  SLC7A6 M80244  SLC7A6 D87432  SLC7A6 D87432  SLC9A1 S68616  SON X63753  AF03446  SNX2 AF034546  SNX3 AF034546  SNX4 AA524345  SNX7 AL049989  It SC-35 X75755  at SC-35 X75755		_			L-GICIAAC)	
SLC4A7 AB012130  SLC6A7 S80071  SLC7A5 M80244  SLC7A6 D87432  SLC7A6 D87432  SLC9A1 S68616  SLC9A6 AF030409  SON X63753  AF034546  SNX2 AF034546  SNX4 AA524345  SNX7 AL049989  H2A X57985  H2A X57985  H2A X57985  H2A X57985  H2A X57985	2313	38208_at	SLC35A3			UDP-N-acety/glucosamine transporter
SLC4A7 AB012130  SLC6A7 S80071  SLC7A6 M80244  SLC7A6 D87432  SLC9A1 S68616  SLC9A6 AF030409  SON X63753  AF034546  SNX2 AF034545  SNX3 AF034546  SNX4 AA524345  SNX7 AL049989  It SC-35 X75755  at SC-35 X75755					dium bicarbonate	
SLC6A7 S80071  SLC7A5 M80244  SLC7A6 D87432  SLC9A1 S68616  SLC9A6 AF030409  SON X63753  SON X63753  SON X63753  SON X63753  SON X63753  SON X63753  AF030409  SNX2 AF034546  SNX2 AF034546  SNX3 AF034546  SNX4 AA524345  SNX7 AL049989  It SC-35 X75755  at SC-35 X75755	2314	34936_at	SLC4A7	AB012130		sodium bicarbonate cotransporterz
SLC6A7 S80071  SLC7A5 M80244  SLC7A6 D87432  SLC9A1 S68616  SLC9A6 AF030409  SON X63753  AF030409  SONX AF034545  SNXA AF0355  SNXA AF034545					mitter	
SLC7A5 M80244  SLC7A6 D87432  SLC9A1 S68616  SLC9A6 AF030409  SON X63753  SON X63753  SON X63753  SON X63753  SON X63753  AF034546  SNX2 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034545	2315	34166_at	SLC6A7	S80071		brain-specific L-proline transporter
SLC7A5 M80244  SLC7A6 D87432  SLC9A1 S68616  SLC9A6 AF030409  SON X63753  SON X63753  SON X63753  SON X63753  SON X63753  SON X63753  AF034345  SNX2 AF065482  SNX2 AF065482  SNX2 AF065482  SNX2 AF065482  SNX2 AF065482  SNX4 AA524345  SNX7 AL049989  It SC-35 X75755  at SC-35 X75755					colute cerrier family 7 (cationic amino acid	solute carrier family 7 (cationic amino acid
SLC7A6 D87432  SLC7A6 D87432  SLC9A1 S68616  SLC9A6 AF030409  SON X63753  SON X63753  SON X63753  SON X63753  SON X63753  AF034546  SNX2 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX4 AA524345  SNX7 AL049989  It SC-35 X75755  at SC-35 X75755	- 0,00	40 00	245	W000044	transporter vt evetem) member 5	transporter, v+ system), member 5
SLC7A6 D87432  SLC9A1 S68616  SLC9A6 AF030409  SON X63753  SON X63753  SON X63753  SON AF03409  SNX2 AF065482  SNX3 AF03456  SNX4 AA524345  SNX7 AL049989  It SC-35 X75755  at SC-35 X75755	210	32186 at	SLC/A5	Mouz44		
SLC7A6 D87432  SLC9A1 S68616  SLC9A6 AF030409  SON X63753  SON X63753  SONZ L13858  SNX2 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX3 AF034546  SNX4 AA524345  SNX7 AL049989  It SC-35 X75755  at SC-35 X75755			-		solute carrier family 7 (cationic amino acid	solute carrier family 7 (cationic amino acid
SLC9A1 S68616 amiloride sensitive) SLC9A1 S68616 amiloride sensitive) SLC9A6 AF030409 exchanger), isoform 1 (antiporter, Na+/H+, amiloride sensitive) SLC9A6 AF030409 exchanger), isoform 6 SON X63753 SON DNA binding protein SNX2 AF03454 son of sevenless homolog 2 (Drosophila) SNX3 AF03454 sorting nexin 2 SNX3 AF03454 sorting nexin 3 SNX3 AF03454 sorting nexin 3 SNX1 AA524345 sorting nexin 4 SNX2 AL049989 sorting nexin 7 SNX3 AF03456 sorting nexin 7 SNX3 AF03456 sorting nexin 7 SNX5 AL049989 sorting nexin 7 SOUTCE: H.sapiens genes for histones at SC-35 SOUTCE: H.sapiens PR264 gene.	2317	39533 at	SLC7A6	D87432	transporter, y+ system), member 6	transporter, y+ system), member 6
SLC9A1 S68616 amiloride sensitive) SLC9A1 S68616 amiloride sensitive) SLC9A6 AF030409 exchanger), isoform 1 (antiporter, Na+/H+, amiloride sensitive) SON X63753 Solute carrier family 9 (sodium/hydrogen exchanger), isoform 6 SON X63753 SON DNA binding protein SNX2 AF036482 sorting nexin 2 SNX3 AF034546 sorting nexin 3 SNX3 AF034546 sorting nexin 3 SNX4 AA524345 sorting nexin 3 SNX7 AL049989 sorting nexin 4 SNX7 AL049989 sorting nexin 7 SNX7 AL049989 sorting nexin 7 SOUTCE: H.sapiens genes for histones at SC-35 SOUTCE: H.sapiens PR264 gene.						
SLC9A1   S68616   amiloride sensitive)   SLC9A1   S68616   amiloride sensitive)   SLC9A6   AF030409   exchanger), isoform 6   SCON   X63753   SON DNA binding protein   SON2   L13858   son of sevenless homolog 2 (Drosophila)   SNX2   AF034345   sorting nexin 3   SNX3   AF034345   sorting nexin 3   SNX7   AL049989   sorting nexin 7   SNX7   AL049989   sorting nexin 7   SOUTCE: H.sapiens genes for histones   H2A   X57985   H2B.1 and H2A.   SOUTCE: H.sapiens PR264 gene.   Source: H.sapiens PR264 gene.					solute carrier family 9 (sodium/hydrogen	
SLC9A6 AF030409 exchanger), isoform 6 SLC9A6 AF030409 exchanger), isoform 6 SON X63753 SON DNA binding protein SOS2 L13858 son of sevenless homolog 2 (Drosophila) SNX2 AF065482 sorting nexin 2 SNX3 AF034546 sorting nexin 3 SNX4 AA524345 sorting nexin 4 SNX7 AL049989 sorting nexin 7 SNX7 AL049989 sorting nexin 7 SOUTCE: H.sapiens genes for histones H2A X57985 H2B.1 and H2A. It SC-35 SOUTCE: H.sapiens PR264 gene.	2318	32681_at	SLC9A1	S68616	amiloride sensitive)	Na+/H+ exchanger NHE-1 isoform
SLC9A6         AF030409         exchanger), isoform 6           SON         X63753         SON DNA binding protein           SOS2         L13858         son of sevenless homolog 2 (Drosophila)           SNX2         AF034546         sorting nexin 2           SNX3         AF034546         sorting nexin 3           SNX4         AA524345         sorting nexin 7           SNX7         AL049989         sorting nexin 7           SNX7         AL049989         sorting nexin 7           SOURCE: H.sapiens genes for histones           HZA         X57985         H2B.1 and H2A.           ALC-35         X75755         Source: H.sapiens PR264 gene.           SC-35         X75755         Source: H.sapiens PR264 gene.					colite cerrier family 9 (sodium/hydroden	
SON         X63753         SON DNA binding protein           SOS2         L13858         son of sevenless homolog 2 (Drosophila)           SNX2         AF065482         sorting nexin 2           SNX3         AF034546         sorting nexin 3           SNX4         AA524345         sorting nexin 4           SNX7         AL049989         sorting nexin 7           SNX7         AL049989         sorting nexin 7           SOUTCE: H.sapiens genes for histones         H2B.1 and H2A.           A57985         H2B.1 and H2A.           A57555         Source: H.sapiens PR264 gene.           A75755         Source: H.sapiens PR264 gene.	2210	36542 at	21 C 0 A B	A F030409	exchanger) isoform 6	sodium-hydrogen exchanger 6
SOS2         L13858         son of sevenless homolog 2 (Drosophila)           SNX2         AF034546         sorting nexin 2           SNX3         AF034546         sorting nexin 3           SNX4         AA524345         sorting nexin 4           SNX7         AL049989         sorting nexin 7           SNX7         AL049989         sorting nexin 7           Source: H.sapiens genes for histones         H2B.1 and H2A.           AK57985         H2B.1 and H2A.           AK5755         Source: H.sapiens PR264 gene.           SC-35         X75755           Source: H.sapiens PR264 gene.	2320	39097_at	SON	X63753	SON DNA binding protein	SON DNA-binding protein
SNX2         AF035482         sorting nexin 2           SNX3         AF034546         sorting nexin 3           SNX4         AA524345         sorting nexin 4           SNX7         AL049989         sorting nexin 7           SOUTCE: H.sapiens genes for histones         Source: H.sapiens for histones           NX7         X57985         H2B.1 and H2A.           NX5755         Source: H.sapiens PR264 gene.           SC-35         X75755         Source: H.sapiens PR264 gene.	2321	32857 at	SOS	L13858		guanine nucleotide exchange factor
SNX3         AF034546         sorting nexin 3           SNX4         AA524345         sorting nexin 4           SNX7         AL049989         sorting nexin 7           Source: H.sapiens genes for histones         Source: H.sapiens for histones           H2A         X57985         H2B.1 and H2A.           It         SC-35         X75755           Source: H.sapiens PR264 gene.         Source: H.sapiens PR264 gene.	2322	41462 at	SNX2	AF065482	sorting nexin 2	sorling nexin 2
SNX4         AA524345         sorting nexin 4           SNX7         AL049989         sorting nexin 7           SNX7         AL049989         sorting nexin 7           Source: H.sapiens genes for histones         HZB.1 and HZA.           NX57985         HZB.1 and HZA.           NX5755         Source: H.sapiens PR264 gene.           Sc.35         X75755           Source: H.sapiens PR264 gene.	2323	39360 at	SNX3	AF034546	sorting nexin 3	sorting nexin 3
SNX7         AL049989         sorting nexin 7           H2A         X57985         H2B.1 and H2A.           SC-35         X75755         Source: H.sapiens genes for histones           SC-35         X75755         Source: H.sapiens PR264 gene.           SC-35         X75755         Source: H.sapiens PR264 gene.	2324	40605 at	SNX4	AA524345	sorting nexin 4	
Source: H.sapiens genes for histones   H.2A	2325	37808 at	SNX7	AL049989	sorting nexin 7	hypothetical protein
H2A         X57985         H2B.1 and H2A.           SC-35         X75755         Source: H.sapiens PR264 gene.           SC-35         X75755         Source: H.sapiens PR264 gene.					Source: H.sapiens genes for histones	
SC-35         X75755         Source: H.sapiens PR264 gene.           SC-35         X75755         Source: H.sapiens PR264 gene.	2326	33352_at	HZA	X57985	H2B.1 and H2A.	histone H2A
SC-35 X75755 Source: H.sapiens PR264 gene.	2327	36112_r_at	SC-35	X75755	Source: H.sapiens PR264 gene.	splicing factor, arginine/serine-rich 2
	2328	36111_s_at	SC-35	X75755	Source: H.sapiens PR264 gene.	splicing factor, arginine/serine-rich 2



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329	2329 1173 a at		HG172-HT3924	Source: Homo sapiens chromosome 10 clone RP11-96B5, WORKING DRAFT SEQUENCE, 8 unordered pieces.	
				Source: Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete	Landhadian Installand
2330	2330 40617_at	44M2.1	AC004381	sednence.	nypoinetical protein reacozy
				Source: Homo sapiens clk2 kinase	
		-100		(CLK2), propin1, cote1,	
				genes, complete cds; metaxin	
				pseudogene and glucocerebrosidase	
			,	pseudogene; and thrombosponding	
2331	2331 33740_at	COTE1	AF023268	(THBS3) gene, partial cds.	chromosome 1 open reading Irame 2
				Source: Homo sapiens hJTB gene,	
2332	2332 41834_g_at	HJTB PAR	AB016492	complete cds.	jumping translocation breakpoint
				Source: Homo sapiens hJTB gene,	
2333	2333 41833_at	HJTB PAR	AB016492	complete cds.	jumping translocation breakpoint
				Source: Homo sapiens mRNA for	
2334	2334 32335_r_at	UbC2	AB009010	polyubiquitin UbC, complete cds.	polyubiquitin UbC
				Source: Homo sapiens mRNA for	
2335	2335 32334_f_at	UbC2	AB009010	polyubiquitin UbC, complete cds.	polyubiquitin UbC
				Source: Human CCAAT-box-binding	
2336	2336 32194_at	CBF	M37197	factor (CBF) mRNA, complete cds.	CCAAT-box-binding transcription factor
				Source: Human CCAAT-box-binding	
2337	2337 229_at	CBF	M37197	factor (CBF) mRNA, complete cds.	CCAAT-box-binding transcription factor
				Source: Human Chromosome 16 BAC	
				clone CIT987SK-A-101F10, complete	
2338	2338 41791 at	101F10.3	AC002550	sequence.	hypothetical protein
				Source: Human Chromosome 16 BAC	
		-		clone CIT987SK-A-211C6, complete	
2339	2339 41488_at	A-211C6.1	AC002394	sequence.	hypothetical protein A-211C6.1
				Source: Human Chromosome 16 BAC	
2340	2340 35742 at	A-362G6 1	U95740	sequence.	hypothetical protein A-362G6.1
	13.				

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		٥		O of our Change Change at a DAC	
		-		clone CIT987SK-A-61E3, complete	•
2341	2341 41733_at	61E3.1	AC003007	sequence.	Unknown gene product (partial)
				Source: Human DNA sequence from	
0340	00004		0707074	clone RP4-742C19 on chromosome 22,	
75.5	2342 30034 al		ALUS 1040	complete sequence.	
				Source: Human mRNA for HLA class I	
2343	2343 37383_f_at	HLA class I - locus	ocus X58536	locus C heavy chain.	HLA class I heavy chain
				Source: Human N-	
				acetylglucosaminyltransferase I (GlcNAc-	acetylglucosaminytransferase I (GlcNAc-  mannosyl (alpha-1,3-)-glycoprotein beta-1,2-
2344	2344 39778_at	T1 GLCN	AC-1M55621	Ti) mRNA, complete cds.	N-acetylglucosaminyltransferase
2345	2345 41573_at	SP3	X68560	Sp3 transcription factor	
				spastic ataxia of Charlevoix-Saguenay	
2346	2346 32102_at	SACS	AB018273	(sacsin)	KIAA0730 protein
				spastic paraplegia 4 (autosomal dominant;	
2347	2347 35171_at	SPG4	AB029006	spastin)	KIAA1083 protein
2348	39423_f_at	SPOP	AJ000644	speckle-type POZ protein	SPOP
2349	2349 38924_s_at	SSH3BP1	AF001628	spectrin SH3 domain binding protein 1	interactor protein AbIBP4
2350	33886_at	SSH3BP1	AF006516	spectrin SH3 domain binding protein 1	e3B1
2351	2351 39556_at	SPTBN1	M96803	spectrin, beta, non-enythrocytic 1	beta-spectrin
2352	2352 34304 s at	SAT	AI 050290	snamidina/sparmina N1-acetytransferase	
			0000000		
				sphingomyelin phosphodiesterase 1, acid	
2353	2353 32574_at	SMPD1	X59960	lysosomal (acid sphingomyelinase)	sphingomyelin phosphodiesterase
				spinocerebellar ataxia 1	
				(olivopontocerebellar ataxia 1, autosomal	
2354	2354 36142_at	SCA1	X79204	dominant, ataxin 1)	ataxin-1
				spinocerebellar ataxia 2	
				(olivopontocerebellar ataxia 2, autosomal	
2355	2355 36998_s_at	SCA2	Y08262	dominant, ataxin 2)	ataxin 2
				splicing factor 30, survival of motor neuron	
2356	2356 38040_at	SPF30	AF107463	related	splicing factor
2357	2357 36973_at	SF3B2	U41371	splicing factor 3b, subunit 2, 145kD	spliceosome associated protein



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37.8	2358 36224 d. at		A1827895	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	
	1000		V70044	or proline/glutamine rich line tract binding protein	PTB-associated splicing factor
ROSS S	2359 40536 at		7,0376	or, arginine/serine-rich 1	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
2361	2360 36096_81 2361 140 s at	0	W(2703	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	transformer-2 beta
2362	2362 32183 at		M74002		arginine-rich nuclear protein
2363	2363 35258 f at	SFRS2IP	AF030234		splicing factor Sip1
2364	40457 at		AF038250		
2365	2365 36991_at	SFRS4	L14076		pre-mRNA splicing factor
2366	40453_s_at	SFRS5	U30826		SRp40-1
2367	2367 40262 at	SRP46	AF031166	Splicing factor, arginine/serine-rich, 46kD	SRp46 splicing factor
2368	2368 35839 at	SOLE	D78130	squalene epoxidase	squalene epoxidase
2360	2369 39047 at	SART3	AB020880	squamous cell carcinoma antigen recognised by T cells 3	squamous cell carcinoma antigen SART-3
232	2370/41784 at	DKFZp564B0769		SR rich protein	hypothetical protein
2371	2371 36091 at	SCAP2	AF051323	src family associated phosphoprotein 2	Src-associated adaptor protein
2372	2372 41354_at	STC1	U25997	stanniocalcin 1	stanniocalcin precursor
2373	32043 at	STC2	AF098462	stanniocalcin 2	stanniocalcin-related protein
2374	2374 41295_at	STARD7	AL041780	START domain containing 7	
2375	2375 38800_at	STMN2	D45352	stathmin-like 2	
2376	2376 41823 at	STAU	AJ132258	staufen, RNA binding protein (Drosophila)	
2377	2377 38669 at	SLK	D86959	Ste20-related serine/threonine kinase	KIAA0204 protein
2378	2378 37147 at	SCGF	AF020044	stem cell growth factor, lymphocyte secreted C-type lectin	lymphocyte secreted C-type lectin precursor
2375	2379 36913_at	SLBP	U75679	stem-loop (histone) binding protein	histone stem-loop binding protein
2380	2380 38034 at	STS	M16505	steroid sulfatase (microsomal), arylsulfatase C, isozyme S	steroid suffatase (microsomai), aryisuliatase C, isozyme S

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T					steroid-5-alpha-reductase, alpha polypeptide
				polypeptide 1 (3-oxo-5 alpha-steroid delta	1 (3-oxo-5 alpha-steroid delta 4-
2381	2381 589 at	SRD5A1	M32313	4-dehydrogenase alpha 1)	dehydrogenase alpha 1)
2382	2382 33369 at	SC4MOL	AI535653	sterol-C4-methyl oxidase-like	
				sterol-C5-desaturase (ERG3 delta-5-	
2383 33421	33421_s_at	SCSDL	AB016247	desaturase homolog, fungal)-like	sterol-C5-desaturase
2384	40419_at	EPB72	X85116	stomatin; H.sapiens epb72 gene exon 1.	band 7 integral membrane protein
2385	2385 33322 i at	SFN	X57348	stratifin	stratifin
				stress-associated endoplasmic reticulum protein 1; ribosome associated membrane	
2386	2386 37035_at	SERP1	AI557272	protein 4	
					stromal cell derived factor receptor 1 isotorm
2387	2387 35747 at	SDFR1	AF035287	stromal cell derived factor receptor 1	b, submigical delived factor receptor is isoform a
2388	2388 32666 at	SDF1	U19495	stromal cell-derived factor 1	intercrine-alpha
2389	2389 33834 at	SDF1	L36033	stromal cell-derived factor 1	pre-B cell stimulating factor homologue
2390	2390 41627 at	SDF2	D50645	stromal cell-derived factor 2	SDF2
				succinate dehydrogenase complex,	succinate dehydrogenase flavoprotein
2391	2391 34826_at	SDHA	121936	subunit A, flavoprotein (Fp)	subunit
				succinate dehydrogenase complex,	
				subunit C, integral membrane protein,	
2392	2392 34385_at	SDHC	U57877	15kD	integral membrane protein CII-3
				succinate dehydrogenase complex,	
2393	2393 40467_at	SDHD	AB006202	subunit D, integral membrane protein	cytochrome b small subunit of complex II
7000	10000	2	AEOEGOES	succinate-CoA ligase, AUP-torming, beta	ATP-specific succinyi-coA synificiase Deta
2305	2305 35832 at	KIAA1077	AR029000	sulfatase FP	KIAA1077 protein
396	2396 33712 at	SULT4A1	N63574	sulfotransferase family 4A, member 1	
2397	2397 34814 at	UBA2	AL041443	SUMO-1 activating enzyme subunit 2	
				superkiller viralicidic activity 2-like (S.	
2398	2398 37998_at	SKIV2L	U09877	cerevisiae)	helicase-like protein
				superoxide dismutase 1, soluble	superoxide dismutase 1, soluble
2399	2399 36620_at	SOD1	X02317	(amyotrophic lateral sclerosis 1 (adult))	(amyotrophic lateral sclerosis 1 (adult))
240	40069_at	SVIL	AF051850	supervillin	supervillin
2401	2401 36676 at	GHRF GRF	AL031659	supported by FGENESH	growth hormone releasing hormone

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				GENEWISE, GENSCAN	nuclear transcription factor Y, alpha, isotorm
707	2402 33297_at	CBF-B HAP2 NF-	NF- AL031 / /8	and ruenes	
2403	2403 34825 at	TTRAP	AL031775	supported by GENSCAN	TRAF and TNF receptor-associated protein
				nicity 13 (colon	
2404	2404 1640_at	ST13	U17714		putative turnor suppressor ST13
2405	2405 37745_s_at	ST5	U15780	suppression of tumorigenicity 5	p82
2406	2406 37805 at	SRPUL	AF060567		sushi-repeat protein
				sushi-repeat-containing protein, X	
2407	2407 31855_at	SRPX	U61374	сhromosome	
2408	2408 31869 at	KIAA0640	AB014540	SWAP-70 protein	KIAA0640 protein
				SWI/SNF related, matrix associated, actin	
				dependent regulator of chromatin,	
2409	2409 40213 at	SMARCA1	M88163	subfamily a, member 1	transcription activator
				SWI/SNF related, matrix associated, actin	
				dependent regulator of chromatin,	
2410	2410 40961_at	SMARCA2	X72889	subfamily a, member 2	HBRM
				SWI/SNF related, matrix associated, actin	
				dependent regulator of chromatin,	
2411	2411 32579_at	SMARCA4	U29175	subfamily a, member 4	transcriptional activator
				SWI/SNF related, matrix associated, actin	
				dependent regulator of chromatin,	
2412	39132_at	SMARCA5	AB010882	subfamily a, member 5	hSNF2H
2413	34753_at	SYBL1	X92396	synaptobrevin-like 1	synaptobrevin-like 1
2414	41692 at	SYNJ1	AB020717	synaptojanin 1	KIAA0910 protein
2415	38075_at	SYPL	X68194	synaptophysin-like protein	synaptophysin-like protein
2416	2416 36452_at	KIAA1029	AB028952	synaptopodin	KIAA1029 protein
					synaptosome associated protein of 23
2417	2417 32178_r_at	SNAP23	AJ011915	synaptosomal-associated protein, 23kD	kilodaltons, isoform A
				syndecan 2 (heparan sulfate proteoglycan	
2418	2418 39757_at	SDC2	J04621	1, cell surface-associated, fibroglycan)	_
2419	2419 32092 at	SDC3	AB007937	syndecan 3 (N-syndecan)	KIAA0468 protein
2420	2420 38110_at	SDCBP	AF000652	syndecan binding protein (syntenin)	syntenin
2421	38685_at	STX12	AL035306	syntaxin 12	hypothetical protein
2422	2422 38381_at	STX3A	U32315	syntaxin 3A	syntaxin 3

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242313	2423 38774 at	STX7	U77942	syntaxin 7	syntaxin 7
24243					syntaxin 8
24253	at		AF004563	nding protein 1	hUNC18b
24263		STXBP3	D63506		unc-18homologue
				ric DNA-binding	,
2427 3	2427 33315 at		M29204	_	chimeric DNA-binding factor
				TAF7 RNA polymerase II, TATA box	
				tor,	-
2428 192 at	192 at	TAF7	U18062		TFIID subunit TAFII55
				TAF9 RNA polymerase II, TATA box	
_				g protein (TBP)-associated factor,	
2429	2429 193 at	TAF9	U21858		TAFII32 precursor
				TAFII20; contains homology to histone	
				H2B; TFIID subunit; TAFII15; contains	
				homology to histone H2B; TFIID subunit;	
				Human TFIID subunits TAF20 and TAF15	
2430	2430 37620 at	TAF12; TAF2J; TAU57693	U57693	mRNA, complete cds.	TAF20; TAF15
2431	2431 32166 at	TLN1	AB028950	talin 1	KIAA1027 protein
2432	2432 39765_at	TLN2	AB002318	talin 2	
2433	41168 at	TAPBP	AF029750	TAP binding protein (tapasin)	tapasin
2434	2434 39779 at	TARBP1	U38847	TAR (HIV) RNA binding protein 1	TAR RNA loop binding protein
2435	2435 32241 at .	TARDBP	AL050265	TAR DNA binding protein	hypothetical protein
2436	2436 39416 at	TIP-1	U90913	Tax interaction protein 1	Tax interaction protein 1
				Tax1 (human T-cell leukemia virus type I)	
2437	2437 498 at	TAX1BP1	U33821	binding protein 1	tax1-binding protein TXBP151
				Tax1 (human T-cell leukemia virus type I)	
2438	2438 35279 at	TAX1BP1	U33821	binding protein 1	tax1-binding protein TXBP151
2439	36702 at	TBX19	AJ010277	T-box 19	TBX19 protein
2440	2440 32196 at	TIP120A	AB020636	TBP-interacting protein	KIAA0829 protein
2441	2441 34791 at	TCP1	X52882	t-complex 1	t-complex 1
				t-complex-associated-testis-expressed 1-	
2442	2442 36921_at	TCTE1L	U02556	like	(-complex-associated-lestis-expressed 1-ine
				t-complex-associated-testis-expressed 1-	f-complex-associated-testis-expressed 1- f-complex-associated-testis-expressed 1-like
2443	2443 946_at	TCTEL1	D50663	like 1	

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				TEIG; EGRa; Homo sapiens TGFb inducible early profein and early growth	
			=- <b>=</b>		TGFb inducible early protein; early growth
444	2444 38374_at	TIEG; EGRA; KLH	KLFAF050110		response protein alpha
					telomeric reneat hinding factor 1, isoform 2:
2445	2445 32255 i at	TERF1	U40705	interacting) 1	telomeric repeat binding factor 1, isoform 1
2446			AL050162	i transcript (3 LIM domains)	hypothetical protein
				-	testis enhanced gene transcript (BAX
2447	2447 33988_at	TEGT	X75861		inhibitor 1)
2448	32080_at		L11669	tetracycline transporter-like protein	tetracycline transporter-like protein
2449	2449 38612_at	_	M69023	tetraspan 3	
2450	2450 37321 at	TTC1	U46570	tetratricopeptide repeat domain 1	tetratricopeptide repeat protein
2451	at	TTC3	D83077	tetratricopeptide repeat domain 3	TPRD
2452	2452 224 at	TIEG	S81439	TGFB inducible early growth response	zinc finger transcription factor
				TGFB-induced factor (TALE family	
2453	2453 38805 at	TGIF	X89750	homeobox)	TGIF protein
				The AAs encoded by bases 5728-5736	
				and 5917-5926 may be ASN-linked	
				glycosylation sites; insulin-like precursor;	
				Homo sapiens growth factor-binding	
				protein-3 precursor (IGFBP3) gene,	
2454	2454 37319 at	IGFBP3	M35878	complete cds.	growth factor-binding protein-3 precursor
				The AAs encoded by bases 5728-5736	
				and 5917-5926 may be ASN-linked	
				glycosylation sites; insulin-like precursor;	
				Homo sapiens growth factor-binding	
				protein-3 precursor (IGFBP3) gene,	
2455	2455 1586 at	IGFBP3	M35878	complete cds.	growth factor-binding protein-3 precursor

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				The first in-frame ATG codon is located at nucleotides 17-19, followed by a second ATG codon 52 codons downstream. And the second ATG codon is potential initiation point for translation of NPPase Human mRNA for nucleotide	esedo
2456 342_a	2456 342 at	ENPPT: M6ST; NF	1; NHU12485 Al653621		
2458	H I	TXNDC	AL080080	thioredoxin domain-containing	hypothetical protein
2459	2459 31508 at	TXNIP	S73591	thioredoxin interacting protein	brain-expressed HHCPA78 homolog VDUP1
2460	2460 39425 at	TXNRD1	X91247	-	thioredoxin reductase (NAUPH)
2461	2461 32214_at	TXNL	AF003938		thioredoxin-like protein
2462	2462 38473_at	TARS	M63180	thetase	threonyl-tRNA synthetase
2463	2463 659_g_at	THBS2	L12350		thrombospondin 2
2464	2464 658_at	THBS2	L12350	thrombospondin 2	Thrombospondin 2
2465	2465 40865 at	TD6	U51166	thymine-DNA glycosylase	G/T mismatch-specific thymine DNA glycosylase
2468	2466 31557 at	TMSB4X	M17733	osome	thymosin, beta 4
	-			thyroid hormone receptor coactivating	
2467	2467 32654_g_at	SMAP	AW020536	protein	thursid hormone recentor interactor 12
2468	2468 39699_at	TRIP12	D28476	thyroid hormone receptor interactor 12	thursid recentor interactor
2469	2469 41251_at	TRIP3	L40410	thyroid hormone receptor interactor 3	Inyroid receptor interactor
2470	2470 39341_at	TRIP6	AJ001902	thyroid hormone receptor interactor 6	IRIPO
2471	2471 37348_s_at	TRIP7	AA845349	thyroid hormone receptor interactor /	
	44006	TDA D240	AB011165	thyroid hormone receptor-associated	KIAA0593 protein
2472	2472 41023 at	TRIP15	AF084260	thyroid receptor interacting protein 15	signalosome subunit 2
	in-0.300			TIA1 cytotoxic granule-associated RNA	TIA1 protein, isoform 1; TIA1 protein,
2474	2474 33852 at	TIA1	M77142	binding protein	isoform 2
2475	2475/41763 g at	TIAL1	D64015	TIA1 cytotoxic granule-associated RNA binding protein-like 1	T-cluster binding protein
2476	2476 36655 at	TJP2	127476	tight junction protein 2 (zona occludens 2)	tight junction protein 2 (zona occludens 2) tight junction protein 2 (zona occludens 2)
2477	2477 37801 at	TJ6	AF112972	TJ6 protein	TJ6

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24783	2478 35238_at	TRAFS	AB000509	ated factor 5	TRAF5
24793	2479 33243 at	GG2-1	AF099935	TNF-induced protein	MDC-3.13 isoform 2
2480	2480 40310_at	TLR2	AF051152		Toll/interleukin-1 receptor-like protein 4
24811	2481 1030_s_at	TOP1	U07806		DNA topoisomerase I
2482 3	2482 36571 at	TOP2B ·	X68060	II beta (180kD)	DNA topoisomerase II
24833	2483 32233 at	TOR1B	AF007872	torsin family 1, member B (torsin B)	torsinB
24843	2484 32219 at	TLK1	D50927		KIAA0137 protein
2485	2485 35321 at	TLK2	AB004884		PKU-alpha
				TRAF family member-associated NFKB	
2486	2486 39742_at	TANK	U59863	activator	I-TRAF
2487 40051	t0051_at	KIAA0057	D31762		TRAM-like protein
2488	2488 1073 at	TCEA1	M81601		transcription elongation factor SII
		)		-like	
2489 38317	38317_at	TCEAL1	M99701		transcription elongation factor A (SII)-like 1
	1 000	, d	0.77	transcription elongation factor B (SIII),	RNA polymerase II elongation factor SIII,
2430	2490 1399_at	I CEB I	79087	polypepide ( 19hD, eloligiii O)	RNA polymerase II elongation factor-like
2491	41759 at	TCEB11	247087	polypeptide 1-like	protein
				transcription elongation regulator 1	
2492	2492 39426_at	TCERG1	AF017789	(CA150)	putative transcription factor CA150
				transcription factor 12 (HTF4, helix-loop-	
2493	2493 33348_at	TCF12	M80627	helix transcription factors 4)	helix-loop-helix protein
7407	0404 1373 of	TOES	M31503	transcription factor 3 (E2A immunoglobulin anhancer binding factors E12/E47)	
	1070 81	2		transcription factor 8 (represses	
2495	2495 33440 at	TCF8	U19969	interleukin 2 expression)	ZEB
				transcription factor AP-4 (activating	
2496	2496 39638_at	TFAP4	S73885	enhancer binding protein 4)	AP-4
2497	2497 37757_at	TFDP1	L23959	transcription factor Dp-1	E2F-related transcription factor
2498	2498 32578_at	TCFL4	AW005997	transcription factor-like 4	
		i i	7070	transcription factor-like 5 (basic helix-loop-	transcription factor. like 5
2499	2499 35614_at	TADAS	AB012124	transcriptional adantor 3-like	ADA3-like protein
300	2300 337 43 at	LAUASL	200100		

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					KIAA1080 protein; Golgi-associated, gamma- adaptin ear containing, ARF-binding protein
501	2501 35297 at	GGA2 VEAR	AC002400	Transcriptional coactivator P15 like	2
2502	2502 33876_at	TAZ	AL050107		hypothetical protein
				transcriptional co-repressor; Human	
				roid	
				0	silencing mediator of retinoid and thyroid
2503	2503 39358 at	SMRT	U37146	cds.	hormone action
				transcriptional regulator interacting with	
2504	2504 37312_at	TRIP-Br2	D50917	the PHS-bromodomain 2	KIAA0127 gene product
2505	2505 40631 at	T081	D38305	transducer of ERBB2, 1	Tob
2506	2506 32554 s at	TBL1	Y12781	transducin (beta)-like 1	transducin (beta) like 1 protein
2507	2507 37324 at	TFRC	X01060	transferrin receptor (p90, CD71)	transferrin receptor (p90, CD71)
2508	2508 39344 at	HSU53209	U53209	transformer-2 alpha (htra-2 alpha)	transformer-2 alpha
				transforming growth factor beta-stimulated	
2509	2509 39032 at	TSC22	AJ222700	protein TSC-22	TSC-22
				transforming growth factor, beta 1	transforming growth factor, beta 1 (Camurati-
2510	2510 41445 at	TGFB1	X02812	(Camurati-Engelmann disease)	Engelmann disease)
	ı			transforming growth factor, beta receptor	
2511	2511 1815 g at	TGFBR2	D50683	II (70-80kD)	TGF-betallR alpha
				transforming growth factor, beta receptor	
2512	2512 1814 at	TGFBR2	D50683	II (70-80kD)	TGF-betailR alpha
				transforming growth factor, beta-induced,	
2513	2513 1385 at	TGFBI	M77349	68kD	transforming growth factor induced protein
				transforming, acidic coiled-coil containing	
2514	2514 40841 at	TACC1	AF049910	protein 1	TACCI
				transforming, acidic coiled-coil containing	
2515	2515 38816 at	TACC2	AF095791	protein 2	TACC2 protein
2516	2516 36931 at	TAGLN	M95787	transgelin	smooth muscle protein
2517	2517 36678 at	TAGLN2	D21261	transgelin 2	transgelin 2
2518	2518131829 r at	TGOLN2	AF027515	trans-golgi network protein 2	hTGN48
				transient receptor potential cation channel	
2519	39124_r_at	TRPC1	99068X	subfamily C, member 1	TRPC1 protein
25.00	2520 39123 s. at	TBPC1	X89066	transient receptor potential cation channel subfamily C, member 1	TRPC1 protein
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				RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP); Human homolog of sploot 853ITERA_MOUSE TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP) piril225197 transitional andoplasmic reticulum ATPase - mouse gil55217 (214044) murine valosin-containing protein; 99% identical to complementing gene 9; Putative DNA repair protein; Hypothetical 96.6 kDa putative membrane protein; Most similar to hypothetical proteins in fission and budding yeast, and C. elegans: (AB004539) ORF YLL031c (Schizosaccharomyces pombe); probable membrane protein (AL021766) [Schizosaccharomyces cerevisiae]; (AF003137) C27A12.9 [Caenorhabditis elegans]; Hypothetical 38.8 kDa putative membrane protein; Most similar to hypothetical 38.8 kDa putative membrane protein; snipar to hypothetical selevans; snipar25851Y828P1,11659_5; concered and protein; snipar to hypothetical selevans; snipar25851Y828P1,11659_5; concered and protein sniparative membrane protein; snipar25851Y828P1,11659_5; concered and protein sniparative membrane protein; snipar25851Y828P1,11659_5; concered and protein sniparative membrane protein; sniparative membrane protein; sniparative membrane protein; snipar25851Y828P1,11659_5; concered and protein sniparative membrane protein; snipar25851Y828P1,11659_5; concered and protein sniparative membrane protein; sniparative membrane protein; sniparative membrane protein; sniparative membrane protein; sniparative membrane protein; sniparative membrane protein sniparative membrane protein sniparative membrane protein; sniparative membrane protein; sniparative membrane protein; sniparative membrane protein; sniparative membrane protein; sniparative membrane protein; sniparative membrane protein; sniparative membrane protein; sniparative membrane protein; sniparative membrane protein; sniparative membrane protein; sniparative membrane protein; sniparative membrane protein; sniparative membrane protein; sniparative membrane prot	TERA_HUMAN; XRCC9; P1.11659_3;
2521	34380	ARCCS	AC004412	translation factor suit homolog	GC20 protein
2522	33351	GC20	AP04607	translation initiation factor IE9	KIAA0741 protein
2523	2523 40537_at	IF2	AB018284	translation initiation factor inc	
2524	2524 32173 at	UK114	X95384	translational inhibitor protein p14.5	14.5 kDa translational inhibitor protein, p14.5
3	10-11-01				

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2525 41051	41051_at	TSNAX	X95073	translin-associated factor X	Translin associated protein X
2526	2526 32831_at	TIMM17A	AA453183	translocase of inner mitochondrial membrane 17 homolog A (yeast)	
2527	2527 36198 at	핕	NDIND13641	translocase of outer mitochondrial membrane 20 (yeast) homolog	mitochondrial outer membrane protein 19
2528	2528 37050 r at	TOMM34	A1130910	translocase of outer mitochondrial membrane 34	
2529	2529 32853 at	TOMM70A	AB018262	translocase of outer mitochondrial membrane 70 homolog A (yeast)	KIAA0719 protein
2530	2530 34796 at	TRAM	X63679	translocating chain-associating membrane protein	TRAM protein
2531	2531 38100_at	TLOC1	D87127	translocation protein 1	translocation protein-1
2532	2532 950_at	TLOC1	D87127	translocation protein 1	translocation protein-1
2533	2533 41531_at	TM4SF1	A1445461	transmembrane 4 superfamily member 1	
2534	2534 39362_r_at	TM4SF6	AF043906	transmembrane 4 superfamily member 6	T245 protein
2535	2535 32083_at	TM7SF1	AF027826	transmembrane 7 superfamily member 1 (upregulated in kidney)	putative seven pass transmembrane protein
2536	2536 38835_at	TM9SF1	U94831	transmembrane 9 superfamily member 1	multispanning membrane protein
2537	2537 34307 at	TM9SF2	U81006	transmembrane 9 superfamily member 2	p76
2538	2538 37955_at	TMEM4	AB015631	transmembrane protein 4	type II membrane protein
2539	2539 37445_at	TMEMS	AB015633	transmembrane protein 5	type II membrane protein
2540	36128_at	TMP21	L40397	transmembrane trafficking protein	
2541	2541 38982 at	RAP1	W28865	TRF2-interacting telomeric RAP1 protein	
2542	2542 39382_at	TRIM2	AB011089	tripartite motif-containing 2	KIAA0517 protein
2543	2543 36825_at	TRIM22	X82200	tripartite motif-containing 22	gpStaf50
2544	2544 38537_at	TRIM32	U18543	tripartite motif-containing 32	zinc-finger protein
2545	2545 32635_at	TRIM33	AB029036	tripartite motif-containing 33	KIAA1113 protein
2546	2546 33107_at	TRIM37	AB020705	tripartite motif-containing 37	KIAA0898 protein
2547	2547 40461_at	TIX1	AB007855	triple homeobox 1	
2546	2548 36791_g_at	TPM1	M19267		tropomyosin 1 (alpha)
2545	2549 36790_at	TPM1	M19267	(tropomyosin 1 (alpha)	tropomyosin 1 (alpha)

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TPM1						
36792_at         TPM1         224727         tropomyosin 1 (alpha)         11           38792_at         TPM2         M12125         tropomyosin 1 (alpha)         11           38777_at         WARS         X59892         tryptophan rich basic protein         1           38121_at         WARS         X59892         tryptophanyi-tRNA synthetase         1           38121_at         WARS         X59892         tryptophanyi-tRNA synthetase         1           39867_at         TULPA         S75463         mitochondrial         1           39873_at         TULBA         ARC38290         tubulin, beta polypeptide         1           39333_at         TUBB         ARC385316         tubulin, beta polypeptide         1           39333_at         TUBB         ARC385316         tubulin, beta polypeptide         1           39346_at         TUBB         ARC38531         tubulin, beta polypeptide         1           33346_at         TUBB         ARC3853         tubulin, beta polypeptide         1           33346_at         TUBB         ARC3853         tubulin-specific chaperone c         1           3516_at         TDE1         U61234         tubulin-specific chaperone c         1           3516_at <t< th=""><th></th><th>¥</th><th>89</th><th></th><th>O</th><th>'n</th></t<>		¥	89		O	'n
at         TPM2         M12125         tropomyosin 2 (beta)         t           at         WARS         Y12478         tryptophan/cHNA synthetasen         4           at         WARS         X59892         tryptophanyLRNA synthetasen         1           at         TULP3         A022290         tubblike protein 3         1           at         TULP3         A022290         tubblin, beta polypeptide         1           at         TUBB         X79535         tubulin, beta polypeptide         1           at         TUBG1         M61724         tubulin, beta polypeptide         1           at         TDE1         U49188         tubulin, beta polypeptide         1           at         TDE2         Ubulin, peta polypeptide         1           at         TDE1         U49188         tubulin, beta polypeptide         1           at         TDE1         U49188         tubulin, beta polypeptide         1	2550		TPM1		tropomyosin 1 (alpha)	tropomyosin isoform
at         WRB         Y12478         ttyptophan rich basic protein         o           at         WARS         X59892         ttyptophanyl-RNA synthetase         4           at         TULP3         A1028290         tubby like protein 3         1           at         TULP3         A1028290         tubby like protein 3         1           at         TUBB         AF035316         tubulin, beta polypeptide         1           at         TUBB         AF03531         tubulin, beta polypeptide         1           at         TDE1         U61234         tubulin, specific chaperone c         1           at         TDE2         U61232         tubulin, specific chaperone c         1           at         TNFRSF10B         AF016266         superfamily, member 12 (transfocating         1           at         TNFRSF12         U83598         cha	2551		TPM2		tropomyosin 2 (beta)	tropomyosin 2 (beta)
WARS         X59892         tryptophany44RNA synthetase           TUFM         S75483         Tu translation elongation factor, mitochondial           TULP3         AI028290         tubbulin, bela polypeptide           TUBB         X79536         tubbulin, bela polypeptide           TUBB         X79535         tubbulin, bela polypeptide           TUBB         X79535         tubbulin, bela polypeptide           TUBB         X79535         tubulin, pela polypeptide           TUBB         X79535         tubulin, pela polypeptide           TUBB         X79535         tubulin, pela polypeptide           TBCC         U61234         tubulin, pela polypeptide           TBCC         U61234         tubulin, pela polypeptide           TBCC         U61234         tubulin, pela polypeptide           TBCC         U61334         tubulin, pela polypeptide           TDE1         U49188         tumor necrosis factor receptor           TNFRSF10B         AF016266         superfamily, member 12 (translocating           AF016266         superfamily, member 12 (translocating           AF016267         superfamily, member 14           AF016268         superfamily, member 14           AF016269         superfamily, member 14	2552	1 1	WRB		tryptophan rich basic protein	congenital heart disease 5 protein
TUFM         S75483         mitochondrial           TULP3         AI028290         tubby like protein 3           TULP3         AI028290         tubbulin, alpha, ubiquitous           TUBB         AF035316         tubulin, belta polypeptide           TUBG1         M61764         tubulin, belta polypeptide           TUBG1         M61784         tubulin, belta polypeptide           TUBC         U61234         tubulin, pelta polypeptide           TUBC         U61234         tubulin, pelta polypeptide           TUBC         U61234         tubulin, pelta polypeptide           TUBC         U61232         tubulin, pelta polypeptide           TUBC         U61234         tubulin, pelta polypeptide           TUBC         U61232         tubulin, pelta po	2553		WARS	X59892	tryptophanyl-tRNA synthetase	471 aa polypeptide (gamma2)
TUFM         S75463         mitochondrial           TULP3         Al028290         tubby like protein 3           TULP3         Al028290         tubby like protein 3           TUBB         AF035316         tubulin, beta polypeptide           TUBB         AF035316         tubulin, beta polypeptide           TUBB         AF03535         tubulin, beta polypeptide           TUBB         AF035316         tubulin, peta polypeptide           TUBB         AF035316         tubulin, peta polypeptide           TUBB         AF046266         tubulin, specific chaperone c           TUBB         AF046266         tubulin-specific chaperone c           TUBB         AF046266         tumor necrosis factor receptor           TUBB         AF046266         superfamily, member 13           TUBB         AF046266         superfamily, member 5           TUMOR         tumor necrosis factor receptor           TUMOR         tumor necrosis factor aceptor           TUMOR         tumor necrosis factor, alpha-induced           TOB237					Tu translation elongation factor,	
TULP3         Al028290         tubby like protein 3           K-ALPHA-1         K00558         tubulin, beta polypeptide           TUBB         AF035316         tubulin, beta polypeptide           TUBB         M81764         tubulin, specific chaperone c           TUBG1         M61764         tubulin-specific chaperone c           TBCE         U61232         tubulin-specific chaperone c           TBCE         U61232         tubulin-specific chaperone c           TDE1         U49188         tumor necrosis factor receptor           TDF1         U49188         tumor necrosis factor receptor           TNFRSF10B         AF016266         superfamily, member 10b           try         tumor necrosis factor receptor           try         tumor ne	2554	39867_at	TUFM	S75463	mitochondrial	P43
K-ALPHA-1         K00558         tubulin, alpha, ubiquitous           TUBB         AF035316         tubulin, beta polypeptide           TUBB         X79535         tubulin, beta polypeptide           TUBG1         M61764         tubulin, specific chaperone c           TBCC         U61234         tubulin-specific chaperone c           TBCE         U61234         tubulin-specific chaperone c           TDE1         U49188         tumor necrosis factor receptor           TNFRSF10B         AF016266         superfamily, member 10b           try         tumor necrosis factor receptor           try         tum	2555	31944_at	TULP3	Al028290	tubby like protein 3	,
TUBB         AF035316         tubulin, beta polypeptide           TUBB         X79535         tubulin, beta polypeptide           TUBG1         M61764         tubulin, parma 1           TBCC         U61234         tubulin-specific chaperone c           TBCE         U61234         tubulin-specific chaperone c           TDE1         U4918B         tumor differentially expressed 1           t         tumor necrosis factor receptor           t         TNFRSF10B         AF016266         tumor necrosis factor receptor           t         tumor necrosis factor receptor         tumor necrosis factor receptor           t         TNFRSF1         U8359B         tumor necrosis factor receptor           t         TNFRSF6         X60592         superfamily, member 1A           t         tumor necrosis factor receptor           t         X60592         superfamily, member 5           t         tumor necrosis factor, alpha-induced           t	2556	32272_at	K-ALPHA-1	K00558	tubulin, alpha, ubiquitous	tubulin, alpha, ubiquitous
at         TUBB         X79535         tubulin, beta polypeptide           r_at         TUBG1         M61764         tubulin, gamma 1           at         TBCC         U61234         tubulin-specific chaperone c           at         TBCE         U61232         tubulin-specific chaperone c           at         TDE1         U49188         tumor differentially expressed 1           at         TNFRSF10B         AF016266         tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein)           at         TNFRSF12         U83598         chain-association membrane protein)           at         TNFRSF1A         M58286         superfamily, member 14           tumor necrosis factor receptor         tumor necrosis factor receptor           at         TNFRSF6         X63717         superfamily, member 5           at         TNFAIP1         M80783         tumor necrosis factor, alpha-induced           at         TNFAIP2         M92357         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           at         TPD52L2         AF004430         tumor protein D53 binding protein, 1 <td>2557</td> <td>39332_at</td> <td>TUBB</td> <td>AF035316</td> <td>tubulin, beta polypeptide</td> <td></td>	2557	39332_at	TUBB	AF035316	tubulin, beta polypeptide	
r_at         TUBG1         M61764         tubulin, gamma 1           at         TBCC         U61234         tubulin-specific chaperone c           at         TBCE         U61232         tubulin-specific chaperone o           at         TDE1         U49188         tumor necrosis factor receptor           at         TNFRSF10B         AF016266         superfamily, member 10b           at         TNFRSF12         U83598         chain-association membrane protein)           at         TNFRSF1A         M58286         superfamily, member 12 (translocating tumor necrosis factor receptor tumor necrosis factor receptor superfamily, member 14           at         TNFRSF5         X60592         tumor necrosis factor receptor superfamily, member 5           at         TNFRSF6         X63717         superfamily, member 14           at         TNFAIP1         M80783         protein 1 (endothelial)           at         TNFAIP2         M92357         protein 2           tumor necrosis factor, alpha-induced           tumor protein p53 binding protein,	2558	39331_at	TUBB	X79535	tubulin, beta polypeptide	beta tubulin
at         TBCC         U61234         tubulin-specific chaperone c           at         TBCE         U61232         tubulin-specific chaperone e           at         TDE1         U49188         tumor necrosis factor receptor           at         TNFRSF10B         AF016266         superfamily, member 10b           at         TNFRSF12         U83598         chain-association membrane protein)           at         TNFRSF1A         M58286         superfamily, member 12 (translocating chain)           at         TNFRSF6         X60592         superfamily, member 5           at         TNFRSF6         X63717         superfamily, member 6           at         TNFRIPA         M80783         protein 1 (endothelial)           at         TNFAIP2         M80783         protein 1 (endothelial)           t         TNFAIP2         M59465         protein 2           t         tumor necrosis factor, alpha-induced           t         tumor	2559	<b>-</b> '.	TUBG1	M61764	tubulin, gamma 1	gamma-tubulin
TBCE         U61232         tubulin-specific chaperone e           TDE1         U49188         tumor differentially expressed 1           TNFRSF10B         AF016266         superfamily, member 10b           TNFRSF12         U83598         tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein)           TNFRSF12         U83598         chain-association membrane protein)           TNFRSF1A         M58286         superfamily, member 12 (translocating chain)           TNFRSF3         X60592         superfamily, member 1A           TNFRSF6         X63717         superfamily, member 5           tumor necrosis factor receptor         tumor necrosis factor receptor           tumor necrosis factor receptor         tumor necrosis factor alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha	2560		TBCC	U61234	tubulin-specific chaperone c	cofactor C
TDE1 U49188 tumor necrosis factor receptor TNFRSF10B AF016266 tumor necrosis factor receptor superfamily, member 10b tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein) tumor necrosis factor receptor tumor necrosis factor receptor TNFRSF X60592 superfamily, member 5 tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor, alpha-induced	2561	35159_at	TBCE	U61232	tubulin-specific chaperone e	cofactor E
TNFRSF10B AF016266 superfamily, member 10b tumor necrosis factor receptor superfamily, member 12 (translocating tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein) tumor necrosis factor receptor superfamily, member 5 tumor necrosis factor receptor superfamily, member 5 tumor necrosis factor receptor superfamily, member 6 tumor necrosis factor, alpha-induced tumor	2562	37007_at	TDE1	U49188	tumor differentially expressed 1	tumor differentially expressed 1
TNFRSF10B AF016266 tumor necrosis factor receptor tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein)  TNFRSF12 U83598 tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor superfamily, member 1A tumor necrosis factor receptor superfamily, member 5 tumor necrosis factor receptor superfamily, member 6 tumor necrosis factor, alpha-induced tumor necrosis factor, a					tumor necrosis factor receptor	
TNFRSF12 U83598 chain-association membrane protein)  TNFRSF14 M58286 tumor necrosis factor receptor superfamily, member 14 tumor necrosis factor receptor superfamily, member 14 tumor necrosis factor receptor superfamily, member 5 tumor necrosis factor receptor superfamily, member 5 tumor necrosis factor receptor superfamily, member 5 tumor necrosis factor receptor superfamily, member 6 tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor protein 3 tumor protein 53 binding protein, 1 tumor protein 53 binding protein, 2 tumor protein 54 binding protein, 2 tumor protein 54 binding protein, 2 tumor protein 54 binding protein, 2 tumor 54 binding protein, 2 tumor 54 binding protein, 2 tumor 54 binding protein, 2 tumor 54 binding protein, 2 tumor 54 binding protein, 2 tumor 54 binding protein, 2 tumor 54 binding protein, 2 tumor 54 binding protein, 2 tumor 54 binding protein, 2 tumor 54 bi	2563	34892_at	TNFRSF10B	AF016266	superfamily, member 10b	TRAIL receptor 2
TNFRSF12 U83598 chain-association membrane protein) tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor superfamily, member 1A tumor necrosis factor receptor tumor necrosis factor receptor superfamily, member 6 tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor protein 3 tumor protein 53 binding protein, 1 tumor protein 53 binding protein, 2					tumor necrosis factor receptor	
TNFRSF12 U83598 chain-association membrane protein)  tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor superfamily, member 5 tumor necrosis factor receptor tumor necrosis factor alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor protein 3 tumor protein 52-like 2 tumor protein 53 binding protein, 1 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2 tumor protein 53 binding protein, 2					superfamily, member 12 (translocating	
TNFRSF1A         M58286         tumor necrosis factor receptor           TNFRSF5         X60592         superfamily, member 5           TNFRSF6         X63717         tumor necrosis factor receptor           TNFAIP1         M80783         tumor necrosis factor receptor           TNFAIP2         M92357         tumor necrosis factor, alpha-induced           TNFAIP2         M92357         protein 1 (endothelial)           TNFAIP3         M59465         protein 2           TPD52L2         tumor necrosis factor, alpha-induced           TPD52L2         tumor necrosis factor, alpha-induced           TPD53BP1         tumor protein 3           TP53BP1         tumor protein 53 binding protein, 1           TP53BP2         tumor protein 553 binding protein, 1           TP53BP2         tumor protein 553 binding protein, 2           tumor protein 553 binding protein, 2         tumor protein 553 binding protein, 2	2564	41190_at	TNFRSF12	U83598	chain-association membrane protein)	death domain receptor 3 soluble form
TNFRSF1A         M58286         superfamily, member 1A           TNFRSF5         X60592         superfamily, member 5           TNFRSF6         X63717         superfamily, member 5           TNFAIP1         M80783         protein 1 (endothelial)           TNFAIP2         M92357         protein 2           TNFAIP3         M59465         protein 3           TPD52L2         AF004430         tumor protein D52-like 2           TP53BP1         U09477         tumor protein D52-like 2           TP53BP2         U58334         tumor protein D53 binding protein, 1           TP53BP2         tumor protein D53 binding protein, 2           tumor protein D53 binding protein, 2         tumor protein D53 binding protein, 2					tumor necrosis factor receptor	
TNFRSF5 X60592 superfamily, member 5  TNFRSF6 X63717 superfamily, member 6  TNFAIP1 M80783 protein 1 (endothelial)  TNFAIP2 M92357 protein 2  TNFAIP3 M59465 protein 3  TP53BP1 U09477 tumor protein 52 binding protein, 1  TP53BP2 U58334 tumor protein 52 binding protein, 2  TNFAIP3 W59346 tumor protein 53 binding protein, 2  TP53BP2 U58334 tumor protein 53 binding protein, 2  TUPS STATE STA	2565	1563_s_at	TNFRSF1A	M58286	superfamily, member 1A	tumor necrosis factor receptor
TNFRSF5         X60592         superfamily, member 5           TNFRSF6         X63717         tumor necrosis factor receptor           TNFAIP1         M80783         protein 1 (endothelial)           TNFAIP2         M92357         protein 2           TNFAIP3         M59465         protein 2           TPD52L2         AF004430         tumor protein D52-like 2           TP53BP1         U09477         tumor protein D53 binding protein, 1           TP53BP2         U58334         tumor protein D53 binding protein, 2           TP53BP2         U58334         tumor protein D53 binding protein, 2					tumor necrosis factor receptor	
TNFRSF6         X63717         tumor necrosis factor receptor superfamily, member 6           TNFAIP1         M80783         tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor protein 3           TPE3BP1         U09477         tumor protein D52-like 2           TP53BP2         U58334         tumor protein p53 binding protein, 1           TP53BP2         U58334         tumor protein p53 binding protein, 2	2566	35150_at	TNFRSF5	X60592	superfamily, member 5	CDw40
TNFRISF         X63717         superfamily, member 6           TNFAIP1         M80783         tumor necrosis factor, alpha-induced           TNFAIP2         M92357         protein 2           TNFAIP3         M59465         protein 3           TPD52L2         AF004430         tumor protein D52-like 2           TP53BP1         U09477         tumor protein D52-like 2           TP53BP2         U58334         tumor protein D53 binding protein, 1           TP53BP2         U58334         tumor protein p53 binding protein, 2					tumor necrosis factor receptor	
th TNFAIP1 M80783 protein 1 (endothelial)  th TNFAIP2 M92357 protein 2  tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor protein D52-like 2  TNFAIP3 M59465 protein 3  TNFAIP3 M59465 tumor protein D52-like 2  TP53BP1 U09477 tumor protein p53 binding protein, 1 tumor protein p53 binding protein, 2	2567	37643_at	TNFRSF6	X63717	superfamily, member 6	APO-1 cell surface antigen precursor
TNFAIP1   M80783   protein 1 (endothelial)					turnor necrosis factor, alpha-induced	
tumor necrosis factor, alpha-induced           tt         TNFAIP2         M92357         protein 2           TNFAIP3         M59465         protein 3           at         TPD52L2         AF004430         tumor protein D52-like 2           at         TP53BP1         U09477         tumor protein p53 binding protein, 1           at         TP53BP2         U58334         tumor protein p53 binding protein, 2	2568	36988_at	TNFAIP1	M80783	protein 1 (endothelial)	B12 protein
TNFAIP2 M92357 protein 2   TNFAIP2   M92357   tumor necrosis factor, alpha-induced   TNFAIP3   M59465   protein 3   TPD52L2   AF004430   tumor protein D52-like 2   TP53BP1   U09477   tumor protein p53 binding protein, 1   TP53BP2   U58334   tumor protein p53 binding protein, 2   TP53BP2   U58334   tumor protein p53 binding protein p53 binding p53 bindi					tumor necrosis factor, alpha-induced	
tumor necrosis factor, alpha-induced           TNFAIP3         M59465         protein 3           at         TPD52L2         AF004430         tumor protein D52-like 2           tumor protein p53 binding protein, 1         tumor protein p53 binding protein, 1           at         TP53BP2         U58334         tumor protein p53 binding protein, 2	2569	38631_at	TNFAIP2	M92357	protein 2	B94 protein
TNFAIP3         M59465         protein 3           at         TPD52L2         AF004430         tumor protein D52-like 2           TP53BP1         U09477         tumor protein p53 binding protein, 1           at         TP53BP2         U58334         tumor protein p53 binding protein, 2					tumor necrosis factor, alpha-induced	
at         TPD52L2         AF004430         tumor protein D52-like 2           TP53BP1         U09477         tumor protein p53 binding protein, 1           at         TP53BP2         U58334         tumor protein p53 binding protein, 2	2570	595_at	TNFAIP3	M59465	protein 3	A20
TP53BP1 U09477 tumor protein p53 binding protein, 1 tumor protein p53 binding protein, 2 tumor protein p53 binding protein, 2	2571	40076_at	TPD52L2	AF004430	turnor protein D52-like 2	hD54+ins2 isoform
TP53BP2 U58334 tumor protein p53 binding protein, 2	2572	1711_at	TP53BP1	U09477		p53-binding protein
	2573	34822_at	TP53BP2	U58334		8bp/53BP2
U82939 tumor protein post-binding protein	2574	38568_at	TP53BPL	U82939	tumor protein p53-binding protein	p53 binding protein

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2575	2575 31584 at	TPT1	X16064	tumor protein, translationally-controlled 1	tumor protein, translationally-controlled 1
				Τ	
2576	2575 21888 c at	TOSC3	AE001294	turnor suppressing subtrains of able	<u>a</u>
	2575 5 1555 3 at	TO 200	1100400	ntibility gene 101	fumor eneceptibility protein
	14/_ai	10150	002130		mand fundament
				twist homolog (acrocephalosyndactyly 3:	
2578	2578 40328 at	TWIST	X99268		B-HLH DNA binding protein
2579	2086_s_at	TYRO3	D17517	TYRO3 protein tyrosine kinase	Sky
2580	2580 35246_at	TYRO3	U18934		receptor tyrosine kinase
				otophan 5-	tyrosine 3-monooxygenase/tryptophan 5-
					monooxygenase activation protein, beta
2581	2581 32324_at	YWHAB	X57346	polypeptide	polypeptide
				tyrosine 3-monooxygenase/tryptophan 5-	
				monooxygenase activation protein, theta	
2582	2582 409_at	YWHAQ	X56468	polypeptide	14.3.3 protein
				tyrosine 3-monooxygenase/tryptophan 5-	
				monooxygenase activation protein, theta	
2583	2583 32530_at	YWHAQ	X56468	polypeptide	14.3.3 protein
				tyrosine 3-monooxygenase/tryptophan 5-	
				monooxygenase activation protein, zeta	
2584	2584 1235_at	YWHAZ	M86400	polypeptide	phospholipase A2
2585	2585 32718_at	TPST1	AF038009	tyrosylprotein sulfotransferase 1	tyrosytprotein suffotransferase-1
2586	2586 35172_at	TPST2	AF049891	tyrosylprotein sulfotransferase 2	tyrosylprotein sulfotransferase-2
2587	2587 38977_at	YARS	U89436	tyrosyl-tRNA synthetase	tyrosyl-tRNA synthetase
				U2(RNU2) small nuclear RNA auxillary	
2588	2588 36517_at	U2AF1	M96982	factor 1	U2 snRNP auxiliary factor small subunit
2589	2589 32858_at	UBN1	Al341565	ubinuclein 1	
2590	2590 34824_at	UBQLN2	AB015344	ubiquilin 2	ubiquilin 2
				ubiquinol-cytochrome c reductase (6.4kD)	
2591	2591 38451_at	UQCR	T58471	subunit	
				ubiquinol-cytochrome c reductase binding	
2592	2592 39427_at	UQCRB	T79616	protein	
2593	2593 40854 at	UQCRC2	J04973	ubiquinol-cytochrome c reductase core protein II	ubiquinol-cytochrome c reductase core protein II

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Γ				ubiquinol-cytochrome c reductase hinge	
2594	36104_at	UQCRH	97		
2595	1366_i_at	UBC	M26880	ubiquitin C	ubiquitin C
2596	2596 1367_f_at	UBC	M26880		ubiquitin C
				urboxyl-terminal esterase L1	ubiquitin carboxyl-terminal esterase L1
2597	36990_at	UCHL1	X04741	(ubiquitin thiolesterase)	(ubiquitin thiolesterase)
2598 811	811_at	UFD1L	U6444	ation 1-like	ubiquitin fusion-degradation 1 like protein
2599	2599 40623_at	UBE3B	AI749193	ubiquitin protein ligase	
				ubiquitin protein ligase E3A (human	
	-			papilloma virus E6-associated protein,	E6-associated protein E6-AP/ubiquitin-
2600	2600 41205_at	UBE3A	U84404	Angelman syndrome)	protein ligase
2601	2601 34383_at	USP1	AB014458	ubiquitin specific protease 1	ubiquitin specific protease
2602	2602 37683_at	USP10	D80012	ubiquitin specific protease 10	
2603	2603 162_at	USP11	U44839	ubiquitin specific protease 11	UHX1 protein
				ubiquitin specific protease 14 (tRNA-	
2604	2604 36982_at	USP14	U30888	guanine transglycosylase)	tRNA-Guanine Transglycosylase
2605	2605 39866_at	USP22	AB028986	ubiquitin specific protease 22	KIAA1063 protein
2606	2606 35847_at	USP24	AB028980	ubiquitin specific protease 24	KIAA 1057 protein
				ubiquitin specific protease 4 (proto-	
2607	2607 1357_at	USP4	U20657	oncogene)	ubiquitin protease
				ubiquitin specific protease 5 (isopeptidase	
2608	2608 34405_at	USP5	U47927	ር (T	isopeptidase T
				ubiquitin specific protease 7 (herpes virus- herpesvirus associated ubiquitin-specific	herpesvirus associated ubiquitin-specific
2609	2609 37672_at	USP7	Z72499	associated)	protease (HAUSP)
2610	2610 39794_at	USP8	D29956	ubiquitin specific protease 8	ubiquitin specific protease 8
				ubiquitin specific protease 9, X	3
2611	32572_at	USP9X	X98296	chromosome (tat tacets-like Drosopnila)	ubiquitin nyarolase
			*:	ubiquitin-activating enzyme E1C (UBA3	
2612	2612 40066_at	UBE1C	AF046024	homolog, yeast)	UBA3
				ubiquitination factor E4A (UFD2 homolog,	ubiquitination factor E4A (UFD2 homolog,
2613	2613 36579_at	UBE4A	D50916	yeast)	yeast)
				ubiquitination factor E4B (UFD2 homolog,	•
2614	261441339_at	UBE4B	AF043117	yeast)	ubiquitin-fusion degradation profein 2
2615	2615 36959 at	UBE2V1	U49278	ubiquitin-conjugating enzyme E2 variant 1 UEV-1	UEV-1
2		1.1.22	0.120		

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				ubiquitin-conjugating enzyme E2A (RAD6  ubiquitin-conjugating enzyme E2A (RAD6	ubiquitin-conjugating enzyme E2A (RAD6
2616	890_at	UBEZA	M74524	homolog)	homolog)
				ubiquitin-conjugating enzyme E2D 1	
2617	2617 37826_at	UBE2D1	AF020761	(UBC4/5 homolog, yeast)	
Γ				ubiquitin-conjugating enzyme E2D 2	
2618	2618 38705_at	UBE2D2	Al310002	(UBC4/5 homolog, yeast)	
				ubiquitin-conjugating enzyme E2D 2	
2619	2619 832 at	UBE2D2	U39317	(UBC4/5 homolog, yeast)	UbcH5B
				ubiquitin-conjugating enzyme E2D 3	
2620	2620 39083 at	UBE2D3	U39318	(UBC4/5 homolog, yeast)	UbcH5C
				ubiquitin-conjugating enzyme E2D 3	
2621	2621 504_at	UBEZD3	U39318	(UBC4/5 homolog, yeast)	UbcH5C
				ubiquitin-conjugating enzyme E2E 3	•
2622	2622 34850_at	UBE2E3	AB017644	(UBC4/5 homolog, yeast)	ubiquitin-conjugating enzyme E2
				ubiquitin-conjugating enzyme E2G 2	
2623	2623 32236_at	UBE2G2	AF032456	(UBC7 homolog, yeast)	ubiquitin conjugating enzyme G2
				ubiquitin-conjugating enzyme E2I (UBC9	
2624	2624 38480_s_at	UBEZI	U66867	homolog, yeast)	ubiquitin conjugating enzyme 9
				ubiquitin-conjugating enzyme E2I (UBC9	
2625	2625 838_s_at	UBE2I	U45328	homolog, yeast)	ubiquitin-conjugating enzyme
2626	2626 223 at	UBE2L3	S81003	ubiquitin-conjugating enzyme E2L 3	L-UBC
2627	2627 40505 at	UBE2L6	AA883502	ubiquitin-conjugating enzyme E2L 6	
				ubiquitin-conjugating enzyme E2N	
2628	2628 36604_at	UBEZN	D83004	(UBC13 homolog, yeast)	ubiquitin-conjugating enzyme E2 UbcH-ben
2629	2629 457_s_at	UBL1	U67122	ubiquitin-like 1 (sentrin)	SUMO-1
2630	2630 155_s_at	UBL1	U61397	ubiquitin-like 1 (sehtrin)	ubiquitin-homology domain protein PIC1
2631	2631 40839_at	UBL3	AL080177	ubiquitin-like 3	hypothetical protein
2632	2632 37336_at	UBXD2	D87684	UBX domain-containing 2	KIAA0242 protein
				UDP-Gal:betaGlcNAc beta 1,4-	
2633	2633 40960 at	B4GALT1	D29805	galactosyttransferase, polypeptide 1	beta-1,4-galactosyltransferase
				UDP-Gal:betaGlcNAc beta 1,4-	
2634	2634 34177_at	B4GALT2	AF038660	galactosyltransferase, polypeptide 2	beta-1,4-galactosyltransferase
L				UDP-Gal:betaGlcNAc beta 1,4-	
2635	2635 39445_at	B4GALT3	AF038661	galactosytransferase, polypeptide 3	beta-1,4-galactosyltransferase
	1	000	040040	UDP-glucose ceramide	reremide africocultransferase
2636	2636 40215_at	UGCG	USUBAU	giucosyiiraiisi erase	וכפומוזוותם אותכסאווומו וצופומפס

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A B C C   DD-glucose dehydrogenese						
UGDH   AF061016   UDP-glucose dehydrogenase   UGP2   UZ7460   UDP-N-acetyl-alpha-D-glactosamine; polypeptide N-acetylgalactosaminyltransferase 1   UDP-N-acetylgalactosaminyltransferase 1   UDP-N-acetylgalactosaminyltransferase 1   UDP-N-acetylgalactosamine dinase 1	F	V	В	O		'n
UGP2 UDP-glucose pyrophosphorylase 2 UDP-wacetyl-alpha-D-galetosamine-to-oppreptide N-acetyl-alpha-D-galetosamine-to-oppreptide N-acetyl-alpha-D-galetosamine-to-oppreptide N-acetyl-alpha-D-galetosamine-to-oppreptide N-acetyl-alpha-D-galetosamine-to-oppreptide N-acetyl-galetosamine-to-oppreptide N-acetyl-galeto-oppreptide N-ac	637	5214 at	ł			UDP-glucose dehydrogenase
UGP2   U27460   UDP-glucose pyrophosphorylase 2   E						uridine diphosphoglucose
CALNT1   U41514   GalNAc-T1)   GalNAc-T1)   GaLNAc-T1)   GaLNAc-T1)   GaLNAc-T1)   GaLNAc-T1)   GaLNAc-T1)   GaLNAc-T1)   UAP1   GaLNAc-T1)   UDP-N-acety/glucosamine-2-epimerase/N-acety/glucosamine-2-epimerase/N-acety/glucosamine kinase   UDP-N-acety/glucosamine pinase   UDP-N-acety/glucosamine-2-epimerase/N-acety/glucosamine kinase   UDP-N-acety/glucosamine kinase   UDP-N-acety/glucosamine-2-epimerase/N-acety/glucosamine kinase   UDP-N-acety/glucosamine-2-epimerase/N-ace	2638 <u> :</u>	37373_at	UGP2	U27460		pyrophosphorylase
galactosamine:polypeptide N- acay/galactosaminytransferase 1 GALNT1 U41514 (GalNAc-T1)  GALNT1 UUP-N-acay/galactosamine-2-epimerase/N-V acay/mannosamine kinase UDP-N-acay/mannosamine kinase UDP-N-acay/mannosamine kinase UDP-N-actey/glucosamine Uncharacterized bypothalamus protein Uncharacterized bypothalamus protein Uncharacterized hypothalamus Uncharact					UDP-N-acetyl-alpha-D-	
GALNT1   U41514   GalNAc-T1)   GALNT1   U41514   GalNAc-T1)   GALNT1   U41514   GALNAc-T1)   GALNT1   UDP-N-acety/glucosamine-S-epimerase/N-UDP-N-acety/glucosamine kinase   GNE   AJ238764   acety/mannosamine kinase   GNE   AB011004   DVP-N-actety/glucosamine   GNE   UDP-N-actety/glucosamine   GNE   UDP-N-actety/glucosamine   GNE   UDP-N-actety/glucosamine   GNE   UDP-N-actety/glucosamine   GNE   UDP-N-actety/glucosamine   GNE   UDP-N-actety/glucosamine   GNE   UNCATO   UNCA						
GALNT1   U41514   (GalNAc-T1)	-					UDP-GalNAc:polypeptide N-
GNE AJ238764 acetyflatrosamine-2-epimerase/N-1  UDP-N-actetyfglucosamine kinase (UDP-N-actetyfglucosamine kinase)  UDP1 AB011004 DV-N-actetyfglucosamine file kinase (UDP-N-actetyfglucosamine file kinase (UDP-N-actetyfglucosamine file kinase (UDP-N-actetyfglucosamine file kinase (UDP-N-actetyfglucosamine file kinase (C. elegans) structure file kinase	2639	38041 at	GALNT1	U41514	(GalNAc-T1)	acetylgalactosaminyftransferase
CONE   AJ238764   acety/mannosamine kinase   COUP-IN-acets/rigiucosamine   COUP-IN-Acets/rigiu					No social control of the social control of t	IDD-N-scendolicosamine-2-epimetase / N-
GNE   AJ238764   acetyfmannosamine knase   10				-	UDP-N-acety/glucosarmine-z-epimerasarm	
UAP1 AB011004 pyrophosphorylase 1 ULK1 AF045458 unc-51-like kinase 1 (C. elegans) at BM036 A1057607 BM036  HT010 AL049948 HT010  HT010 AL049948 HT010  HT010 AL049948 HT010  HT010 Incharacterized hypothalamus protein HT012 A1760162 HT012  HT012 A1760162 Unncharacterized hypothalamus protein HT012 A1760162 Unncharacterized hypothalamus protein HT012 AB024327 Unn-interacting protein t UNRIP AB024327 unr-interacting protein t UNRIP AB022310 protein 10.  HEB1 AB022310 protein 1  AB002310 uracil-DNA glycosylase uracil-DNA glycosylase uracil-DNA glycosylase uracil-DNA glycosylase uracil-DNA glycosylase UNRaciation Resistance Associated Gene; H.sapiens mRNA; UV Radiation HORAG X99050 Resistance Associated	2640	36515_at	GNE	AJ238764	acetylmannosamine kinase	acetylmannosamine kinase
UAP1         AB011004         pyrophosphorylase 1         Interpretable (C. elegans)           at         ULK1         AF045458         unc-51-like kinase 1 (C. elegans)         interpretable kinase 1 (C. elegans)           at         BM036         AI057607         BM036         uncharacterized bone marrow protein           at         HT010         AL049948         HT010         uncharacterized hypothalamus protein           at         HT012         AI760162         HT012         HT012           at         HT012         AI760162         HT012           at         HT012         AI760162         HT012           at         UNRIP         AB024327         unrinteracting protein           at         UNRIP         AB002310         protein           at         UNREB1         AB002310         protein           at         UMPS         V99008         uracii-DNA glycosylase           at         UMPS         J03626         orotidine-5'-decarboxylase)           at         UMPS         J03626         orotidine-5'-decarboxylase)           at         UNF         uronyl-2-sulfotransferase and           at         UVRadiation Resistance Associated Gene.           AB020316         uronyl-2-sulfotransferase					UDP-N-acteylglucosamine	UDP-N-acetyglucosamine
unc-51-like kinase 1 (C. elegans)         ist           at         BM036         AI057607         BM036         uncharacterized bone marrow protein           in         HT010         AL049948         HT010         uncharacterized hypothalamus protein           in         HT012         HT012         HT012         HT012           in         UNRIP         AB024327         unrelineracting protein           in         V0903         unre	2641	41242 at	UAP1	AB011004	pyrophosphorylase 1	pyrophosphorylase
at BM036 AI057607 BM036 uncharacterized bone marrow protein HT010 AL049948 HT010  HT0112 AI760162 HT012  HT012 AI760162 HT012  HT012 AI760162 HT012  THT012 AI760162 HT012  THT012 AI760162 Unnemed protein product; Human gene for acidic (type !) cytokeratin 10.  THT012 AB024327 unr-interacting protein THT013 AB022310 protein 1  THT014 AB020310 protein 1  THT015 AB020310 protein 1  THT016 AB020310 protein 1  THT017 AB020310 protein 1  THT018 AB020310 protein 1  THT019 AB020310 protein 1  THT010 AB020310 protein 1  THT010 AB020310 protein 1  THT010 AB020310 protein 1  THT010 AB020310 p	2642	34827 at	ULK1	AF045458	unc-51-like kinase 1 (C. elegans)	serine/threonine kinase ULK1
BM036   A1057607   BM036   Uncharacterized hypothalamus protein					uncharacterized bone marrow protein	
HT010 AL049948 HT010  HT012 Al760162 Uncharacterized hypothalamus protein HT012 Al760162 HT012  HT012 Al760162 Uncharacterized hypothalamus protein HT012 Al760162 Unnamed protein product; Human gene to X14487 (type !) cytokeratin 10.  UNRIP AB024327 unr-interacting protein UNRIP AB022310 unr-interacting protein upstream regulatory element binding uracil-DNA glycosylase uridine monophosphate synthetase and (orotate phosphoribosyl transferase and UNPS J03626 orotidine-5'-decarboxylase)  UNPS AB020316 uronyl-2-sulfotransferase UV Radiation Resistance Associated Gene; H.sapiens mRNA; UV Radiation HVRAG X99050 Resistance Associated	2643	37315 f at	BM036	A1057607	BM036	
HT010         AL049948         HT010           HT012         AI760162         HT012           HT012         AI760162         Uncharacterized hypothalamus protein           HT012         AI760162         Unnamed protein product; Human gene           KRT10; KPP         X14487         for acidic (type I) cytokeratin 10.           UNRIP         AB024327         unn-interacting protein           UNRIP         AB002310         protein 1           UNG         Y09008         uracil-DNA glycosylase           UMPS         J03626         uracil-DNA glycosylase           UMPS         J03626         orotidine-5'-decarboxylase)           UST         AB020316         uronyl-2-sulfotransferase           UV Radiation Resistance Associated Gene.         Gene; H.sapiens mRNA; UV Radiation           UVRAG         X99050         Resistance Associated Gene.					uncharacterized hypothalamus protein	
HT012 AI760162 HT012 HT012 AI760162 Uncharacterized hypothalamus protein HT012 AI760162 Unnamed protein product; Human gene KRT10; KPP X14487 (or acidic (type I) cytokeratin 10. UNRIP AB024327 unr-interacting protein UNREB1 AB002310 protein 1 UNG Y09008 uracil-DNA glycosylase UNG (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)  UMPS J03626 orotidine-5'-decarboxylase) UNF AB020316 uronyl-2-sulfotransferase  UNF AB020316 uronyl-2-sulfotransferase Gene; H.sapiens mRNA; UV Radiation Gene; H.sapiens mRNA; UV Radiation Resistance Associated Gene.	2644	35750 at	HT010	AL049948	HT010	
HT012 AI760162 HT012  HT012 AI760162 Uncharacterized hypothalamus protein HT012 AI760162 HT012  UNRIP X14487 (or acidic (type I) cytokeratin 10.  UNRIP AB024327 unr-interacting protein UNREB1 AB002310 protein 1  UNG Y09008 uracil-DNA glycosylase Unidine monophosphate synthetase and (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)  UMPS J03626 orotidine-5'-decarboxylase)  UST AB020316 uronyl-2-sulfotransferase  UV Radiation Resistance Associated Gene; H.sapiens mRNA; UV Radiation UVRAG X99050 Resistance Associated Gene.		-			uncharacterized hypothalamus protein	
HT012 AI760162 HT012 Unnamed protein product; Human gene KRT10; KPP X14487 for acidic (type l) cytokeratin 10.  UNRIP AB024327 unn-interacting protein upstream regulatory element binding protein 1 V09008 uracil-DNA glycosylase (orotate phosphoribosyl transferase and unidine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)  UMPS J03626 orotidine-5'-decarboxylase)  UST AB020316 uronyl-2-sulfotransferase  UV Radiation Resistance Associated Gene.  Resistance Associated Gene.	2645	41058 g at	HT012	AI760162	HT012	
HT012 AI760162 HT012  Unnamed protein product; Human gene KRT10; KPP X14487 for acidic (type I) cytokeratin 10.  UNRIP AB024327 unr-interacting protein UNEB1 AB002310 upstream regulatory element binding UNG Y09008 uracil-DNA glycosylase uridine monophosphate synthetase and (orotate phosphoribosyl transferase and UMPS J03626 orotidine-5'-decarboxylase)  UST AB020316 uronyl-2-sulfotransferase Gene; H.sapiens mRNA; UV Radiation Gene; H.sapiens mRNA; UV Radiation Resistance Associated Gene.					uncharacterized hypothalamus protein	
KRT10; KPP X14487 for acidic (type I) cytokeratin 10.  UNRIP AB024327 unr-interacting protein  UREB1 AB002310 upstream regulatory element binding  UNG Y09008 uracil-DNA glycosylase  uridine monophosphate synthetase and  uridine monophosphate synthetase and  (orotate phosphoribosyl transferase and  ONST AB020316 uronyl-2-sulfotransferase  UV Radiation Resistance Associated  Gene; H.sapiens mRNA; UV Radiation  Resistance Associated Gene.	2646	41057 at	HT012	AI760162	HT012	
KRT10; KPP   X14487   for acidic (type I) cytokeratin 10.		6			unnamed protein product; Human gene	
UNRIP AB024327 unr-interacting protein  UREB1 AB002310 protein 1  UNG Y09008 uracil-DNA glycosylase  UNG uridine monophosphate synthetase and orotidine-5'-decarboxylase)  UMPS J03626 orotidine-5'-decarboxylase)  UST AB020316 uronyl-2-sulfotransferase  UV Radiation Resistance Associated Gene, H.sapiens mRNA; UV Radiation  Gene, H.sapiens mRNA; UV Radiation  Resistance Associated Gene.	2647	38610 s at	KRT10; KPP	X14487	for acidic (type I) cytokeratin 10.	keratin 10
UNEB1 AB002310 protein 1  UNG Y09008 uracil-DNA glycosylase  UNG V09008 uracil-DNA glycosylase  uridine monophosphate synthetase and orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)  UMPS J03626 orotidine-5'-decarboxylase)  UST AB020316 uronyl-2-sulfotransferase  UV Radiation Resistance Associated Gene, H.sapiens mRNA; UV Radiation  Resistance Associated Gene.	2648	34402 at	UNRIP	AB024327	unr-interacting protein	WD-40 repeat protein
at UNG Y09008 uracil-DNA glycosylase UNG Y09008 uridine monophosphate synthetase (orotate phosphoribosyl transferase and UMPS J03626 orotidine-5'-decarboxylase)  UST AB020316 uronyl-2-sulfotransferase UV Radiation Resistance Associated Gene; H.sapiens mRNA; UV Radiation Gene; H.sapiens mRNA; UV Radiation Resistance Associated Gene.					upstream regulatory element binding	upstream regulatory element binding protein
at UNG Y09008 uracil-DNA glycosylase uridine monophosphate synthetase (orotate phosphoribosyl transferase and UMPS J03626 orotidine-5'-decarboxylase)  UST AB020316 uronyl-2-sulfotransferase UV Radiation Resistance Associated Gene; H.sapiens mRNA; UV Radiation Gene; H.sapiens mRNA; UV Radiation Resistance Associated Gene.	2649	34372 at	UREB1	AB002310	protein 1	
UMPS J03626 uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)  UST AB020316 uronyl-2-sulfotransferase UV Radiation Resistance Associated Gene; H.sapiens mRNA; UV Radiation UVRAG X99050 Resistance Associated Gene.	2650	37686 s at	UNG	Y09008	uracil-DNA glycosylase	uracil-DNA glycosylase
UMPS J03626 orotidine-5'-decarboxylase)  UST AB020316 uronyl-2-sulfotransferase UV Radiation Resistance Associated Gene; H.sapiens mRNA; UV Radiation UVRAG X99050 Resistance Associated Gene.		1			uridine monophosphate synthetase	uridine monophosphate synthetase (orotate
UST AB020316 uronyl-2-sulfotransferase UST AB020316 uronyl-2-sulfotransferase UV Radiation Resistance Associated Gene; H.sapiens mRNA; UV Radiation Cene; H.sapiens mRNA; UV Radiation NVRAG X99050 Resistance Associated Gene.					(orotate phosphoribosyl transferase and	phosphoribosyl transferase and orotidine-5'-
UST AB020316 uronyl-2-sulfotransferase UV Radiation Resistance Associated Gene; H.sapiens mRNA; UV Radiation X99050 Resistance Associated Gene.	2651	33815 at	UMPS	J03626	orotidine-5'-decarboxylase)	decarboxylase)
UST AB020316 uronyl-2-sulfotransferase UV Radiation Resistance Associated Gene; H.sapiens mRNA; UV Radiation X99050 Resistance Associated Gene.						dermatan/chondroitin sulfate 2-
UV Radiation Resistance Associated Gene; H.sapiens mRNA; UV Radiation LVRAG X99050 Resistance Associated Gene.	2652	41859 at	UST	AB020316	uronyl-2-sulfotransferase	suffotransferase
Gene; H.sapiens mRNA; UV Hadiation UVRAG X99050 Resistance Associated Gene.					UV Radiation Resistance Associated	
UVRAG   X99050   Hesistance Associated Gene.					Gene; H.sapiens mHNA; UV Hadiation	(may) broscores/ com
	2653	39429_at	UVRAG	X99050	Resistance Associated Gene.	pos (processed roun)

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T					v-abl Abelson murine leukemia viral
	•				oncogene homolog 1 isoform a; v-abl
		-		v-abl Abelson murine leukemia viral	Abelson murine leukemia viral oncogene
2654			X16416		homolog 1 isoform b
2655	2655 35779_at	5A	AJ133421	vacuolar protein sorting 45A (yeast)	vacuolar protein sorting
				VAMP (vesicle-associated membrane	
2656	2656 38801_at	VAPA	AI742846	protein)-associated protein A (33kD)	
					vascular cell adhesion molecule 1, isoform a
					precursor; vascular cell adhesion molecule
2657 583	583 s at	VCAM1	M30257	vascular cell adhesion molecule 1	1, isoform b precursor
2658	3 at		AF024710	vascular endothelial growth factor	vascular endothelial growth factor
2659	o at	VEGF	AF022375	vascular endothelial growth factor	vascular endothelial growth factor
					VEGF related factor isoform VRF186
2660	2660 37268 at	VEGFB	U43368	vascular endothelial growth factor B	precursor
100	100		1142340		vascular endothelial growth factor related protein
007	2001 139_at		043142		
				VDAC protein; similar to mouse VDAC 3;	
				Homo sapiens voltage dependent anion	
2662	2662 36102_at	VDAC3; HD-VDA	DA0AF038962	channel protein mRNA, complete cds.	voltage dependent anion channel protein
2663	2663 40147_at		U18009	vesicle amine transport protein 1	vesicle amine transport protein 1
2664	2664 33930_at	RA410	AB020724	vesicle transport-related protein	KIAA0917 protein
				vesicle-associated membrane protein 2	
2665	2665 32254_at	VAMP2	AL050223	(synaptobrevin 2)	
				vesicle-associated membrane protein 3	
2666	2666 35783_at	VAMP3	H93123	(cellubrevin)	
2667	2667 40103_at	VIL2	X51521	villin 2 (ezrin)	villin 2
2668	2668 34091 s at	WIX	Z19554	vimentin	vimentin
					vinculin isoform VCL; VCL isoform meta-
2669	2669 36601_at	VCL	M33308	vinculin	NCL
2670	2670 39091 at	-iwa	AF070523	vitamin A responsive: cytoskeleton related JWA protein	JWA protein
	-			vitamin D (1,25- dihydroxyvitamin D3)	vitamin D (1,25- dihydroxyvitamin D3)
2671	2671 1388 g_at	VDR	J03258	receptor	receptor
				v-Ki-ras2 Kirsten rat sarcoma 2 viral	
2672	2672 1940_at	KRAS2	M54968	oncogene homolog	K-ras oncogene protein
				•	

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				v-maf musculoaponeurotic fibrosarcoma	
2673	2673 41504_s_at	MAF	AF055376	oncogene homolog (avian)	short form transcription factor C-MAF
				v-maf musculoaponeurotic fibrosarcoma	
2674	2674 32835_at	MAFF	AA725102	oncogene homolog F (avian)	
2675	2675 40198 at	VDAC1	L06132	voltage-dependent anion channel 1	voltage-dependent anion channel
2676	2676 37696 at	VDAC2	L06328	voltage-dependent anion channel 2	voltage-dependent anion channel
2677	2677 171 at	VBP1	U56833	von Hippel-Lindau binding protein 1	VHL binding protein-1
				v-raf-1 murine leukemia viral oncogene	
2678	2678 38743_f_at	RAF1	X06409	homolog 1	
				v-ral simian leukemia viral oncogene	
				homolog B (ras related; GTP binding	v-ral simian leukemia viral oncogene
2679	2679 32776 at	RALB	M35416	protein)	homolog B
				v-rel reticuloendotheliosis viral oncogene	
				homolog A, nuclear factor of kappa light	
				polypeptide gene enhancer in B-cells 3,	
2680	2680 36645_at	RELA	L19067	p65 (avian)	NF-kappa-B transcription factor subunit
				v-rel reticuloendotheliosis viral oncogene	
				homolog A, nuclear factor of kappa light	
				polypeptide gene enhancer in B-cells 3,	
2681	2681 1295 at	RELA	L19067	p65 (avian)	NF-kappa-B transcription factor subunit
				v-yes-1 Yamaguchi sarcoma viral	v-yes-1 Yamaguchi sarcoma viral oncogene
2682	2682 1674 at	YES1	M15990	oncogene homolog 1	homolog 1
				v-yes-1 Yamaguchi sarcoma viral related	v-yes-1 Yamaguchi sarcoma viral related
268	2683 1402 at	LXN	M16038	oncogene homolog	oncogene homolog
268	2684 1058 at	WASF3	S69790	WAS protein family, member 3	
268	2685 38736_at	WDR1	AL050108	WD repeat domain 1	hypothetical protein
2686	2686 41430_at	WDR7	AB011113	WD repeat domain 7	KIAA0541 protein
268.	2687 36009_at	CI 683	AE091092	weakly similar to dutathione peroxidase 2	weakh similar to glutathione peroxidase 2
	SERRIZEGNO at	WEE1	X62048	WEE1+ homolog (S. pombe)	wee1 tyrosine kinase
	m_0000				eukaryotic translation initiation factor 4H,
				Williams-Beuren syndrome chromosome	isoform 1; eukaryotic translation initiation
268	2689 41212_r_at	WBSCR1	D26068	region 1	factor 4H, isoform 2
269	2690 41635_at	WTAP	D14661	Wilms' tumour 1-associating protein	Wilms' turnour 1-associating protein
_				wingless-type MMTV integration site	wingless-type MMTV integration site family,
269	2691 31862_at	WNT5A	120861	family, member 5A	member 3A precursor

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T					Wolf-Hirschhorn syndrome candidate 2
:1692	34225 at	WHSC2	AF101434	Wolf-Hirschhorn syndrome candidate 2	protein
2693	2693 33438 at	WBP2	AL049981	WW domain binding protein 2	
				WW domain binding protein 4 (formin	•
2694	35213 at	WBP4	AF071185	binding protein 21)	formin binding protein 21
2695	2695 39995 s at	WWOX	U13395	ining oxidoreductase	oxidoreductase
2696	2696 36822 at	WAC	U51334		putative RNA binding protein RBP56
				xeroderma pigmentosum,	
2697 1307	1307 at	XPA	D14533	complementation group A	XPAC protein
				xeroderma pigmentosum,	
2698	2698 1873 at	XPC	D21089	complementation group C	XP-C repair complementing protein (p125)
				XPA binding protein 1; putative ATP(GTP)-	
2699	2699 41756_at	NTPBP	AJ010842	binding protein	ATP(GTP)-binding protein
				X-ray repair complementing defective	
				repair in Chinese hamster cells 5 (double-	
				strand-break rejoining; Ku autoantigen,	
2700	2700 38733 at	XRCCS	M30938	80kD)	ATP-dependant DNA helicase II
				X-ray repair complementing defective	-
				repair in Chinese hamster cells 5 (double-	
				strand-break rejoining; Ku autoantigen,	:
2701	2701 585 at	XRCC5	M30938	80kD)	ATP-dependant DNA helicase II
				X-ray repair complementing defective	
			•	repair in Chinese hamster cells 5 (double-	
				strand-break rejoining; Ku autoantigen,	:
2702	2702 2093 s at	XRCC5	J04977	80KD)	ATP-dependant DNA helicase II
2703	2703 35827 at	KIAA0905	AB020712	yeast Sec31p homolog	KIAA0905 protein
2704	2704 40988 at	YME1L1	AJ132637	YME1-like 1 (S. cerevisiae)	ATP-dependent metalloprotease YME1L
2705	2705 891 at	1771	M77698	YY1 transcription factor	GLI-Krupple related protein
				zb29g04.s1	
				Soares_parathyroid_tumor_NbHPA Homo	
				sapiens cDNA clone IMAGE:305046 3,	
2706	2706 34887_at		N92548	mRNA sequence.	
				Zic family member 1 (odd-paired homolog,	
2707	2707 36308_at	ZIC1	D76435	Drosophila)	Zic protein
2708	2708 35681 r at	ZFHX18	AB011141	zinc finger homeobox 1b	KIAA0569 protein



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2709 34786	4786_at	TSGA	AB018285		KIAAU/42 protein
2710 39977		ZNF-U69274	U69274		zinc finger protein
27114	9711 40140 at	ZFP103	D76444	zinc finger protein 103 homolog (mouse)	zinc finger protein 103 homolog
27123	2712 36295 at	ZNF134		zinc finger protein 134 (clone pHZ-15)	zinc finger protein ZNF134
27133	2713 32192 a at	ZNF144		zinc finger protein 144 (Mel-18)	Mel-18 protein
27143		ZNF146	X70394	zinc finger protein 146	zinc finger protein
27154	2715 41532 at	ZNF151	Y09723	zinc finger protein 151 (pHZ-67)	Miz-1 protein
2716	2716 32628 at	ZNF161		zinc finger protein 161	DB1
2717	2717 41436 at	ZNF198	5	zinc finger protein 198	ZNF198 protein
27184	2718 40724 at	ZNF200	Y14443	zinc finger protein 200	zinc finger protein
2719	2719 35368 at	ZNF207	9	zinc finger protein 207	zinc finger protein 207
2720	2720 41542 at	ZNF216	AF062346	zinc finger protein 216	zinc finger protein 216 splice variant 1
2721	2721840 at	ZNF220	U47742	zinc finger protein 220	monocytic leukaemia zinc finger protein
2722	2722 39762 at	ZNF262	AB007885	zinc finger protein 262	zinc finger protein 262
2723	2723 34299 at	ZNF278	AL096880	zinc finger protein 278	hypothetical protein
2724	2724 39005 s at	ZNF294	AB018257	zinc finger protein 294	KIAA0714 protein
2725	2725 37860 at	ZNF337	AL049942	zinc finger protein 337	hypothetical protein
	1			zinc finger protein 36, C3H type, homolog	
2726	2726 40448 at	ZFP36	M92843	(mouse)	zinc finger transcriptional regulator
7777	2727 38740 at	ZFP36L1	X79067	zinc finger protein 36, C3H type-like 1	butyrate response factor 1
977g	2728 36046 at	7NF363	AI 050144	zinc finger protein 363	hypothetical protein
37,7	מבססס				hypothetical protein, similar to (U06944)
9226	2729 32129 at	ZNF364	AL079314	zinc finger protein 364	PRAJA1 [Mus musculus]
2730		ZNF84	M27878	zinc finger protein 84 (HPF2)	DNA binding protein
2731	<b>1</b> 1 :	ZFR	AI743507	zinc finger RNA binding protein	
2732		ZDHHC3	AF052182	zinc finger, DHHC domain containing 3	
				zinc metalloproteinase (STE24 homolog,	
2733	2733 33912_at	ZMPSTE24	Y13834	yeast)	farnesylated-proteins converting enzyme 1
2734	2734 36521 at	DZIP1	AB023213	zinc-finger protein DZIP1	KIAA0996 protein
2735	2735 35995 at	ZWINT	AF067656	ZW10 interactor	ZW10 interactor Zwint
2736	2736 706 at		HG4582-HT4987		
2737	2737 960_g_at		HG2463-HT2559		
2738	2738 956_at		HG1980-HT2023		
2739	2739 955_at		HG1862-HT1897		
2740	2740 324_f_at		HG1515-HT1515		

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2741	2741 327_f_at		HG1800-HT1823		
2742	2742 333_s_at		HG2639-HT2735		
2743	2743 1840 g at		HG1112-HT1112		
2744	2744 1664_at	٠	HG3543-HT3739		
2745	2745 1624_at		HG2036-HT2090		
2746	2746 1278_at		HG162-HT3165		
2747	2747 1179_at		HG2855-HT2995		
2748	2748 1180_g_at		HG2855-HT2995		
2749	2749 32243_g_at		AL038340		
2750	2750 311_s_at		HG3044-HT3742		
2751	2751 297_g_at		HG4322-HT4592		
2752	2752 296_at		HG4322-HT4592		
2753	2753 1839_at		HG1112-HT1112		
2754	2754 723_s_at		HG1322-HT5143		
					guanine nucleotide binding protein (G
2755	2755 33300_at	dJ283E3.1	AL031282		protein), beta polypeptide 1
Ŀ					guanine nucleotide binding protein (G
2756	2756 41249_at	dJ283E3.1	AL031282		protein), beta polypeptide 1

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<u> </u>	Systematic	Common	Genbank	Description	Product
				***ALU WARNING: Human Alu-Sq	
2	AFFX-hum alu at	31	U14573	subfamily consensus sequence.	
T	38820 at		15-Sep AF051894	15 kDa selenoprotein	15 kDa selenoprotein
Т				26S proteasome-associated pad1	
4	33247 at	POH1	U86782	homolog	26S proteasome-associated pad1 homolog
				35 kDa protein; Homo sapiens splicing	
				factor, arginine/serine-rich 7 (SFRS7)	
ည	32165_at	SFRS7	L41887	gene, complete cds.	splicing factor, arginine/serine-rich 7
				39 kDa protein; Human N33 protein form	
y	36851 g at	N33	U42360		N33 protein form 2
				3-hydroxy-3-methylglutaryl-Coenzyme A	3-hydroxy-3-methylglutaryl-Coenzyme A
7	39328 at	HMGCR	M11058	reductase	reductase
					succinyl CoA:3-oxoacid CoA transferase
∞	41142 at	OXCT	U62961	3-oxoacid CoA transferase	precursor
L				3'-phosphoadenosine 5'-phosphosulfate	
6	34411_at	PAPSS1	Y10387	synthase 1	PAPS sunthetase
2	738_at	NT5C2	D38524	5'-nucleotidase, cytosolic II	5'-nucleotidase
=	31794_at	NT5C2	D38524	5'-nucleotidase, cytosolic II	5'-nucleotidase
				5-aminoimidazole-4-carboxamide	
				ribonucleotide formytransferase/IMP	5-aminoimidazole-4-carboxamide-1-beta-D-
12	38811 at	ATIC	D82348	cyclohydrolase	ribonucl eotide transformylase/inosinicase
				5-methyltetrahydrofolate-homocysteine	
13	38383_at	MTR	U73338	methyltransferase	methionine synthase
14	39025 at	LOC54543	AI557912	6.2 kd protein	
	_				

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ä		divalent cation tolerant protein CUTA	delta7-sterol reductase	ADAM10		metalloprotease/disintegrin/cysteine-rich		graviii		KIAA0629 protein	KIAA0920 protein
0	60S Ribosomal Protein L35A LIKE pseudogene match: proteins P04646 P02434 P18077 P05744 P41056 CE04362 match: cDNAs Y16430 X52966 X03475 V01440 X55030 J00995 match: ESTs AA554649 AA747384 AA572868 AA329139 AA745138 AA330809 AA483371 AA507788 AA483213 D55111 N90267 N91909 AA662153 AA720551 AA836920 AA501529 AA526745 AA608598 AA649846 AA654164 match: genomic DNAs Z32550 X05705 X05706	X05704 123465 145758	7-dehydrocholesterol reductase	a disintegrin and metalloproteinase domain 10	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha,	a disintegrin and metalloproteinase	A kinase (PRKA) anchor protein (gravin)	71	A kinase (PHKA) anchor protein 10	A kinase (PRKA) anchor protein 11	A kinase (PRKA) anchor protein 2
O		AL021366	AF034544	AF009615	AA142964	1141766	200701	08160/	AA114830	AB014529	AB023137
8		cICK0721Q.1	DHCR7	ADAM10	ADAM17	ADAMo		AKAP12	AKAP10	AKAP11	AKAP2
A	·	40446_at	39059_at	40797_at	41601 at				36633_at	22 34657_at	35985_at
		15	16	17	<u>α</u>	2 9		ន	21	22	23

Fig 21

ABL is the cellular honcogene of Abelso virus and is associate chromosomal translegene in chronic mye lymphoblastic leuken splicing using altern ABL is the cellular honcogene of Abelso virus and is associat chromosomal translegene in chronic mye lymphoblastic leuken splicing using altern ABL is the cellular honcogene of Abelso virus and is associat chromosomal translegene in chronic mye lymphoblastic leuken splicing using exon oncogene tyrosine-Figene, exon 1a and concogene tyrosine-Igene, exon 1a and acetyl-Coenzyme A (mitochondrial 3-ox AB016294 thiolase)  AA669799 acetylserotonin O-macidic (leucine-rich) phosphoprotein 32 acidic (leucine-rich) 211559 acidic (leuc	_				1	$\overline{}$						$\neg$	
A B C C  1636_g_at ABL U07563  41724_at DXS1357E X81817  41724_at ACAA2 D16294  3468_at ACATN D88152  36553_at ANP32A U73477  38479_at ANP32B Y07969  34397_at OA48-18 AF069250  39168_at ACO1 Z11559  40077_at ACO1 Z11559  37578_at ARPC U50523	<b>W</b>	proto-oncogene tyrosine-protein kinase	accessory proteins BAP31/BAP29	mitorhondrial 3-oxoacyl-CoA thiolase	acetyl-coenzyme A transporter		acidic nuclear phosphoprotein pp32	APRIL	okadaic acid-inducible phosphoprotein	KIAA0785 protein	iron regulatory factor	actin filament associated protein	actin related protein 2/3 complex, subunit 2 (34 kD)
A B C C  1636_9_at ABL U07563  41724_at DXS1357E X81817  41724_at DXS1357E X81817  41530_at ACAA2 D16294  34668_at ACATN D88152  36553_at ACATN D88152  36553_at ANP32A U73477  38479_at ANP32B Y07969  34397_at OA48-18 AF069250  39168_at ALTE AB018328  40077_at ACO1 Z11559  37578_at AFAP D25248	D	ABL is the cellular homolog proto- oncogene of Abelson's murine leukemia virus and is associated with the 19:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; alternative splicing using alternative first exon 1b; ABL is the cellular homolog proto- oncogene of Abelson's murine leukemia virus and is associated with the 19:22 chromosomal translocation with the BCR gene in chronic myelogenous and acute lymphoblastic leukemia; alternative splicing using exon 1a; Human proto- oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete	accessory proteins BAP31/BAP29	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A	acetyl-Coenzyme A transporter	acetylserotonin O-methyltransferase-like	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	acid-inducible phosphoprotein	Ac-like transposable element	aconitase 1, soluble	actin filament associated protein	actin related protein 2/3 complex, subunit 2 (34 kD)
A 1636_g_at 41724_at 41724_at 41724_at 34668_at 34668_at 36553_at 36553_at 36553_at 37034_at 37034_at 37034_at 37558_at 3757_at	C		X81817	D16204	D88152	AA669799	U73477	Y07969	AF069250	AB018328	Z11559	D25248	U50523
	В	ABL	DXS1357E	640	ACATN	ASMTL	ANP32A	ANP32B	OA48-18	ALTE	ACO1	AFAP	ARPC2
	A	1636_g_at	41724_at	41620 of	41550_at 34668_at	36553_at	37034_at	38479_at	34397_at	39168_at	40077_at	37578_at	1718_at
			_				29	8			i	1 1	35

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	A	8	ပ	0	u
				ed protein 2/3 complex, subunit	
39	34692_r_at	ARPC4	AF006087		p20-Arc
1				ed protein 2/3 complex, subunit	
ကို	38392 at	ARPC5	AF006088		p16-Arc
17		ACTA2	X13839	actin, alpha 2, smooth muscle, aorta	alpha 2 actin
11:	AC07/	ACTB	X00351	actin, beta	beta actin
-	AFFX-HSAC07/AACTB	ACTB	X00351	actin, beta	beta actin
رتوا	32318 s at	ACTB	X63432	actin, beta	mutant beta-actin (beta'-actin)
15		ACTG1	X04098	actin, gamma 1	gamma-actin
12		ACTN1	X15804	actinin, alpha 1	actinin, alpha 1
1:-1	at	ACTN4	U48734	actinin, alpha 4	alpha actinin
_ <b>≂</b>	38642 at	ALCAM	Y10183	activated leucocyte cell adhesion molecule MEMD protein	MEMD protein
				activated RNA polymerase II transcription	
	36171_at	PC4	AI521453	cofactor 4	
1	39764_at	ACVR1	Z22534	activin A receptor, type I	ALK-2
110	sat	ACVR2	D31770	activin A receptor, type II	activin typell A receptor precursor
1 ***		ADNP	AB018327	activity-dependent neuroprotector	KIAA0784 protein
				acyl-Coenzyme A dehydrogenase,	
£ 7	40673_at	ACADSB	U12778		acyl-CoA dehydrogenase
ľ	40459_at	ACOX1	Se9189	acyl-Coenzyme A oxidase 1, palmitoyl	peroxisomal acyl-coenzyme A oxidase
1				adaptor-related protein complex 1, beta 1	
-c	40745_at	AP1B1	L13939	subunit	beta-prime-adaptin
				adaptor-related protein complex 1,	•
ഥ	35275_at	AP1G1	AL050025	gamma 1 subunit	hypothetical protein
1				adaptor-related protein complex 2, mu 1	adaptor-related protein complex 2, mu 1
Ο,	39795_at	AP2M1	D63475	subunit	subunit
1				adaptor-related protein complex 2, sigma	
တ	39347 at	AP2S1	X97074	1 subunit	clathrin-associated protein
1				adaptor-related protein complex 3, beta 1	
Ċ	32039_at	AP3B1	U81504	subunit	beta-3A-adaptin subunit of the AP-3 complex
1				adaptor-related protein complex 3, delta 1	
بي	36172_s_at	AP3D1	AF002163	subunit	delta-adaptin
l l				adaptor-related protein complex 3, sigma	
==	38074_at	AP3S1	U91932	1 subunit	AP-3 complex sigma3A subunit
1.7	33102 at	ADD3	D67031	adducin 3 (gamma)	adducin-like protein



38748_at ADARB1 U76421 168_at ADARB1 U76421 168_at ADK U50196 33865_at ADCY3 AB0110 40585_at ADCY7 D25538 33800_at ADCY7 D25538 40788_at ADCY7 D25538 33405_at ADSL AF0376 33405_at ADFP X97324 334378_at ADFP X97324 33587_at ARF1 M3634 33587_at ARF4 M3634 33585_at ARF4 M3634 33585_at ARF4 M3634 33585_at ARF1 AA49 33585_at ARF1 AA49 33585_at ARF1 AA49 33585_at ARF4 M3634 317296_at ARF6AP1 L28997 34777_at ADPRT J03477 332218 at ADPRT D1487	r	4	В	ပ	Q	ш
38014_at   ADAR   X79448   adenosine dearninase, RNA-specific adenosine dearninase, RNA-specific adenosine dearninase, RNA-specific, B1 (RED1 homolog rat)	T					
38014_at   ADAR   X79448   adenosine dearninase, RNA-specific B1						adenosine deaminase, RNA-specific,
38748 at ADARB						isoform ADAR-a; adenosine deaminase,
38014_at         ADAR         X7948         adenosine deaminase, RNA-specific           38748_at         ADARB1         U76421         (RED1 homolog rat)           186_at         ADARB1         U76421         (RED1 homolog rat)           186_at         ADK         U50196         adenosine deaminase, RNA-specific, B1           186_at         ADK         U50196         adenovirus S E1A binding protein           1868_at         ADCY3         AB011083         adenylate cyclase 3           33800_at         ADCY3         AR03827         adenylate cyclase 9           40788_at         ADCY3         AF067853         adenylate kinase 2           33653_at         ADCY3         AF067853         adenylate kinase 2           3405_at         ADCY3         AF067853         adenylate kinase 2           3405_at         ADCY3         AF067853         adenylate kinase 2           3405_at         ADCAP         ADG785         adenylate kinase 2           3405_at         ADCAP         ADG785         adenylate kinase 2           3405_at         ADCAP         ADG785         adenylate cyclase 3sociated protein           3406_at         ADFF         ADG4896         adlenylate kinase 2           3405_at         ADFF						RNA-specific, isoform ADAR-b; adenosine
38748_at         ADARB1         U76421         (RED1 homolog rat)           168_at         ADK         U50196         adenosine deaminase, RNA-specific, B1           168_at         ADK         U50196         adenosine kinase           33865_at         ADCY3         AB011083         adenovirus E1A binding protein           40585_at         ADCY7         D25538         adenylate cyclase 7           33800_at         ADCY9         AF036927         adenylate cyclase 7           33800_at         ADCY9         AF036927         adenylate cyclase 7           33800_at         ADCY9         AF067853         adenylate cyclase 9           40788_at         ADCY9         AF067853         adenylate cyclase 9           33659_at         ADCY9         AF067853         adenylate kinase 2           36539_at         ADCP         N90755         adenylate kinase 2           36539_at         ADFP         ADFP         ADFP           3340_bat         CAP2         N90755         adenylate kinase 2           3343_bat         CAP2         N90755         adenylate kinase 2           3343_bat         ABF1         M36340         ADF-ribosylation factor 1           35856_at         ARF4         M36341         ADF-ri		38014 at	ADAR	X79448	adenosine deaminase, RNA-specific	deaminase, RNA-specific, isoform ADAR-c
38748_at         ADARB1         U76421         (RED1 homolog ral)           158_at         ADK         U50196         adenosine kinase           33865_at         BS69         AA127624         adenovirus E E1A binding protein           33134_at         ADCY3         AB011083         adenylate cyclase 3           40565_at         ADCY3         AF038927         adenylate kinase 2           33800_at         ADCY9         AF038927         adenylate kinase 2           40788_at         ADSL         AF067853         adenylate kinase 2           36539_at         ADSL         AF067853         adenylate kinase 2           36539_at         ADSL         AF067853         adenylate kinase 2           36539_at         ADSL         L12168         adenylate kinase 2           36631_at         ADSL         AF067853         adenylate kinase 2           36861_at         ADSL         L12168         adenylate kinase 2           36861_at         ADF         X97324         adipose differentiation-related protein           36861_at         ARF1         M36340         ADP-ribosylation factor 1           38368_at         ARF4         M36341         ADP-ribosylation factor 3           38368_at         ARFA         ARFGA	_	-			adenosine deaminase, RNA-specific, B1	
168_at   ADK   U50196   adenosine kinase   33865_at   BS69   AA127624   adenovirus 5 E1A binding protein   33865_at   ADCY3   AB011083   adenylate cyclase 3   ADCY7   D25538   adenylate cyclase 9   ADCY3   AF036927   adenylate cyclase 9   ADCY9   AF036927   adenylate cyclase 9   ADCY9   AF036927   adenylate kinase 2   33805_at   ADCY9   AF036927   adenylate kinase 2   33659_at   ADCY9   AF036927   adenylate kinase 2   33659_at   ADCY9   AF036927   adenylate kinase 2   33405_at   ADCY9   AF036927   adenylate kinase 2   33405_at   ADCY9   61	38748 at		U76421	(RED1 homolog rat)	dsRNA adenosine deaminase DRADA2b	
333855_at         BS69         AA127624         adenovirus 5 E1A binding protein           33134_at         ADCY3         AB011083         adenylate cyclase 3           40585_at         ADCY7         D25538         adenylate cyclase 7           33800_at         ADCY7         D25538         adenylate cyclase 9           40788_at         ADCY9         AF036927         adenylate cyclase 9           40788_at         ADCY9         AF036927         adenylate cyclase 9           33800_at         ADCY         AF067853         adenylate cyclase 9           33405_at         CAP         L12168         adenylate cyclase 9           33405_at         CAP         L12168         adenylyl cyclase-associated protein 2           34378_at         ADFP         N90755         adenylyl cyclase-associated protein 2           34378_at         ADFP         ADF-ribosylation factor 1           33987_at         ARFT         ADF-ribosylation factor 1           33987_at         ARFT         ADF-ribosylation factor 1           35585_at         ARFGAP1         AA402332         ADP-ribosylation factor 1           3553_at         ARFGAP1         AA402332         ADP-ribosylation factor 1           3553_at         ARLI         AA402332	Т		ADK	U50196	adenosine kinase	adenosine kinase
33134_at         ADCY3         AB011083         adenylate cyclase 3           40585_at         ADCY7         D25538         adenylate cyclase 7           33800_at         ADCY9         AF036927         adenylate kinase 2           40788_at         AKZ         U84371         adenylate kinase 2           40788_at         AAPC         U84371         adenylate kinase 2           40788_at         ADSL         AF067853         adenylosuccinate lyase           33405_at         CAP         L12168         adenylosuccinate lyase           33405_at         CAPZ         N97524         adenylosuccinate lyase           33405_at         CAPZ         N97524         adenylosuccinate lyase           33405_at         ADFP         X97324         adenylosuccinate lyase           33887_at         ADFP         X97324         adiconnormation factor 1           38861_at         ARF1         M36340         ADP-ribosylation factor 1           38862_at         ARF4         M36341         ADP-ribosylation factor GTPase activating           38585_at         ARFA         AAA02332         protein 1           3753_at         ARFGAP1         L04510         64kD           38572_r         ARLIP         L28997	1	at	BS69	AA127624	adenovirus 5 E1A binding protein	
40585_at         ADCY7         D25538         adenylate cyclase 7           33800_at         ADCY9         AF036927         adenylate cyclase 9           40788_at         ADCY9         AF036927         adenylate kinase 2           36639_at         ADSL         AF067853         adenylate kinase 2           36639_at         ADSL         AF067853         adenylyl cyclase-associated protein           3653_at         CAP         N90755         adenylyl cyclase-associated protein           34378_at         ADFP         X97324         adenylyl cyclase-associated protein           36861_at         ADFP         X97324         adenylyl cyclase-associated protein           36861_at         ADFP         X97324         adenylyl cyclase-associated protein           36861_at         ABFT         M36340         ADP-ribosylation factor 1           38336_at         ARFT         M36341         ADP-ribosylation factor 3           38586_at         ARFT         ADP-ribosylation factor GTPase activating           37537_at         ARFGAP1         L04510         ADP-ribosylation factor GTPase activating           37537_at         ARFGAP1         AA402332         ADP-ribosylation factor GTPase activating           385572_r at         ARL6IP         AA402332         ADP	T -		ADCY3	AB011083	adenylate cyclase 3	KIAA0511 protein
33800_at         ADCY9         AF036927         adenylate kinase 2           40788_at         AK2         U84371         adenylate kinase 2           40788_at         AK2         U84371         adenylosuccinate lyase           36539_at         ADSL         AF067853         adenylosuccinate lyase           935_at         CAP         L12168         adenylyl cyclase-associated protein           33405_at         CAP2         N90755         adenylyl cyclase-associated protein           34378_at         ADF         N90755         adenylyl cyclase-associated protein           34378_at         ARF1         N907324         adipose differentiation-related protein           33881_at         ARF3         M74491         ADP-ribosylation factor 1           39336_at         ARF4         M36341         ADP-ribosylation factor 1           39336_at         ARF7         ADP-ribosylation factor 4           35585_at         ARFA         ADP-ribosylation factor domain protein 1,           37537_at         ARFGAP1         L04510         64kD           37537_at         ARLGAP1         AA402332         ADP-ribosylation factor-like 6 interacting           37532_r         ARLGAP1         AA402332         ADP-ribosylation factor-like 6 interacting			ADCY7	D25538	adenylate cyclase 7	adenylate cyclase 7
40788_at         AK2         U84371         adenylate kinase 2           36639_at         ADSL         AF067853         adenylosuccinate lyase           36639_at         ADSL         AF067853         adenylyl cyclase-associated protein           3345_at         CAP         L12168         adenylyl cyclase-associated protein           334578_at         ADFP         X97324         adjpose differentiation-related protein           36861_at         DKFZp56411922         AL049946         adilican           39887_at         ARF1         M36340         ADP-ribosylation factor 1           39336_at         ARF4         M36341         ADP-ribosylation factor 3           36585_at         ARF4         ADP-ribosylation factor 4           37537_at         ARFA         ADP-ribosylation factor GTPase activating           37536_at         ARL1         L28997         ADP-ribosylation factor GTPase activating           36572_r_at         ARLGP         AA402332         ADP-ribosylation factor GTPase activating           34777_at <td>99</td> <td></td> <td>ADCY9</td> <td>AF036927</td> <td>adenylate cyclase 9</td> <td>adenylyl cyclase type IX</td>	99		ADCY9	AF036927	adenylate cyclase 9	adenylyl cyclase type IX
36639_at         ADSL         AF067853         adenylosuccinate lyase           935_at         CAP         L12168         adenylyl cyclase-associated protein           935_at         CAP2         N90755         adenylyl cyclase-associated protein           334378_at         ADFP         X97324         adipose differentiation-related protein           3661_at         DKFZp56411922         AL049946         adilcan           35861_at         DKFZp56411922         AL049946         adilcan           39861_at         DKFZp56411922         AL049946         adilcan           39886_at         ARFA         M74491         ADP-ribosylation factor 1           39805_i_at         ARFD1         L04510         6AkD           37537_at         ARFD1         L04510         ADP-ribosylation factor GP ase activating protein 1           37596_at         ARFL1         L28997         ADP-ribosylation factor-like 1           37296_at         ARL1         L28997         ADP-ribosylation factor GP activating protein 1           36572_r_at         ARL6IP         D31885         protein 1           41146_at         ADPRT         J03473         ribose) polymerase)           34777_at         ADPRT         J03473         ribosyltransferase (NAD+; poly (ADP-polymerase)	т		AK2	U84371	adenylate kinase 2	adenylate kinase 2A
935_at         CAP         L12168         adenylyl cyclase-associated protein           33405_at         CAP2         N90755         adenylyl cyclase-associated protein           33405_at         ADFP         X97324         adipose differentiation-related protein           34378_at         ADFP         ADFP         ADFP           38861_at         DKFZp56411922         AL049946         adlican           39887_at         ARF1         M36340         ADF-ribosylation factor 1           399336_at         ARF3         M74491         ADF-ribosylation factor 3           39585_at         ARF4         ADF-ribosylation factor 4           39586_at         ARFGAP1         ADP-ribosylation factor 4           39586_at         ARFGAP1         ADP-ribosylation factor 4           ADP-ribosylation factor Momain protein 1         ADP-ribosylation factor 4           37296_at         ARFGAP1         AA402332         ADP-ribosylation factor-like 6 interacting protein           36572_r_at         ARLI         L28997         ADP-ribosylation factor-like 6 interacting protein           36572_rat         ADPRT         J03473         ADP-ribosyltransferase (NAD+; poly (ADP-ribosyltransferase (NAD+; poly (ADP-ribosylt	1		ADSL	AF067853	adenylosuccinate lyase	adenylosuccinate lyase
33405_at         CAP2         N90755         adenylyl cyclase-associated protein 2           34378_at         ADFP         X97324         adipose differentiation-related protein 3           36861_at         DKFZp56411922         AL049946         adilican adipose differentiation-related protein 2           38987_at         ARF1         M36340         ADP-ribosylation factor 1           39336_at         ARF3         M74491         ADP-ribosylation factor 3           36585_at         ARF4         M36341         ADP-ribosylation factor 4           37537_at         ARFD1         L04510         64kD           39005_i_at         ARFGAP1         AA40232         protein 1           37296_at         ARL1         AA40232         protein 1           37296_at         ARL6P         AA40232         ADP-ribosylation factor-like 6 interacting protein 1           36572_r_at         ARL6P         D31885         ADP-ribosylation factor-like 6 interacting protein ADP-ribosyltransferase (NAD+; poly (ADP-ribosyl adprenance) polymerase)           41146_at         ADPRT         J03473         ribose) polymerase)           34777_at         ADM         D14874         Adrenomedullin Approaches (NAD+; poly (ADP-ribosyl adprenance) Approaches (NAD+; poly (ADP-ribosyl adprenance) Approaches (NAD+; poly (ADP-ribosyl adprenance) Approaches (NAD+; poly (ADP-ribosyl adpren	Т	935 at	CAP	L12168	adenylyl cyclase-associated protein	adenylyl cyclase-associated protein
34378_at         ADFP         X97324         adipose differentiation-related protein           36861_at         DKFZp56411922         AL049946         adlican           33987_at         ARF1         M36340         ADP-ribosylation factor 1           39336_at         ARF3         M74491         ADP-ribosylation factor 3           36585_at         ARFA         M36341         ADP-ribosylation factor 4           37537_at         ARFD1         L04510         ADP-ribosylation factor domain protein 1, ADP-ribosylation factor domain protein 1, ADP-ribosylation factor domain protein 1           37296_at         ARL1         L28997         ADP-ribosylation factor-like 1           37296_at         ARL6IP         ADP-ribosylation factor-like 1           36572_r_at         ARL6IP         ADP-ribosylation factor-like 6 interacting protein           36572_r_at         ARL6IP         D31885         protein           41146_at         ADPRT         J03473         ribose) polymerase)           41747_at         ADM         D14874         adrenomedullin           AF034176         Homo sapiens cDNA clone           AF034176         Intcon5 contig.	$\Gamma$	33405 at	CAP2	N90755	adenylyl cyclase-associated protein 2	
36861_at         DKFZp56411922         AL049946         adlican           33987_at         ARF1         M36340         ADP-ribosylation factor 1           39336_at         ARF3         M74491         ADP-ribosylation factor 3           36585_at         ARF4         M36341         ADP-ribosylation factor 4           37537_at         ARFD1         L04510         64kD           37296_at         ARFGAP1         AA402332         protein 1           37296_at         ARL1         L28997         ADP-ribosylation factor-like 1           36572_r_at         ARL6IP         D31885         protein 1           41146_at         ADPRT         J03473         ribose) polymerase (NAD+; poly (ADP-ribosyltransferase (NAD-ribody) (ADP-ribody)	T-		ADFP	X97324	adipose differentiation-related protein	adipophilin
33987_at         ARF1         M36340         ADP-ribosylation factor 1           39536_at         ARF3         M74491         ADP-ribosylation factor 3           36585_at         ARF4         M36341         ADP-ribosylation factor 4           37537_at         ARFD1         L04510         64kD           37296_at         ARFGAP1         AA402332         Protein 10           37296_at         ARL1         AA402332         ADP-ribosylation factor GTPase activating protein 1           37296_at         ARL1         AA402332         ADP-ribosylation factor GTPase activating protein 1           36572_r_at         ARL6IP         AA402332         ADP-ribosylation factor-like 1           41146_at         ABDRT         J03473         ADP-ribosyltransferase (NAD+; poly (ADP-1058) famerase)           41146_at         ADDRT         J03473         ribose) polymerase)           34777_at         ADM         D14874         adrenomedullin           AF034176         Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone         AF034176	Г	36861_at	5641192	AL049946	adlican	hypothetical protein
39336_at         ARF3         M74491         ADP-ribosylation factor 3           36585_at         ARF4         M36341         ADP-ribosylation factor 4           37537_at         ARFD1         L04510         64kD           37537_at         ARFGAP1         AA402332         Protein 1           37296_at         ARFGAP1         AA402332         Protein 1           37296_at         ARL1         L28997         ADP-ribosylation factor GTPase activating protein 1           36572_r_at         ARL6IP         D31885         ADP-ribosylation factor-like 1           41146_at         ADPRT         ADP-ribosylation factor-like 6 interacting protein 1           41146_at         ADPRT         J03473         ribose) polymerase (NAD+; poly (ADP-1058) fangerase (NAD+1058) fangerase (NAD	Г	33987_at	ARF1	M36340	ADP-ribosylation factor 1	ADP-ribosylation factor 1
36585_at         ARF4         M36341         ADP-ribosylation factor 4           37537_at         ARFD1         L04510         64kD           39905_i_at         ARFGAP1         AA402332         protein 1           37296_at         ARFGAP1         AA402332         protein 1           37296_at         ARL1         L28997         ADP-ribosylation factor GTPase activating protein 1           36572_r_at         ARL6IP         D31885         ADP-ribosylation factor-like 1           41146_at         ADPRT         ADP-ribosylation factor-like 6 interacting protein           41146_at         ADPRT         ADP-ribosylation factor-like 6 interacting protein           41146_at         ADPRT         J03473         ribose) polymerase (NAD+; poly (ADP-105) (ADP-105)           1287_at         ADPRT         J03473         ribose) polymerase (NAD+; poly (ADP-105) (ADP-105)           34777_at         ADM         D14874         AF034176 Human mRNA (Tripodis and PAF034176 Human mRNA (Tripodis and PAF034176 Intcon5 contig.	74	39336_at	ARF3	M74491	ADP-ribosylation factor 3	ADP-ribosylation factor 3
37537_at         ARFD1         L04510         64kD           39905_i_at         ARFGAP1         AA402332         ADP-ribosylation factor GTPase activating protein 1           37296_at         ARL1         L28997         ADP-ribosylation factor-like 1           36572_r_at         ARL6IP         D31885         ADP-ribosylation factor-like 6 interacting protein           41146_at         ADPRT         J03473         ribose) polymerase (NAD+; poly (ADP-ribosyltransferase (NAD+ribosyltransferase (NAD+ribosyltransferase (NAD+ribosyltransferase (NAD+ribosyltransferase (NAD+ribosyltransferase (NAD	75	36585 at	ARF4	M36341	ADP-ribosylation factor 4	ADP-ribosylation factor 4
37537_at         ARFD1         L04510         64kD           39905_i_at         ARFGAP1         AA402332         protein 1           37296_at         ARL1         L28997         ADP-ribosylation factor-like 1           37296_at         ARL1         L28997         ADP-ribosylation factor-like 1           36572_r_at         ARL6IP         D31885         ADP-ribosylation factor-like 6 interacting protein           41146_at         ADPRT         ADP-ribosyltransferase (NAD+; poly (ADP-ribosyltransferase (NAD+ribosyltransferase (NAD+ribosyltransferase (NAD+ribosyltransferase (NAD+ribosy					ADP-ribosylation factor domain protein 1.	
39905_i_at         ARFGAP1         AA402332         protein 1           37296_at         ARL1         L28997         ADP-ribosylation factor-like 1           37296_at         ARL1         L28997         ADP-ribosylation factor-like 6 interacting           36572_r_at         ARL6IP         D31885         ADP-ribosyltransferase (NAD+; poly (ADP-ribosyltransferase (NAD+; poly (ADP-ribosyltransferase)           41146_at         ADPRT         J03473         ribose) polymerase)           1287_at         ADM         D14874         adrenomedullin           34777_at         ADM         D14874         AF034176 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone           32218 at         AF034176         ntcon5 contig.	9/	37537 at	ARFD1	L04510	64kD	nucleotide binding protein
39905_i_at         ARFGAP1         AA402332         protein 1           37296_at         ARL1         L28997         ADP-ribosylation factor-like 1           36572_r_at         ARL6IP         D31885         ADP-ribosylation factor-like 6 interacting protein           41146_at         ADPRT         J03473         ribose) polymerase (NAD+; poly (ADP-ribosyltransferase (NAD+; poly (ADP-ribosyltransferase (NAD+; poly (ADP-ribosyltransferase (NAD+; poly (ADP-ribosyltransferase)           1287_at         ADPRT         J03473         ribose) polymerase)           34777_at         ADM         D14874         adrenomedullin           AF034176         Homo sapiens cDNA clone ntcon5 contig.					ADP-ribosylation factor GTPase activating	<u></u>
37296_at         ARL1         L28997         ADP-ribosylation factor-like 1           36572_r_at         ARL6IP         D31885         protein           41146_at         ADPRT         J03473         ribose) polymerase)           1287_at         ADPRT         J03473         ribose) polymerase)           34777_at         ADM         D14874         adrenomedullin           32218 at         AF034176         ntcon5 contig.	11	39905_i_at	ARFGAP1	AA402332	protein 1	
36572_r_at         ARL6IP         D31885         protein           41146_at         ADPRT         J03473         ribose) polymerase)           1287_at         ADPRT         J03473         ribose) polymerase)           34777_at         ADM         D14874         adrenomedullin           32218 at         AF034176         ntcon5 contig.		37296_at	ARL1	L28997	ADP-ribosylation factor-like 1	ADP-ribosylation factor-like 1
36572_r_at         ARL6IP         D31885         protein           41146_at         ADPRT         J03473         ribose) polymerase)           1287_at         ADPRT         J03473         ribose) polymerase)           34777_at         ADM         D14874         adrenomedullin           AF034176         Homo sapiens c'DNA clone           32218 at         AF034176         ntcon5 contig.					ADP-ribosylation factor-like 6 interacting	
41146_at         ADPRT         J03473         ribose) polymerase)           1287_at         ADPRT         J03473         ribose) polymerase)           34777_at         ADP         ribose) polymerase         NAD+; poly (ADP-ribosyltransferase (NAD+; poly (ADP-ribosyltransferase)           34777_at         ADM         D14874         adrenomedullin           AF034176         Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone           AF034176         ntcon5 contig.	.79	_	ARLGIP	D31885	protein	
41146_at         ADPRT         J03473         ribose) polymerase)           1287_at         ADPRT         J03473         ribose) polymerase)           34777_at         ADM         D14874         adrenomedullin           AF034176         Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone ntcon5 contig.					ADP-ribosyltransferase (NAD+; poly (ADP	_
ADPRT         J03473         ribose) polymerase)           34777_at         ADM         D14874         adrenomedullin           AF034176         Homo sapiens cDNA clone           AF034176         Intcon5 contig.	8	41146_at	ADPRT	J03473	ribose) polymerase)	poly(ADP-ribosyl)transferase
1287_at         ADPRT         J03473         ribose) polymerase)           34777_at         ADM         D14874         adrenomedullin           AF034176 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone appears to the result of					ADP-ribosyltransferase (NAD+; poly (ADP	
34777_at ADM D14874 adrenomedullin AF034176 Human mRNA (Tripodis and Ragoussis) Homo sapiens c'DNA clone AF034176 ntcon5 contig.	81	1287_at	ADPRT	J03473	ribose) polymerase)	poly(ADP-ribosyl)transferase
32218 at AF034176	82		ADM	D14874	adrenomedullin	adrenomedullin precursor
32218 at AF034176					AF034176 Human mRNA (Tripodis and Rangussis) Homo saniens cONA clone	
	83	_		AF034176	Intcon5 contig.	

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AFG3L2         Y18314         AFG3ATPase family gene 3-like 2 (yeast) pagin           AGRN         AF016903         AHIVAK         M80899         AHIVAK nucleoprotein (desmoyokin)         AHIVAK           AARS         D32050         aldehyde dehydrogenase 1 family.         aldehyde dehydrogenase 2 family.         aldehyde dehydrogenase 2 family.           ALDH1A3         U07919         member A3         aldehyde dehydrogenase 2 family.         aldehyde dehydrogenase 2 family.           ALDH2         X05409         member A2         aldehyde dehydrogenase 3 family.         aldehyde dehydrogenase 4 family.           ALDH3A2         U46689         member A2         aldehyde dehydrogenase 4 family.         aldehyde dehydrogenase 7 family.           ALDH3A2         U24266         member A1         aldehyde dehydrogenase 9 family.         aldehyde dehydrogenase 9 family.           ALDH3A1         U34252         member A1         aldehyde dehydrogenase 9 family.         aldehyde dehydrogenase 9 family.           AKR1B1         X15414         (aldehyde dehydrogenase 9 family.         aldehyde dehydrogenase 9 family.           AKR1B1         X15414         (aldehyde dehydrogenase 9 family.         aldehyde dehydrogenase 9 family.           AKR1B1         X15414         (aldehyde dehydrogenase 9 family.         aldeh-keto reductase family 1, member A1           AKR		•	α	C	G	u
AKR1C3						
33454_at         AGRN         AF016903         agrin           37027_at         AHINAK         M80899         AHINAK nucleoprotein (desmoyokin)         6           36185_at         AARS         D32050         alany-IRINA synthetase         1 alachyde dehydrogenase 1 family.           36686_at         ALDH1A3         U07919         member A3         aldehyde dehydrogenase 2 family.           32747_at         ALDH2         X05409         (mitochondrial)         6           37331_g_at         ALDH3A2         U46689         member A3         aldehyde dehydrogenase 3 family.           37331_g_at         ALDH3A1         U24266         member A1         aldehyde dehydrogenase 4 family.           38780_at         ALDH3A1         U24266         member A1         aldehyde dehydrogenase 7 family.           38780_at         ALDH3A1         U34252         member A1         aldehyde dehydrogenase 9 family.           38780_at         AKR181         X15414         (aldehyde dehydrogenase 9 family.         aldehyde dehydrogenase 9 family.           38589_at         ALDH3A1         U34252         member A1         aldehyde dehydrogenase 9 family.           38780_at         AKR181         X15414         (aldehyde dehydrogenase 9 family.           38589_at         AKR181 <td< th=""><th>84</th><th>34315_at</th><th>AFG3L2</th><th>Y18314</th><th>AFG3 ATPase family gene 3-like 2 (yeast)</th><th>paraplegin-like protein</th></td<>	84	34315_at	AFG3L2	Y18314	AFG3 ATPase family gene 3-like 2 (yeast)	paraplegin-like protein
37027_et         AHNAK         M80899         AHNAK nucleoprotein (desmoyckin)           36186_at         AARS         D32050         alanyl-IRNA synthetase           36686_at         ALDH1A3         U07919         member A3           32747_at         ALDH2         X05409         (mitochondrial)           40409_at         ALDH3A2         U46689         member A2           37331_g_at         ALDH3A1         U24266         member A1           38132_at         ALDH3A1         U24266         member A1           38132_at         ALDH3A1         U34252         member A1           38132_at         ALDH9A1         U34256         member A1           381389_at         ALDH9A1         U34252         member A1           38189_at         AKR1A1         U34252         member A1           38589_at         AKR1A1         U34252         member A1           38589_at         AKR1B1         X15414         (aldebyde dehydrogenase 9 family, member B1           38589_at         AKR1B1         X15414         (aldebyde dehydrogenase 9 family 1, member B1           38589_at         AKR1B1         X15414         (aldebyde dehydrogenase 9 family 1, member B1           38589_at         AKR1C2         D17793		33454_at	AGRN	AF016903		agrin precursor
36185_at         AARS         D32050         alanyl-IRNA synthetase         4 AARS           36686_at         ALDH1A3         U07919         member 40         aldehyde dehydrogenase 2 family.         aldehyde dehydrogenase 2 family.         aldehyde dehydrogenase 2 family.           40409_at         ALDH2         X05409         (mitochondrial)         aldehyde dehydrogenase 2 family.         inember A2           37331_g_at         ALDH3A2         U46689         member A1         aldehyde dehydrogenase 4 family.         inember A2           33899_at         ALDH3A1         S74728         member A1         aldehyde dehydrogenase 9 family.         inember A1           33890_at         AKR1A1         J04794         (aldehyde dehydrogenase 9 family.         inember A1           38589_at         AKR1B1         X15414         (aldehyde dehydrogenase 9 family.         inember A1           3859_at         AKR1B1         X15414         (aldehyde dehydrogenase 9 family.         inember A1           3859_at         AKR1B1         X15414         (aldehyde dehydrogenase 9 family.         inember A1           3859_at         AKR1B1         X15414         (aldehyde dehydrogenase 9 family.         inember A1           3859_at         AKR1C3         D17793         type II)         inember A1	_	37027_at	AHNAK	M80899		
32747_at   ALDH1A3   U07919   member A3   aldehyde dehydrogenase 2 family, aldehyde dehydrogenase 2 family, aldehyde dehydrogenase 2 family, aldehyde dehydrogenase 3 family, aldehyde dehydrogenase 3 family, aldehyde dehydrogenase 4 family, aldehyde dehydrogenase 7 family, aldehyde dehydrogenase 7 family, aldehyde dehydrogenase 7 family, aldehyde dehydrogenase 7 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde reductase family 1, member A1 aldo-keto reductase family 1, member A2 aldo-keto reductase famil	87	36185_at	AARS	D32050		alanyt-tRNA synthetase
356.86_ at         ALDH1A3         U07919         member A3           32747_at         ALDH2         X05409         (mitochondrial)           32747_at         ALDH2         X05409         (mitochondrial)           40409_at         ALDH3A2         U46689         member A2           37331_g_at         ALDH3A1         U24266         member A1           36132_at         ALDH3A1         U24266         member A1           38132_at         ALDH3A1         U34252         member A1           38780_at         AKR1A1         J04794         (aldehyde dehydrogenase 9 family.           38780_at         AKR1B1         X15414         (aldehyde dehydrogenase 9 family.           38589_at         AKR1B1         X15414         (aldehyde dehydrogenase 9 family.           38780_at         AKR1B1         X15414         (aldehyde dehydrogenase 9 family.           38589_at         AKR1B1         X15414         (aldehyde dehydrogenase 9 family.           38589_at         AKR1B1         X15414         (aldehyde reductase family.           38589_at         AKR1B1         X15414         (aldehyde reductase family.           38589_at         AKR1B1         X15414         (aldehyde reductase family.           36589_at         AKR1						
22747_at         ALDH2         X05409         (mitochondrial)         4           40409_at         ALDH3A2         U46689         member A2         aldehyde dehydrogenase 3 family, and the program of	88	36686_at	ALDH1A3	U07919		aldehyde dehydrogenase 6
32747_at         ALDH2         X05409         (mitochondrial)           40409_at         ALDH3A2         U46689         member A2           aldehyde dehydrogenase 3 family, 40409_at         aldehyde dehydrogenase 4 family, aldehyde dehydrogenase 7 family, member A1           37331_a_at         ALDH4A1         U24266         aldehyde dehydrogenase 7 family, member A1           3889_at         ALDH9A1         S74728         member A1           38780_at         AKR1A1         J04794         aldehyde dehydrogenase 9 family, member R1           38780_at         AKR1A1         J04794         aldehyde dehydrogenase 9 family, member R1           38780_at         AKR1B1         X15414         (aldehyde reductase family 1, member R1           36589_at         AKR1B1         X15414         (aldo-keto reductase family 1, member R2           37399_at         AKR1C2         D17793         type II)           32510_at         AKR7A2         AF026947         (aflabyde reductase family 1, member C3           37040_at         AKR7A2         AF026947         (aflatoxin aldehyde reductase)           37040_at         AF1Q         D42041         aldo-keto reductase family 1, member C3           37040_at         AKR7A2         AF026947         (aflatoxin aldehyde reductase family 7, member C3 <td< th=""><th></th><th></th><th></th><th></th><th></th><th>aldehyde dehydrogenase 2 family</th></td<>						aldehyde dehydrogenase 2 family
ALDH3A2   U46689   member A2   aldehyde dehydrogenase 3 family, aldehyde dehydrogenase 4 family, aldehyde dehydrogenase 7 family, aldehyde dehydrogenase 7 family, aldehyde dehydrogenase 7 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, member A1 aldehyde reductase family 1, member A1 aldehyde reductase family 1, member B1 aldehyde reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, 19pe II) aldehyde reductase family 7, member A2 aldehyde aldehyde reductase family 7, member A2 aldehyde aldehyde reductase) aldehyde reductase family 7, member A2 aldehyde aldehyde reductase) aldehyde reductase family 7, member A2 aldehyde aldehyde reductase) aldehyde reductase family 7, member A2 aldehyde aldehyde reductase) aldehyde reductase family 7, member A2 aldehyde aldehyde reductase) aldehyde reductase family 7, member A2 aldehyde aldehyde reductase family 7, member A2 aldehyde aldehyde reductase) aldehyde red	83	32747_at	ALDH2	X05409		(mitochondrial)
40409_at         ALDH3A2         U46689         member A2           37331_g_at         ALDH4A1         U24266         member A1           36132_at         ALDH7A1         S74728         aldehyde dehydrogenase 7 family.           33899_at         ALDH9A1         U34252         member A1           38780_at         AKR1A1         J04794         (aldehyde dehydrogenase 9 family.           38780_at         AKR1B1         X15414         (aldehyde reductase)           38780_at         AKR1B1         X15414         (aldehyde reductase)           38780_at         AKR1B1         X15414         (aldehyde reductase)           38780_at         AKR1B1         X15414         (aldo-keto reductase)           38589_at         AKR1B1         X15414         (aldo-keto reductase)           38589_at         AKR1B1         X15414         (aldo-keto reductase)           37399_at         AKR1B1         X15414         (aldo-keto reductase)           37399_at         AKR1C3         D17793         type II)           38510_at         AKR1A2         AF026947         (aldo-keto reductase family 1, member A2           36541_at         AF1Q         U16954         ALL1-fused gene from chromosome 1q           35223_at         KIAA1017					hydrogenase 3 family,	
ALDHAA1   U24266   member A1   aldehyde dehydrogenase 4 family, aldehyde dehydrogenase 7 family, aldehyde dehydrogenase 7 family, aldehyde dehydrogenase 7 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde dehydrogenase 9 family, aldehyde reductase family 1, member A1 aldehyde reductase family 1, member B1 aldo-keto reductase family 1, member B1 aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, aldo-keto reductase family 7, member A2 aldo-keto reductase family 7, member A2 aldo-keto reductase family 7, member A2 aldo-keto reductase family 7, member A2 aldo-keto reductase family 7, member A2 aldo-keto reductase family 7, member A2 aldo-keto aldo-keto	6	40409_at	ALDH3A2	U46689		aldehyde dehydrogenase
37331_g_at         ALDH4A1         U24266         member A1           36132_at         ALDH7A1         S74728         member A1           33899_at         ALDH9A1         U34252         member A1           338780_at         AKR1A1         J04794         (aldehyde dehydrogenase 9 family.           36589_at         AKR1B1         X15414         (aldehyde reductase family 1, member R1 aldo-keto reductase family 1, member R2 aldo-keto reductase family 1, member C3 aldo-keto reductase family 7, member C3 aldo-keto reductase family 7, member C3 aldo-keto reductase family 7, member A2 aldo-keto reductase family 1, member A2					aldehyde dehydrogenase 4 family,	
36132_at         ALDH7A1         S74728         member A1           33899_at         ALDH9A1         U34252         member A1           38780_at         ALDH9A1         U34252         member A1           38780_at         AKR1A1         J04794         (aldehyde dehydrogenase 9 family.           36589_at         AKR1B1         X15414         (aldehyde reductase family 1, member R1 aldo-keto reductase)           37399_at         AKR1B1         X15414         (aldo-keto reductase)           37399_at         AKR1C3         D17793         (aldo-keto reductase)           372510_at         AKR1C3         D17793         (aldo-keto reductase)           38225_at         AKR7A2         AF026947         (aldo-keto reductase)           36041_at         AKR7A2         AF026947         (altatoxin aldehyde reductase)           36041_at         AKR7A2         AF026947         (altatoxin aldehyde reductase)           36041_at         AF1Q         U16954         ALL1-fused gene from chromosome 1q           37040_at         GGZAN         D42041         alpha glucosidase II alpha subunit           35223_at         KIAA1017         AB023234         alpha integrin binding protein 63           36147_a_at         ATRX         U72936         cerevisiae)	91	37331_g_at	ALDH4A1	U24266	member A1	pyrroline-5-carboxylate dehydrogenase
36132_at         ALDH7A1         S74728         member A1           33899_at         ALDH9A1         U34252         member A1           38780_at         AKR1A1         J04794         (aldehyde dehydrogenase 9 family.           38780_at         AKR1A1         J04794         (aldehyde reductase family 1, member A1 aldo-keto reductase)           36589_at         AKR1B1         X15414         (aldose reductase)           37399_at         AKR1C3         D17793         type II)           38225_at         AKR1C3         D17793         type II)           39225_at         AKR7A2         AF026947         (aflatoxin aldehyde reductase)           35223_at         AKR7A2         AF026947         (aflatoxin aldehyde reductase)           35223_at         AF1Q         U16954         ALL1-fused gene from chromosome 1q           35223_at         KIAA1017         AB023234         alpha glucosidase II alpha subunit           35223_at         KIAA1017         AB023234         alpha integrin binding protein 63           39147_q_at         ATRX         U72936         cerevisiae)	L				aldehyde dehydrogenase 7 family,	
33899_at         ALDH9A1         U34252         member A1           38780_at         AKR1A1         J04794         (aldehyde reductase family 1, member A1           36589_at         AKR1B1         X15414         (aldehyde reductase family 1, member B1 aldo-keto reductase family 1, member C3           37399_at         AKR1C3         D17793         type II)           39225_at         AKR7A2         AF026947         (alfatoxin aldehyde reductase)           37040_at         AKR7A2         AF026947         (alfatoxin aldehyde reductase)           35223_at         AKRA1017         AB023234         alpha glucosidase II alpha subunit           3523_at         KIAA1017         AB023234         alpha integrin binding protein 63           39147_q_at         ATRX         U72936         cerevisiae)	92	36132_at	ALDH7A1	S74728	member A1	antiquitin
33899_at         ALDH9A1         U34252         member A1           38780_at         AKR1A1         J04794         (aldehyde reductase) aldo-keto reductase)           36589_at         AKR1B1         X15414         (alde-keto reductase) aldo-keto reductase)           37399_at         AKR1C3         D17793         type II) aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) aldo-keto reductase family 7, member A2 aldo-keto reductase family 1, member A2 aldo-keto reductase family					aldehyde dehydrogenase 9 family,	
38780_at         AKR1A1         J04794         (aldehyde reductase)           36589_at         AKR1B1         X15414         (aldehyde reductase)           37399_at         AKR1B1         X15414         (aldose reductase)           37399_at         AKR1C3         D17793         type II)           32510_at         AKR7A2         AF026947         (aflatoxin aldehyde reductase)           39225_at         AKR7A2         AF026947         (aflatoxin aldehyde reductase)           36941_at         AF1Q         U16954         ALL1-fused gene from chromosome 1q           35223_at         AF1Q         U16954         ALL1-fused gene from chromosome 1q           35223_at         KIAA1017         AB023234         alpha integrin binding protein 63           39147_gat         ATRX         U72936         cerevisiae)	83	33899_at	ALDH9A1	U34252	member A1	gamma-aminobutyraldehyde dehydrogenase
38780_at         AKR1A1         J04794         (aldehyde reductase)           36589_at         AKR1B1         X15414         (aldose reductase family 1, member B1 aldo-keto reductase family 1, member C3 aldo-keto reductase family 1, member C3 aldo-keto reductase family 7, member A2 aldo-keto reductase family 1, member A2 aldo-keto reductase					aldo-keto reductase family 1, member A1	aldo-keto reductase family 1, member A1
36589_at         AKR1B1         X15414         (aldose reductase)           37399_at         AKR1C3         D17793         type II)           32510_at         AKR7A2         AF026947         (aflatoxin aldehyde reductase)           39225_at         AGPS         Y09443         alkylglycerone phosphate synthase           36941_at         AF1Q         U16954         ALL1-fused gene from chromosome 1q           37040_at         G2AN         D42041         alpha glucosidase II alpha subunit           35223_at         KIAA1017         AB023234         alpha integrin binding protein 63           39147_gat         ATRX         U72936         cerevisiae)	94	38780_at	AKR1A1	J04794	(aldehyde reductase)	(aldehyde reductase)
36589_at         AKR1B1         X15414         (aldose reductase)           37399_at         AKR1C3         D17793         type II)           32510_at         AKR7A2         AF026947         (aflatoxin aldehyde reductase)           39225_at         AKR7A2         AF026947         (aflatoxin aldehyde reductase)           36941_at         AF1Q         U16954         ALL1-fused gene from chromosome 1q           37040_at         G2AN         D42041         alpha glucosidase II alpha subunit           35223_at         KIAA1017         AB023234         alpha integrin binding protein 63           35223_at         ATRX         U72936         cerevisiae)	L				aldo-keto reductase family 1, member B1	aldo-keto reductase family 1, member B1
37399_at   AKR1C3   D17793   type   I)   aldo-keto reductase family 1, member C3   (3-alpha hydroxysteroid dehydrogenase, type   I)   aldo-keto reductase family 7, member A2   39225_at   AKR7A2   AF026947   (aflatoxin aldehydre reductase)   aldo-keto reductase family 7, member A2   36941_at   AF1Q   U16954   ALL1-fused gene from chromosome 1q   alpha glucosidase II alpha subunit   alpha integrin binding protein 63   alpha thalassemia/mental retardation   syndrome X-linked (RAD54 homolog, S. cerevisiae)   cerevisiae)	95	36589_at	AKR1B1	X15414	(aldose reductase)	(aldose reductase)
(3-alpha hydroxysteroid dehydrogenase, type II)   AKR7A2   AF026947   (aflatoxin aldehydr reductase family 7, member A2 aldo-keto reductase family 7, member A2 aldo-keto reductase family 7, member A2 algo-keto reductase family 8, member A2 algo-keto reductase family 8, member A2 algo-keto reductase family 8, member A2 algo					aldo-keto reductase family 1, member C3	
37399_at         AKR1C3         D17793         type II)           32510_at         AKR7A2         AF026947         (aflatoxin aldehyde reductase)           39225_at         AGPS         Y09443         alkylglycerone phosphate synthase           36941_at         AF1Q         U16954         ALL1-fused gene from chromosome 1q           37040_at         G2AN         D42041         alpha glucosidase II alpha subunit           35223_at         KIAA1017         AB023234         alpha integrin binding protein 63           39147_gat         ATRX         U72936         cerevisiae)					(3-alpha hydroxysteroid dehydrogenase,	aldo-keto reductase family 1, member C3 (3-
32510_at         AKR7A2         AF026947         (aflatoxin aldehyde reductase)           39225_at         AGPS         Y09443         alkylglycerone phosphate synthase           36941_at         AF1Q         U16954         ALL1-fused gene from chromosome 1q           37040_at         G2AN         D42041         alpha glucosidase II alpha subunit           35223_at         KIAA1017         AB023234         alpha integrin binding protein 63           39147_g_at         ATRX         U72936         cerevisiae)	96	37399 at	AKR1C3	D17793	(I) edit	alpha hydroxysteroid dehydrogenase, type II)
32510_at         AKR7A2         AF026947         (aflatoxin aldehyde reductase)           39225_at         AGPS         Y09443         alkylglycerone phosphate synthase           36941_at         AF1Q         U16954         ALL1-fused gene from chromosome 1q           37040_at         G2AN         D42041         alpha glucosidase II alpha subunit           35223_at         KIAA1017         AB023234         alpha integrin binding protein 63           39147_g_at         ATRX         U72936         cerevisiae)					aldo-keto reductase family 7, member A2	
39225_at         AGPS         Y09443         alkylglycerone phosphate synthase           36941_at         AF1Q         U16954         ALL1-fused gene from chromosome 1q           37040_at         G2AN         D42041         alpha glucosidase II alpha subunit           35223_at         KIAA1017         AB023234         alpha integrin binding protein 63           alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S.         syndrome X-linked (RAD54 homolog, S.           39147_g_at         ATRX         U72936         cerevisiae)	97		AKR7A2	AF026947	(aflatoxin aldehyde reductase)	aflatoxin aldehyde reductase AFAR
39225_at         AGPS         Y09443         alkylglycerone phosphate synthase           36941_at         AF1Q         U16954         ALL1-fused gene from chromosome 1q           37040_at         G2AN         D42041         alpha glucosidase II alpha subunit           35223_at         KIAA1017         AB023234         alpha integrin binding protein 63           alpha thalassemia/mental retardation         syndrome X-linked (RAD54 homolog, S.           39147_g_at         ATRX         U72936						alkyl-dihydroxyacetonephosphate synthase
36941_at         AFIQ         U16954         ALL1-fused gene from chromosome 1q           37040_at         G2AN         D42041         alpha glucosidase II alpha subunit           35223_at         KIAA1017         AB023234         alpha integrin binding protein 63           alpha thalassemia/mental retardation         syndrome X-linked (RAD54 homolog, S.           39147_g_at         ATRX         U72936	86		AGPS	Y09443	alkylglycerone phosphate synthase	precursor
35223_at KIAA1017 AB023234 alpha integrin binding protein 63 abha integrin binding protein 63 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. O72936 cerevisiae)	66	_	AF1Q	U16954	ALL1-fused gene from chromosome 1q	AF1Q protein
35223_at KIAA1017 AB023234 alpha integrin binding protein 63 alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S.  39147_g_at ATRX U72936 cerevisiae)	18	37040_at	GZAN	D42041	alpha glucosidase II alpha subunit	alpha glucosidase II alpha subunit
alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. U72936 cerevisiae)	5	35223_at	KIAA1017	AB023234	alpha integrin binding protein 63	KIAA1017 protein
Syndrome X-linked (RAD54 homolog, S. U72936 cerevisiae)					alpha thalassemia/mental retardation	-
ATRX U72936 (cerevisiae)					syndrome X-linked (RAD54 homolog, S.	putative DNA dependent ATPase and
	102	39147_g_at	ATRX	U72936	cerevisiae)	helicase

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				X-linked (RAD54 homolog, S.	putative DNA dependent ATPase and
5	818_s_at	ATRX	U72936		helicase
				alternative translation initiation; H.sapiens	
				HLTF gene for helicase-like transcription	
104	34327 at	HLTF	246606	factor.	helicase-like transcription factor
				aminoadipate-semialdehyde	
_				dehydrogenase-phosphopantetheinyl	
105	35761 at	AASDHPPT	AL050073	transferase	hypothetical protein
108	39431 at	NPEPPS	AJ132583	aminopeptidase puromycin sensitive	puromycin sensitive aminopeptidase
107	u	AES	Al951946	amino-terminal enhancer of split	
_		6-80	U41635	amplified in osteosarcoma	OS-9 precurosor
				amylo-1, 6-glucosidase, 4-alpha-	
				glucanotransferase (glycogen	
				debranching enzyme, glycogen storage	-
109	38253 at	AGL	U84011	disease type III)	glycogen debranching enzyme isoform 6
				amyloid beta (A4) precursor protein	amyloid beta (A4) precursor protein
110	41136 s at	АРР	Y00264	(protease nexin-II, Alzheimer disease)	(protease nexin-II, Alzheimer disease)
				amyloid beta (A4) precursor protein-	
Ξ	40148 at	APBB2	U62325	binding, family B, member 2 (Fe65-like)	FE65-like protein
				amyloid beta precursor protein	
112	38471 r at	APPBP2	D86981	(cytoplasmic tail) binding protein 2	KIAA0228 protein
				amyloid beta precursor protein	
113	38470_i_at	APPBP2	D86981	(cytoplasmic tail) binding protein 2	KIAA0228 protein
				amyloid beta precursor protein binding	:
114	35364_at	APPBP1	U50939	protein 1, 59kD ,	amyloid precursor protein-binding protein 1
L				emvotronhic lateral sclerosis 2 (juvenile)	
115	40064 at	ALS2CR3	AB011121	chromosome region, candidate 3	KIAA0549 protein
				androgen receptor (dihydrotestosterone	
				receptor; testicular feminization; spinal	
				and bulbar muscular atrophy; Kennedy	
116	1577_at	AR	M23263	disease)	androgen receptor
117		AMOTL2	AB023206	angiomotin like 2	angiomotin like 2
118		ANGPT1	D13628	angiopoietin 1	angiopoietin 1
119		ANGPT1	U83508	angiopoietin 1	angiopoietin-1

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_	A	В	3		
120 3	36965_at	ANK3	U13616	ankyrin 3, node of Ranvier (ankyrin G)	ankyrın G
121	_	ANXA1	X05908	annexin A1	annexin l
122 3		ANXA11	L19605	1	56K autoantigen
123 7		ANXA2	D00017		lipocortin II
124 3	31684 at	ANXA2P1	M62896	annexin A2 pseudogene 1	
125 3	at	ANXA2P3	M62895	annexin A2 pseudogene 3	
1					annexin IV (placental anticoagulant protein
126 3	37374_at	ANXA4	M82809	annexin A4	(1)
127 3	37670 at	ANXA7	J04543	annexin A7	annexin VII isoform 1; annexin VII isoform 2
	41138 at	MICS	M16279	antigen identified by monoclonal antibodies 12E7 E21 and O13	antigen
	5	11110	2 (22)	nylate	
129	40506_s_at	PABPC4; APP1; A	1; AU75686	APF-1, norms sapers polyage injured binding protein mRNA, complete cds.	polyadenylate binding protein
130	34370_at	ARCN1	X81198	archain 1	archain
_				arginine-glutamic acid dipeptide (RE)	
131	32253_at	RERE	AB007927	repeats	KIAA0458 protein
132	549_at	RARS	S80343	arginyl-tRNA synthetase	arginyl-tRNA synthetase
133	39164_at	ARIH2	AF099149	ariadne homolog 2 (Drosophila)	TRIAD1 type I
				ariadne homolog, ubiquitin-conjugating	
134	134 41729 at	ARIH1	AJ009771	ila)	
135	36057_at	ALEX2	AB011084	armadillo repeat protein ALEX2	KIAA0512 protein
				ARP1 actin-related protein 1 homolog A,	
136	40052_at	ACTR1A	X82206	centractin alpha (yeast)	alpha-centractin
		0 HO 4	, L	ARP2 actin-related protein 2 homolog	
2	35/34_at	ACINZ	Aleccool	ARP2 actin-related protein 2 homolog	
138	35733 at	ACTR2	AF006082	(yeast)	Arp2
				ARP3 actin-related protein 3 homolog	
139	35271_at	ACTR3	AF006083	(yeast)	Arp3
140	140 40516_at	AHR	L19872	aryl hydrocarbon receptor	AH-receptor
141	141 36671_at	ASNS	M27396	asparagine synthetase	asparagine synthetase
142	142 41241_at	NARS	D84273	asparaginyl-tRNA synthetase	Asparaginyl tRNA Synthetase
143	143 38703_at	DNPEP	AF005050	aspartyl aminopeptidase	aspartyl aminopeptidase
144	144 34181_at	AGA	X55330	aspartylglucosaminidase	aspartylglucosaminidase

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	A	В	3		
145	37229 at	ATR	U49844	ataxia telangiectasia and Rad3 related	FHAP-related protein
		A2LP	U70671	ataxin 2 related protein	ataxin-2 related protein
				ATP binding protein associated with cell	
147	379 at	APACD	AB006679	differentiation	ATP binding protein
	148 40881 at	ACLY	X64330	ATP citrate lyase	ATP-citrate (pro-S-)-lyase
	1			ATP synthase, H+ transporting,	
				mitochondrial F0 complex, subunit b,	
149	149 41228 r at	ATP5F1	X60221	isoform 1	H+-ATP synthase subunit b
				ATP synthase, H+ transporting,	
				mitochondrial F0 complex, subunit c	mitochondrial ATP synthase subunit 9
150	34811 at	ATP5G3	U09813	(subunit 9) isoform 3	precursor
				ATP synthase, H+ transporting,	
151	35760 at	ATP5H	AF087135	mitochondrial F0 complex, subunit d	F1FO-type ATPase subunit d
				ATP synthase, H+ transporting,	
152	38751 i at	ATPSI	AA426364	mitochondrial F0 complex, subunit e	
				ATP synthase, H+ transporting,	
153	36107_at	ATP5J	AA845575	mitochondrial F0 complex, subunit F6	
				ATP synthase, H+ transporting,	
154	38693 at	ATP5L	AA917672	mitochondrial F0 complex, subunit g	
				ATP synthase, H+ transporting,	
				mitochondrial F1 complex, gamma	
155	155 40115 at	ATP5C1	D16562	polypeptide 1	ATP synthase gamma-subunit
				ATPase, Ca++ transporting, cardiac	ATPase, Ca++ transporting, cardiac muscle,
156	39791 at	ATP2A2	M23114	muscle, slow twitch 2	slow twitch 2
				ATPase, Ca++ transporting, cardiac	ATPase, Ca++ transporting, cardiac muscle,
157	39790 at	ATP2A2	M23115	muscle, slow twitch 2	slow twitch 2
	_			ATPase, Ca++ transporting, type 2C,	
158	38684 at	ATP2C1	AJ010953	member 1	putative Ca2+-transporting ATPase
159		ATP9A	AB014511	ATPase, Class II, type 9A	KIAA0611 protein
160	40853	ATP10D	Al478147	ATPase, Class V, type 10D	
161	36635 at	ATP11B	AB023173	ATPase, Class VI, type 11B	KIAA0956 protein
	1			ATPase, Cu++ transporting, alpha	1
162	36523 at	ATP7A	L06133	polypeptide (Menkes syndrome)	Cu++-transporting P-type A I Pase
<u> </u>				ATPase, H+ transporting, lysosomal	
163	163 33854_at	ATP6M	AA877795	(vacuolar proton pump)	

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				somal	•
164	37395_at	ATP6S14	D49400		vacuolar ATPase
				ATPase, H+ transporting, lysosomal	
165	36994_at	ATP6L	M62762	(vacuolar proton pump) 16kD	vacuolar H+ ATPase proton channel subunit
				ATPase, H+ transporting, lysosomal	
166	36167_at	ATP6F	D89052	(vacuolar proton pump) 21kD	proton-ATPase-like protein
				ATPase, H+ transporting, lysosomal	
167	37367 at	ATP6E	X76228	(vacuolar proton pump) 31kD	vacuolar H+ ATPase E subunit
				ATPase, H+ transporting, lysosomal	
168	37948_at	ATP6C	J05682	(vacuolar proton pump) 42kD	H+ -ATPase C subunit
				ATPase, H+ transporting, lysosomal	
169	33875_at	ATP6H	AI547262	(vacuolar proton pump) 9kD	
				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump) membrane sector	
170	40903_at	ATP6M8-9	AL049929	associated protein M8-9	hypothetical protein
				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump), alpha	
171	34889_at	ATP6A1	AA056747	polypeptide, 70kD, isoform 1	
				ATPase, H+ transporting, lysosomal	
				(vacuolar proton pump), beta polypeptide,	
172	40568_at	ATP6B2	L35249	56/58kD, isoform 2	vacuolar H+-ATPase 56,000 subunit
				ATPase, H+ transporting, lysosomal	
173	35770_at	ATP6S1	D16469	(vacuolar proton pump), subunit 1	ORF
				ATPase, Na+/K+ transporting, beta 1	•
174	37669_s_at	ATP1B1	U16799	polypeptide	Na,K-ATPase beta subunit
				ATPase, Na+/K+ transporting, beta 3	sodium/potassium-transporting ATPase beta-
175	32563_at	ATP1B3	U51478	polypeptide	3 subunit
				ATP-binding cassette, sub-family A	
176	35717_at	ABCA8	AB020629	(ABC1), member 8	KIAA0822 protein
				ATP-binding cassette, sub-family C	
177	38261_at	ABCC3	AF085692	(CFTR/MRP), member 3	multidrug resistance-associated protein 3B
178	35648_at	KIAA0442	AB007902	autism-related protein 1	autism-related protein 1
179	38068_at	AMFR	M63175	autocrine motility factor receptor	autocrine motility factor receptor
180	38433_at	AXL	M76125	AXL receptor tyrosine kinase	tyrosine kinase receptor
٤		TOXA	AI 050171	incorporation	hypothetical protein DKFZp586F1122 similar to avotrophin
	35268_al	AXOI	ALUSUI / I	laxonopiiii	to avoil optimit

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182	35350_at	GALNAC4S-6ST	AB011170		KIAA0598 protein
Γ				oma Mo-MLV insertion region	murine leukemia viral (bmi-1) oncogene
183	41562_at	BMI1	L13689	1	потпогод
				B lymphoma Mo-MLV insertion region	murine leukemia viral (bmi-1) oncogene
184	1728 at	BMI1	L13689		homolog
185	36578 at	BIRC2	U37547	iral IAP repeat-containing 2	MIHB
	41278 at	BAF53A	AF041474	BAF53	BAF53a
187	33175 at	BBS4	AA156237	Bardet-Biedl syndrome 4	
_				basic helix-loop-helix domain containing,	
188	40790 at	ВНСНВ2	AB004066	class B, 2	1-Dec
189	40108 at	BZAP45	D13630	basic leucine-zipper protein BZAP45	basic leucine-zipper protein BZAP45
				basic transcription element binding protein	
190	40202_at	BTEB1	D31716		GC box binding protein
191	35055 at	BTF3	X53281	basic transcription factor 3	general transcription factor
192	38364_at	BCE-1	AF068197	BCE-1 protein	BCE-1
				B-cell CLL/lymphoma 6 (zinc finger protein	
193	40091_at	BCL6	U00115	51)	zinc-finger protein .
				B-cell translocation gene 1, anti-	
194	37294 at	BTG1	X61123	proliferative	B-cell translocation protein 1
	1			BCL2/adenovirus E1B 19kD interacting	BCL2/adenovirus E1B 19kD-interacting
195	32060 at	BNIP2	U15173	protein 2	protein 2
				BCL2/adenovirus E1B 19kD interacting	
196	38010 at	BNIP3	AF002697	protein 3	E1B 19K/Bcl-2-binding protein Nip3
				BCL2/adenovirus E1B 19kD interacting	BCL2/adenovirus E1B 19kDa-interacting
197	39436 at	BNIP3L	AF079221	protein 3-like	protein 3a
				-	glucocortoid receptor-associated protein
198	34798_at	BAG1	Z35491	BCL2-associated athanogene	RAP46
199	35291 at	BAG2	AL050287	BCL2-associated athanogene 2	hypothetical protein
200	200 36463 at	BAG5	AB020680	BCL2-associated athanogene 5	KIAA0873 protein
S	38050 at	BTF	D79986	Bcl-2-associated transcription factor	KIAA0164 gene product
202	38101 at	BDG-29	AB011151	BDG-29 proten	KIAA0579 protein
				beclin 1 (coiled-coil, myosin-like BCL2	
203	39378_at	BECN1	U17999	interacting protein)	
				beta subunit; Human pyruvate	
204	204 39160 at	PDHB	D9008G	gene, exons 1-10.	pyruvate dehydrogenase (lipoamide) beta
	15.2.2.2.1				

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205 3	34644_at	BZM	AB021288	7	beta 2-microglobulin
	40601 at	88P	Al057115	beta-amyloid binding protein precursor	
				beta-hexosaminidase alpha chain; Human	-
		_		beta-hexosaminidase alpha chain (HEXA)	•
207	39340 at	HEXA	M16424	gene, exon 14.	hexosaminidase A preproprotein
802	38126 at	BGN	J04599		biglycan preproprotein
		BART1	AA206524	binder of Arl Two	
				biotin-amide amidohydrolase; Homo	
	10000	7	A E018631	sapiens biotindase (BTD) gene, exons 2,	biotinidase
\$	3/2/4 at	סומ	200	rine hydrolase:	
211	40912 s at	BPHL	X81372	antigen)	biphenyf hydrolase-related protein
+	35267 q at	BLCAP	AL049288	bladder cancer associated protein	bladder cancer associated protein
213	35266_at	BLCAP	AL049288	ciated protein	bladder cancer associated protein
	37700 at	BLMH	X92106	_	bleomycin hydrolase
				bone morphogenetic protein receptor, type	
215	39565 at	BMPR1A	Z22535		ALK-3
216	39551 at	BHC80	N98667	BRAF35/HDAC2 complex (80 kDa)	
				brain abundant, membrane attached	
217	32607 at	BASP1	AF039656	signal protein 1	neuronal tissue-enriched acidic protein
_	1.			brain abundant, membrane attached	
218	32606 at	BASP1	AA135683	signal protein 1	
219	37945 at	ВАСН	U91316	hydrolase	acyl-CoA thioester hydrolase
220	37958 at	BCMP1	AL049257	brain cell membrane protein 1	brain cell membrane protein 1
221	40023 at	BDNF	X60201	brain-derived neurotrophic factor	brain-derived neurotrophic factor
_	1			branched chain keto acid dehydrogenase	
				E1, beta polypeptide (maple syrup urine	branched chain alpha-ketoacid
222	41683 i at	ВСКОНВ	U50708	disease)	dehydrogenase E1 beta subunit
					breast cancer antiestrogen resistance 3
223	36812 at	BCAR3	U92715	breast cancer anti-estrogen resistance 3	protein
				brefeldin A-inhibited guanine nucleotide-	
224	224 38306_at	BIG1	AA477576	exchange protein 1	
225	225 37947_at	BRD3	D26362	bromodomain containing 3	bromodomain containing protein 3
				BTB and CNC homology 1, basic leucine	BTB and CNC homology 1, basic leucine
226	226 31895_at	BACH1	AB002803	zipper transcription factor 1	zipper transcription factor 1

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	36634_at	BTG2	U72649		BIGZ
1	37218 at	BTG3	D64110		ANA
1_					
229 4	41547_at	BUB3	AF047472	east)	spleen mitotic checkpoint BUB3
<b>↓</b> `	24702 0 04	103	AE047473		testis mitotic checkpoint BUB3
_	n¦ ~	200 a	A A D E 8 7 E 2	//240KD)	
3	02/01_1_a1	200	Angoni of	8	
232	32780_at	BPAG1	AB018271	bullous pemphigoid antigen 1 (230/240kD) KIAA0728 protein	KIAA0728 protein
+	233 32629 1 at	BTN3A1	U90552	butyrophilin, subfamily 3, member A1	butyrophilin
۲	234 39357 at	C2F	U72514	C2f protein	CZ
235	40709 at	LOC58502	W27601	C2H2 (Kruppel-type) zinc finger protein	
236	37031_at	C9orf10	D80005	C9orf10 protein	C9orf10 protein
237	33856 at	CXX1	Y13374	CAAX box 1	putative prenylated protein
_	36976 at	CDH11	D21255	cadherin 11, type 2, OB-cadherin (osteoblast)	OB-cadherin-2
	-			cadherin 11, type 2, OB-cadherin	
239	2087_s_at	CDH11	D21254	(osteoblast)	OB-cadherin-1
240	2053 at	CDH2	M34064	cadherin 2, type 1, N-cadherin (neuronal)	cadherin 2, type 1 preproprotein
.T				calcium/calmodulin-dependent protein	
241	31670 s at	CAMK2G	U81554	kinase (CaM kinase) II gamma	CaM kinase II isoform
Π	,			calcium/calmodulin-dependent protein	
242	38716 at	CAMKK2	AB018330	kinase kinase 2, beta	KIAA0787 protein
273	21854 at	CASK	AF035582	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	CASK
244	41738 at	CAL D1	M64110	caldesmon 1	caldesmon
245	41739 s at	CALD1	M83216	caldesmon 1	caldesmon
1				calmodulin 1 (phosphorylase kinase,	
246	41288_at	CALM1	AL036744	delta)	
1				calmodulin 2 (phosphorylase kinase,	colmodulin 2 (ahoenhondaea kinasa dalta)
247	911_s_at	CALM2	LLEGIM	gena)	calification & (principlication) lase militare, define)
248	40125	CANX	L10284	calnexin	Califexili
249	37001_at	CAPN2	M23254	calpain 2, (π/II) large subunit	neutral protease large subunit
0	36138	CAPNS1	X04106	calpain, small subunit 1	calpain, small subunit 1

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		2	3	0	
251		CAST	D16217	calpastatin	calpastatin
252	33385 g at	CAST	U31346	calpastatin	calpastatin
253		CNN3	S80562	calponin 3, acidic	acidic calponin
254	37345 at	CALU	AF013759	calumenin	calumein
				cAMP responsive element binding protein	cAMP responsive element binding protein 1, isoform A; cAMP responsive element binding
255	37535_at	CREB1	M27691		protein 1, isoform B
		C C C	0001	cAMP responsive element binding protein	transcription (actor   ZIP
007	40849_s_at	CUEBS	02000	cAMP responsive element binding protein-	
257	39438 at	CREBL2	AF039081	like 2	Cre binding protein-like 2
					cyclic AMP-responsive element modulator
258	32065_at	CREM	S68134	cAMP responsive element modulator	beta isoform
259	32067_at	CREM	S68271	cAMP responsive element modulator	cyclic AMP-responsive element modulator
					cyclic AMP-responsive element modulator
260	32066_g_at	CREM	S68134	cAMP responsive element modulator	beta isoform
				capping protein (actin filament) muscle Z-	
261	40910_at	CAPZA1	U56637	line, alpha 1	capping protein alpha subunit isoform 1
L				capping protein (actin filament) muscle Z-	
262	36641_at	CAPZA2	U03851	line, alpha 2	capping protein alpha
				capping protein (actin filament) muscle Z-	
263	37012 at	CAPZB	U03271	line, beta	F-actin capping protein beta subunit
				carbohydrate (chondroitin 6)	
264	32094 at	CHST3	AB017915	sulfotransferase 3	chondroitin 6-sulfotransferase
265	41447 at	CHSY1	AB023207	carbohydrate (chondroitin) synthase 1	KIAA0990 protein
				carbohydrate (keratan sulfate Gal-6)	
266	41395_at	CHST1	AB003791	sulfotransferase 1	keratan sullate Gal-6-sulfotransferase
				carbohydrate (N-acetylglucosamine-6-0)	N-acetylglucosamine-6-O-sulfotransferase
267	37960_at	CHST2	AB014679	sulfotransferase 2	(GlcNAc6ST)
268		CA12	AF037335	carbonic anhydrase XII	carbonic anhydrase precursor
569	34876_at	CPD	U65090	carboxypeptidase D	carboxypeptidase D
270	36606_at	CPE	X51405	carboxypeptidase E	carboxypeptidase E precursor
				Cas-Br-M (murine) ectropic retroviral	
271	35632_at	CBLB	U26710	transforming sequence b	q-lqɔ
272	40184_at	CSNK1A1	L37042	casein kinase 1, alpha 1	casein kinase I-alpha
273	273 36949_at	CSNK1D	U29171	casein kinase 1, delta	casein kinase I delta

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	A	£	٥		
274	38019_at	CSNK1E	L37043		casein Kinase I-epsilon
				containing	
275	1211_s_at	CRADD	U84388	adaptor with death domain	death domain containing protein CRADD
376	1867 at	CEI AB	AE005775	CASP8 and FADD-like apoptosis regulator	CASP8 and FADD-like apoptosis regulator caspase-like apoptosis regulatory protein 2
3	15-			caspase 4 apontosis-related cysteine	
277	195 s at	CASP4	U28014	professe	cysteine protease
				caspase 8, apoptosis-related cysteine	
278	33774 at	CASP8	X98172	protease	MACH-alpha-1
				catenin (cadherin-associated protein),	•
279	41156_g_at	CTNNA1	U03100	alpha 1 (102kD)	alpha2(E)-catenin
				catenin (cadherin-associated protein),	
280	41155_at	CTNNA1	U03100	alpha 1 (102kD)	alpha2(E)-catenin
				catenin (cadherin-associated protein),	
281	2085_s_at	CTNNA1	D14705	alpha 1 (102kD)	'human alpha-catenin'
				catenin (cadherin-associated protein),	
282	2069_s_at	CTNNA1	L23805	alpha 1 (102kD)	alpha1(E)-catenin
				catenin (cadherin-associated protein),	,
283	35331_at	CTNNAL1	U97067	alpha-like 1	alpha-catenin-like protein
				catenin (cadherin-associated protein),	,
284	40777_at	CTNNB1	X87838	beta 1 (88kD)	beta-catenin
				catenin (cadherin-associated protein),	
285	40444_s_at	CTNND1	AB002382	delta 1	
_	38466_at	CTSK	X82153	cathepsin K (pycnodysostosis)	Cathepsin O
287	37391_at	CTSL	X12451	cathepsin L	pro-(cathepsin L)
288	36915_at	CTSO	AI810485	cathepsin O	
289	36119_at	CAV1	AF070648	caveolin 1, caveolae protein, 22kD	
290	339_at	CAV2	AF035752	caveolin 2	caveolin-2
				Cbp/p300-interacting transactivator, with	
291	33113_at	CITED2	U65093	Glu/Asp-rich carboxy-terminal domain, 2	msg-related gene 1
				CCAAT/enhancer binding protein	
292	1052_s_at	CEBPD	M83667	(C/EBP), delta	NF-IL6-beta protein
293	293 39219 at	CEBPG	U20240	CCAAT/enhancer binding protein (C/EBP), gamma	C/EBP gamma
3	1332 13 at	2000	10505.00		



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-				CCR4-NOT transcription complex, subunit	
294	33861_at	CNOIZ	A1123426	CODA NOT transcription complex culturit	
200	** 00000	ATONO.	1171967	CCR4-NOT transcription complex, subdim	potential transcriptional repressor NOT4Hp
200	32020 at	CD164	D14043	D164 antigen, siglomucin	MGC-24 precursor
3 2	24000	O V CO	A1 050105		hynothetical protein
187	24039 at	באסמט	201000		
				CD36 antigen (collagen type I receptor,	
			•	thrombospondin receptor)-like 2	
298	33823_at	CD36L2	D12676	(lysosomal integral membrane protein II)	85kDa human lysosomal sialoglycoprotein
				CD44 antigen (homing function and Indian	
299	2036_s_at	CD44	M59040	blood group system)	cell adhesion molecule
				CD81 antigen (target of antiproliferative	
300	35282_r_at	CD81	M33680	antibody 1)	CD81 antigen
301	39389_at	CD9	M38690	CD9 antigen (p24)	CD9 antigen
				CDC10 cell division cycle 10 homolog (S.	
302	32175_at	CDC10	872008	cerevisiae)	cell division cycle 10
				CDC16 cell division cycle 16 homolog (S.	
303	303 40404_s_at	CDC16	U18291	cerevisiae)	CDC16Hs
				CDC23 (cell division cycle 23, yeast,	
304	31877_at	CDC23	AF053977	homolog)	cell division cycle protein 23
305	40690 at	CKS2	X54942	CDC28 protein kinase 2	Cks1 protein homologue
306	33362_at	CEP3	AF094521	Cdc42 effector protein 3	MSE55-related protein
307	32833_at	CLK1	M59287	CDC-like kinase 1	
308 308	41535_at	CDK2AP1	AF006484	CDK2-associated protein 1	putative oral tumor suppressor protein
				CDP-diacylglycerol synthase	
309	41343_at	CDS2	Y16521	(phosphatidate cytidylyltransferase) 2	CDS2 protein
		-		CDP-diacylglycerolinositol 3-	
				phosphatidyltransferase	
310	33397_at	CDIPT	AL050383	(phosphatidylinositol synthase)	
311	40591	CDC27	S78234	cell division cycle 27	H-NUC
				cell growth regulatory with ring finger	
312	. 450_g_at	CGR19	U66469	domain	cell growth regulator CGR19
313	313 36514 at	CGR19	U66469	cell growth regulatory with ring finger domain	cell growth regulator CGR19
<u>'</u>	- LOSS (	,			

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	A	В	၁	O	ביים ביים ביים ביים ביים ביים ביים ביים
,	24.4 000044	0100	A E084523	cellular repressor of F1A-stimulated genes CREG	cellular repressor of ETA-stimulated genes CREG
1 1	33311 at	CHINE	00000	contains heta 2	centaurin beta 2
2	315 41333_at	CEIVIDE	020003		VIAA1000 protoin
316	316 34676_at	CENTG2	AB029022		NAME OF STREET
317	38410_at	CETN2	X72964		caltractin
Γ				centrin, EF-hand protein, 3 (CDC31	
318	35232 f at	CETN3	A1056696	homolog, yeast)	
319	319 31894 at	CENPC1	M95724		centromere autoantigen C
320	320 33805 at	CAP350	AB007949	ed protein 350	KIAA0480 protein
				cerebellar degeneration-related protein	
321	36190 at	CDR2	M63256	(62kD)	major Yo paraneoplastic antigen
	32262 at	CGI-01	AL049669	CGI-01 protein	hypothetical protein
	40931 at	LOC50999	AL080084	CGI-100 protein	
	38500_at	LOC51014	AB002450	CGI-109 protein	
325		LOC51020	AA524058	CGI-130 protein	
326	38667_at	LOC51031	AA189161	CGI-150 protein	
327	41824_at	LOC51096	Al140114	CGI-48 protein	
328	34862_at	LOC51097	AA005018	CGI-49 protein	
329	329 37199_at	LOC51626	AI760932	CGI-60 protein	
330	41411 at	LOC51103	AI566877	CGI-65 protein	
331	39814 s at	LOC51635	AI052724	CGI-86 protein	
				chaperonin containing TCP1, subunit 2	chaperonin-containing TCP-1 beta subunit
332	35759 at	CCT2	AF026166	(beta)	homolog
				chaperonin containing TCP1, subunit 3	
333	40774 at	CCT3	X74801	(gamma)	gamma subunit of CCT chaperonin
				chaperonin containing TCP1, subunit 4	chaperonin containing t-complex polypeptide
334	32594_at	CCT4	AF026291	(delta)	1, delta subunit
				chaperonin containing TCP1, subunit 6A	
335	38416 at	CCT6A	L27706	(zeta 1)	chaperonin-like protein
				chaperonin containing TCP1, subunit 7	chaperonin containing t-complex polypeptide
336	38720_at	CCT7	AF026292	(eta)	1, eta subunit
				chaperonin containing TCP1, subunit 8	chaperonin containing TCP1, subunit 8
337	39767_at	сств	D13627	(theta)	(theta)
338	41000_at	CHES1	U68723	checkpoint suppressor 1	checkpoint suppressor 1
339	339 37855 at	CTBS	M95767	chitobiase, di-N-acetyl-	di-N-acetylchitobiase

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	CI NS1A	X91788	chloride channel, nucleotide-sensitive, 1A	IcIn protein
	CI IC4	AL080061	-	
	CH25H	AF059214		cholesterol 25-hydroxylase
			ycan 2	(annimary) C anny famous and a second and a second
	CSPG2	X15998		Chondrollin sullate proteogrycan z (versican)
			chondroitin sulfate proteoglycan 2	(accipant) C accidence to the site of the
	CSPG2	X15998	(versican)	chondroitin suitate proteoglycan 2 (versican)
			chondroitin sulfate proteoglycan 6	•
	CSPG6	AF020043	(bamacan)	chromosome-associated polypeptide
			chromobox homolog 1 (HP1 beta homolog	
	CBX1	U35451	Drosophila )	heterochromatin protein p25
			chromobox homolog 3 (HP1 gamma	
	CBX3	AI740522	homolog, Drosophila)	
			chromobox homolog 3 (HP1 gamma	
	CBX3	AA648295	homolog, Drosophila)	
			chromodomain helicase DNA binding	
	CHD4	X86691	protein 4	Mi-2 protein
			chromodomain protein, Y chromosome-	
	CDYL	AL050164	like	hypothetical protein
	Clorf17	AB011156	chromosome 1 open reading frame 17	KIAA0584 protein
	C1orf8	278368	chromosome 1 open reading frame 8	
	C12orf22	AF052105	chromosome 12 open reading frame 22	TGF-beta induced apotosis protein 12
	C14orf3	AJ243310	chromosome 14 open reading frame 3	C14orf3 protein
at	C18orf1	AF009425	chromosome 18 open reading frame 1	clone 22
	C19orf7	AB028987	chromosome 19 open reading frame 7	KIAA1064 protein
	C21orf80	AB023175	chromosome 21 open reading frame 80	KIAA0958 protein
33406 at	C22orf2	AL050345	chromosome 22 open reading frame 2	hypothetical protein
	C22orf4	AL096779	chromosome 22 open reading frame 4	hypothetical protein
	C22orf5	AL096879	chromosome 22 open reading frame 5	hypothetical protein
	C3orf4	AL080097	chromosome 3 open reading frame 4	hypothetical protein
	C4orf1	AF006621	chromosome 4 open reading frame 1	embryonic lung protein
	C5orf8	U10362	chromosome 5 open reading frame 8	GP36b glycoprotein
	C6orf28	AJ245416	chromosome 6 open reading frame 28	G7b protein
	C6orf34	W27949	chromosome 6 open reading frame 34	
	C6orf5	AL050289	chromosome 6 open reading frame 5	hypothetical protein

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367	35193_at	CHC1L	AF060219		RCC1-like G exchanging factor RLG
368	34292_at	CXorf12	X92475	chromosome X open reading frame 12	chromosome X open reading frame 12
		cs	AF047042	citrate synthase	citrate synthase
	41159	CLTC	D21260	clathrin, heavy polypeptide (Hc)	clathrin heavy chain
37.1	38657 c at	OI TA	M20471	clathrin light polypeptide (Lca)	clathrin, light polypeptide A, isoform a; clathrin, light polypeptide A, isoform b
5	2000			cleavage and polyadenylation specific	
372	35743 at	CPSF4	U79569	factor 4, 30kD subunit	no arches
				cleavage stimulation factor, 3' pre-RNA,	
373	32723_at	CSTF1	L02547	subunit 1, 50kD	cleavage stimulation factor
				cleavage stimulation factor, 3' pre-RNA,	
374	41183_at	CSTF3	U15782	subunit 3, 77kD	cleavage stimulation factor 77kDa subunit
375	38711_at	CLASP2	AB014527	CLIP-associating protein 2	KIAA0627 protein
376	36017	LOC57213	AF055016	CLLL6 protein	CLLL6 protein
				clusterin (complement lysis inhibitor, SP-	clusterin (complement lysis inhibitor, SP-
				40,40, sulfated glycoprotein 2,	40,40, sulfated glycoprotein 2, testosterone-
				testosterone-repressed prostate message repressed prostate message 2,	repressed prostate message 2,
377	36780_at	CLU	M25915	2, apolipoprotein J)	apolipoprotein J)
378	378 35180_at	LOC113251	AL050205	c-Mpl binding protein	
379	40811_at	COASTER	AB011148	coactivator for steroid receptors	KIAA0576 protein
380	380 38052_at	F13A1	M14539	coagulation factor XIII, A1 polypeptide	coagulation factor XIII A1 subunit precursor
381	36972_at	RNP24	X92098	coated vesicle membrane protein	transmembrane protein
382	34326_at	COPB	X82103	coatomer protein complex, subunit beta	beta-Coat protein
				coatomer protein complex, subunit beta 2	
383	36677_at	COPB2	X70476	(beta prime)	subunit of coatomer complex
384	35205_at	COBRA1	AL050280	cofactor of BRCA1	hypothetical protein
				cofactor required for Sp1 transcriptional	
382	36648_at	CRSP9	AF031383	activation, subunit 9 (33kD)	hMed7
386	33659_at	CFL1	X95404	cofilin 1 (non-muscle)	cofilin
387	₩	BICD2	AB014599	coiled-coil protein BICD2	KIAA0699 protein
388		CIRBP	D78134	cold inducible RNA binding protein	CIRP
389	39839_at	CSDA	M24069	cold shock domain protein A	cold shock domain protein A
390	32307_s_at	COL1A2	V00503	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein
391	32306_g_at	COL1A2	J03464	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein
392		COL1A2	J03464	collagen, type I, alpha 2	alpha 2 type I collagen preproprotein

П	_		Т	Т	7	П						7	7	<u></u>		_	=		ᆵ		_	T	_							-		Т		
ш			prepro-alpha-1 type 3 collagen	alpha (2) chain	procollagen alpha 2(V)	alpha-1 collagen VI (AA 574-1009)	collagen type VI, alpha 3 chain	alpha 1(VIII) collagen	alpha 1 type XI collagen, isoform A	preproprotein; alpha 1 type XI collagen,	isoform B preproprotein; alpha 1 type XI	collagen, isoform C preproprotein	alpha-1 type XVI collagen	complement component 1, q subcomponent	binding protein precursor		complement component 1, r subcomponent		complement component 1, s subcomponent	connective tissue growth factor		OS-4 protein		IKB kinase alpha subunit	Jun activation domain binding protein	COP9 signalosome subunit 1 CSN1	34 kDa Mov34 homolog	copine I	KIAA0636 protein	-	coproporphyrinogen oxidase	Kruppel-like zinc tinger protein 219	transcription factor	noduinos
Q		collagen, type III, alpha 1 (Ehlers-Danlos	syndrome type IV, autosomal dominant)	collagen, type IV, alpha 2			collagen, type VI, alpha 3	collagen, type VIII, alpha 1				collagen, type XI, alpha 1	collagen, type XVI, alpha 1	complement component 1, q	subcomponent binding protein	complement component 1, r	subcomponent	complement component 1, s	subcomponent	connective tissue growth factor	conserved gene amplified in	osteosarcoma	conserved helix-loop-helix ubiquitous	kinase	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)	COP9 homolog	COP9 subunit 6 (MOV34 homolog, 34 kD) 34 kDa Mov34 homolog	copine I	copine III	coproporphyrinogen oxidase	(coproporphyria, harderoporphyria)	core promoter element binding protein	core-binding factor, beta subunit	ohin-like
ပ			X14420	X05610	Y14690	X15880	X52022	X57527				J04177	M92642		M69039		M14058		J04080	X78947		AF000152		AF009225	U65928	U51205	U70735	U83246	AB014536		D16611	AF001461	L20298	A E 10.4308
8	1		COL3A1	COL4A2	COL5A2	COL6A1	COLEA3	COL 8A1				COL11A1	COL16A1		C1QBP		C1R		C1S	CTGF		0S4		CHUK	COPSE	COP9	MOV34-34KD	CPNE1	CPNE3		CPO	COPEB	CBFB	IIVC
A					395 38420 at		397 38077 at		500			37892 at	35168 t at		37668 at		39409_at		403 40496_at	404 36638 at		41202 s at		33770 at	1789 at	32539 at	40138 at	40452 at	39706 at	_	37999_at	37026_at	41175	0000
			393	394	395	396	397	308				399	400		401		405		403	404		405		406	407	408	400	410	411		412	413	414	7

	A	В	O	Q	Ε
940	04703	7,70	02021	COX11 homolog, cytochrome c oxidase	COX11 homolog
4 10	34123 al		013510	CnG island protein: Human nested gene	6
417	37907 at	F8A: DXS522E	M34677	protein gene, complete cds.	coagulation factor VIII-associated protein
418	38664	CFDP1	AB009285	craniofacial development protein 1	craniofacial development protein 1
				CREB binding protein (Rubinstein-Taybi	
419	33831_at	CREBBP	U47741	syndrome)	CREB-binding protein
420	420 36948_at	CR11	AL109701	CREBBP/EP300 inhibitory protein 1	C15orf3
421	38148_at	CRY1	D83702	cryptochrome 1 (photolyase-like)	photolyase
422	37902_at	CRYZ	L13278	crystallin, zeta (quinone reductase)	zeta-crystallin
423	40167_s_at	LOC55884	AF038187	CS box-containing WD protein	
				CSE1 chromosome segregation 1-like	
424	38804_at	CSE1L	AF053641	(yeast)	cellular apoptosis susceptibility protein
425	1768_s_at	CSK	X59932	c-src tyrosine kinase	c-src-kinase
426	426 41309_g_at	CTBP1	U37408	C-terminal binding protein 1	phosphoprotein CtBP
427	40780_at	CTBP2	AF016507	C-terminal binding protein 2	C-terminal binding protein 2
428	39723_at	CUL1	AF062536	cullin 1	cullin 1
429	40141_at	CUL4B	AB014595	cullin 4B	KIAA0695 protein
				cut-like 1, CCAAT displacement protein	
430	31823_at	CUTL1	M74099	(Drosophila)	cut-like 1, CCAAT displacement protein
431	36872_at	ARPP-19	AL120559	cyclic AMP phosphoprotein, 19 kD	
				cyclin D binding myb-like transcription	cyclin D binding myb-like transcription factor
432	41808_at	DMTF1	AF052102	factor 1	-
				cyclin D1 (PRAD1: parathyroid	
433	433 38418_at	CCND1	X59798	adenomatosis 1)	cyclin
				cyclin D1 (PRAD1: parathyroid	
434	2020_at	CCND1	M73554	adenomatosis 1)	bcl-1
435	36650_at	CCND2	D13639	cyclin D2	cyclin D2
436	436 40225_at	GAK	D88435	cyclin G associated kinase	HsGAK
437	37723_at	CCNG2	U47414	cyclin G2	cyclin G2
438	1913_at	CCNG2	U47414	cyclin G2	cyclin G2
439	1924_at	CCNH	U11791	cyclin H	cyclin H
4 <del>5</del>	440 1836_at	CCNI	D50310	cyclin I	cyclin l
4	441 1792 g_at	CDK2	M68520	cyclin-dependent kinase 2	cdc2-related protein kinase

Fig 2)

A B B C   Cyclin-dependent kinase 7 (MO15   Cyclin-dependent kinase 1 (CDK)						
CDK7		∢	<b>6</b> 0		U	U
1699 s at CDK7					cyclin-dependent kinase 7 (MO15	
1989 s_at						
1969 s_at   CDK7   X77743   kinase   cyclin-dependent kinase   KMO15   kinase   cDK7   X77743   kinase   cDK8   R59697   cyclin-dependent kinase   cyclin-dependent kinase inhibitor 1A (p21, cyclin-dependent kinase inhibitor 1B (p27, cyclin-dependent cyclin-depend		33317 at	CDK7	•		protein serine/threonine kinase
1989 s_at			-		cyclin-dependent kinase 7 (MO15	
1969_s_at   CDK7					homolog, Xenopus laevis, cdk-activating	
35140_at         CDK8         R59697         cyclin-dependent kinase inhibitor 1A (p21, cyclin-dependent kinase inhibitor 1B (p27, cyclin-dependent kinase inhibitor 2C (p18, cyclin-dependent	443	S	CDK7	X77743	kinase)	CDK activating kinase
CORNITA   U03106   Cip1   Cyclin-dependent kinase inhibitor 1A (p21, cyclin-dependent kinase inhibitor 1B (p27, cyclin-dependent kinase inhibitor 1B (p27, cyclin-dependent kinase inhibitor 1B (p27, cyclin-dependent kinase inhibitor 2C (p18, cyclin-dependent cyclin-dependent kinase inhibitor 2C (p18, cyclin-dependent kinase inhibitor 2C (p18, cyclin-dependent cyclin-dependent kinase inhibitor 2C (p18, cyclin-dependent cyclin-dependent kinase inhibitor 2C (p18, cyclin-dependent cyclin-dependent kinase inhibitor 2C (p18, cyclin-dependent kinase inhibitor 2C (p18, cyclin-dependent kinase inhibitor 2C (p18, cyclin-dependent kinase inhibitor 2C (p18, cyclin-dependent kinase inhibitor 2C (p18, cyclin-dependent kinase inhibitor 2C (p18, cyclin-dependen	_	35140 at	CDK8	R59697	cyclin-dependent kinase 8	
CDKN1A   U03106   Cip    _				cyclin-dependent kinase inhibitor 1A (p21,		
38877_s_at         CDKN1B         Al304854         Cyclin-dependent kinase inhibitor 1B (p27, polin-dependent kinase inhibitor 2C (p18, polin-dependent kinase subunit VIIa polypeptide 2C (ilier) polypeptide 2C (ili		2031_s_at	CDKN1A	U03106	Cip1)	cyclin-dependent kinase inhibitor 1A
COKNUE   AI304854   Kip1					cyclin-dependent kinase inhibitor 1B (p27,	
COKN2C   AF041248   inhibits CDK4    1401248   inhibits CDK4    1401241   141401	446	33847_s_at	CDKN1B	AI304854	Kip1)	
36053_at         CDKN2C         AF041248         inhibits CDK4)           38700_at         CSRP1         M33146         cysteline and glycine-rich protein 1         41401_at           41401_at         CSRP2         U57646         cysteline-rich moror neuron 1         6151806           40936_at         CRIM1         AI651806         cysteline-rich molor neuron 1         6151806           40408_at         CYR61         Y11307         cysteline-rich molor neuron 1         6151806           40408_at         CYR61         Y11307         cysteline-rich molor neuron 1         6151806           40408_at         CYR61         Y11307         cysteline-rich molor neuron 1         6151806           40408_at         CARS         L06845         cystelinyl-tRNA synthetase         6178           40408_at         CARS         L06824         N-acetylneuraminate monocxygenase)         6170chrome coxidase subunit VI           41206_rat         COXAB         AA152406         cytochr					cyclin-dependent kinase inhibitor 2C (p18,	
38700_at         CSRP1         M33146         cysteline and glycine-rich protein 1         of cysteline and glycine-rich protein 2           41401_at         CSRP2         U57646         cysteline and glycine-rich protein 2         of cysteline-rich motor neuron 1           40936_at         CRR1         Y11307         cysteline-rich motor neuron 1           38772_at         CYR61         Y11307         cysteline-rich angiogenic inducer, 61           40408_at         CARS         L06845         cysteliny-tRNA synthetase           40408_at         CARS         L06824         cysteliny-tRNA synthetase           40408_at         CARS         CARS         cysteliny-tRNA synthetase           41206_at         CARS         CARS         cysteliny-tRNA synthetase           41206_r         AA152406         cytochrome c oxidase subunit VIIa           41760_at	447	36053_at	CDKN2C	AF041248	inhibits CDK4)	cyclin-dependent kinase inhibitor
41401_at         CSRP2         U57646         cysteine and glycine-rich protein 2           40936_at         CRIM1         Al651806         cysteine-rich molor neuron 1           38772_at         CYR61         Y11307         cysteine-rich molor neuron 1           40408_at         CYR61         Y11307         cysteinyl-tRNA synthetase           40408_at         CARS         L06845         cysteinyl-tRNA synthetase           40408_at         CARS         L06845         cysteinyl-tRNA synthetase           40408_at         CARS         L06845         cytidine monophosphate-N-acetylneuraminate monocxygenase)           39317_at         CMAH         D86324         N-acetylneuraminate monocxygenase)           34340_at         CYBS-M         AA173896         membrane precursor           3921_at         COX5B         Al526089         cytochrome c oxidase subunit VIa           39031_at         COX6A1         AA1526089         cytochrome c oxidase subunit VIa           41760_at         COX7A2         AA978033         polypeptide 1 (muscle)           3933_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2         AB007618         cytochrome c oxidase subunit VIIa           34331_at         COX7C         AA978	448	38700_at	CSRP1	M33146	cysteine and glycine-rich protein 1	cysteine and glycine-rich protein 1
40936_at         CRIM1         AI651806         cysteine-rich motor neuron 1           38772_at         CYR61         Y11307         cysteine-rich, angiogenic inducer, 61           40408_at         CARS         L06845         cysteine-rich, angiogenic inducer, 61           40408_at         CARS         L06845         cysteinyl-tRNA synthetase           39317_at         CMAH         D86324         cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-acetylneuraminic acid hydroxylase subunit VII           39921_at         COX5B         AI526089         cytochrome c oxidase subunit VII           39031_at         COX7A1         AA152406         cytochrome c oxidase subunit VIIa           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7A2         AI708889         cytochrome c oxidase subunit VIIc	449	41401 at	CSRP2	U57646	cysteine and glycine-rich protein 2	cysteine and glycine-rich protein 2
38772_at         CYR61         Y11307         cysteine-rich, angiogenic inducer, 61           40408_at         CARS         L06845         cysteinyl-tRNA synthetase           40408_at         CARS         L06845         cysteinyl-tRNA synthetase           39317_at         CMAH         D86324         cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-acetylneuraminic acid hydroxylase subunit VI           39921_at         COX5B         AA173896         membrane precursor cytochrome coxidase subunit VI           41206_rat         COX6A1         AI526089         cytochrome coxidase subunit VII           39031_at         COX6C         W51774         cytochrome coxidase subunit VIIa           41760_at         COX7A1         AA152406         polypeptide 1 (muscle)           34330_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2         AB007618         polypeptide 2 (liver)           34381_at         COX7A2         AI708889         cytochrome coxidase subunit VIIc	450	40936 at	CRIM1	AI651806	cysteine-rich motor neuron 1	
40408_at         CARS         L06845         cysteinyl-tRNA synthetase           39317_at         CMAH         D86324         vacetylneuraminic acid hydroxylase (CMP-acetylneuraminic acid hydroxylase (CMP-acetylneuraminic acid hydroxylase (CMP-acetylneuraminate monooxygenase)           34340_at         CYB5-M         AA173896         membrane precursor           35818_at         HCS         D00265         cytochrome c oxidase subunit Vb           39921_at         COX5B         AI526089         cytochrome c oxidase subunit Vla           41206_r_at         COX6A1         AI540925         polypeptide 1           39031_at         COX7A1         AA152406         polypeptide 1           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2         AB007618         polypeptide 2 (liver)           34331_at         COX7A2         AB007618         polypeptide 2 (liver)           34331_at         COX7A2         AB007618         cytochrome c oxidase subunit VIIa	451	38772 at	CYR61	Y11307	cysteine-rich, angiogenic inducer, 61	CYR61 protein
Company	452	40408 at	CARS	L06845	cysteinyl-tRNA synthetase	cysteinyl-tRNA synthetase
39317_at         CMAH         D86324         cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-acetylneuraminic acetylneuraminic a						
39317_at         CMAH         D86324         N-acetylneuraminic acid hydroxylase (CMP-acetylneuraministe monooxygenase)           34340_at         CYB5-M         AA173896         membrane precursor           35818_at         HCS         D00265         cytochrome b5 outer mitochondrial           41206_r_at         COX5B         AI526089         cytochrome c oxidase subunit VIa           41206_r_at         COX6C         W51774         cytochrome c oxidase subunit VIa           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2         AB007618         polypeptide 2 like           34331_at         COX7A2         AB007618         polypeptide 2 like           34331_at         COX7A2         AR907618         polypeptide 2 like					cytidine monophosphate-N-	
39317_at         CMAH         D86324         N-acetylneuraminate monooxygenase)           34340_at         CYB5-M         AA173896         membrane b5 outer mitochondrial           35818_at         COX5B         D00265         cytochrome c oxidase subunit Vb           41206_r_at         COX6A1         AI526089         cytochrome c oxidase subunit Vla           41206_r_at         COX6C         W51774         cytochrome c oxidase subunit Vla           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2         AB007618         polypeptide 2 (liver)           34330_at         COX7A2         AB007618         polypeptide 2 (liver)           34331_at         COX7A2         AR978899         cytochrome c oxidase subunit VIIa			-		acetylneuraminic acid hydroxylase (CMP-	
34340_at         CYB5-M         AA173896         membrane precursor           35818_at         HCS         D00265         cytochrome c         .           39921_at         COX5B         AI526089         cytochrome c oxidase subunit Vb           41206_r_at         COX6A1         AI540925         polypeptide 1           39031_at         COX6C         W51774         cytochrome c oxidase subunit Vla           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 (liver)           34331_at         COX7A2L         AB007618         polypeptide 2 like           34331_at         COX7A2L         AB007618         polypeptide 2 like           34331_at         COX7A2         AB007618         cytochrome c oxidase subunit VIIa	453	39317	CMAH	D86324	N-acetylneuraminate monooxygenase)	CMP-N-acetylneuraminic acid hydroxylase
34340_at         CYB5-M         AA173896         membrane precursor           35818_at         HCS         D00265         cytochrome c         ,           39921_at         COX5B         AI526089         cytochrome c oxidase subunit Vb           41206_r_at         COX6A1         AI540925         polypeptide 1           36165_at         COX6C         W51774         cytochrome c oxidase subunit Vla           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         AI708889         cytochrome c oxidase subunit Vlla					cytochrome b5 outer mitochondrial	
35818_at         HCS         D00265         cytochrome c         incorporation           39921_at         COX5B         Al526089         cytochrome c oxidase subunit VIa           41206_r_at         COX6A1         Al540925         polypeptide 1           36165_at         COX6C         W51774         cytochrome c oxidase subunit VIa           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7A2         AB007618         cytochrome c oxidase subunit VIIa           34381_at         COX7C         AI708889         cytochrome c oxidase subunit VIIc	454	34340_at	CYB5-M	AA173896	membrane precursor	
39921_at         COX5B         AI526089         cytochrome c oxidase subunit Vb           41206_r_at         COX6A1         AI540925         polypeptide 1           36165_at         COX6C         W51774         cytochrome c oxidase subunit Vla           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7A2         AI708889         cytochrome c oxidase subunit VIIa	455	35818 at	HCS	D00265	cytochrome c	cytochrome c
41206_r_at         COX6A1         Al540925         polypeptide 1           36165_at         COX6C         W51774         cytochrome c oxidase subunit VIc           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         AI708889         cytochrome c oxidase subunit VIIa	456		COX5B	AI526089	cytochrome c oxidase subunit Vb	
41206_r_at         COX6A1         AI540925         polypeptide 1           36165_at         COX6C         W51774         cytochrome c oxidase subunit VIIa           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         AI708889         cytochrome c oxidase subunit VIIc					cytochrome c oxidase subunit Vla	
36165_at         COX6C         W51774         cytochrome c oxidase subunit VIIa           39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         AI708889         cytochrome c oxidase subunit VIIa	457		COX6A1	AI540925	polypeptide 1	
39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         AI708889         cytochrome c oxidase subunit VIIc	458	36165 at	coxec	W51774	cytochrome c oxidase subunit VIc	
39031_at         COX7A1         AA152406         polypeptide 1 (muscle)           41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         AI708889         cytochrome c oxidase subunit VIIc					cytochrome c oxidase subunit VIIa	
41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 (liver)           34381_at         COX7C         AI708889         cytochrome c oxidase subunit VIIc	459		COX7A1	AA152406	polypeptide 1 (muscle)	
41760_at         COX7A2         AA978033         polypeptide 2 (liver)           34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         AI708889         cytochrome c oxidase subunit VIIc	L			,	cytochrome c oxidase subunit VIIa	
34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         AI708889         cytochrome c oxidase subunit VIIc	460	41760_at	COX7A2	AA978033	polypeptide 2 (liver)	
34330_at         COX7A2L         AB007618         polypeptide 2 like           34381_at         COX7C         AI708889         cytochrome c oxidase subunit VIIc					cytochrome c oxidase subunit VIIa	
COX7C AI708889	461		COX7A2L	AB007618	polypeptide 2 like	COX7RP
	462	34381_at	COX7C	AI708889	cytochrome c oxidase subunit VIIc	

					1
	٧	В		O	Ш
463	38080 at	COX8	AI525665	cytochrome c oxidase subunit VIII	
_	35819 at	CYC1	X06994	cytochrome c-1	cytochrome c-1
				cytochrome P450, 51 (lanosterol 14-alpha-	
465	33389_at	CYP51	U23942	demethylase)	lanosterol 14-demethylase cytochrome P450
				cytochrome P450, subfamily I (dioxin-	
				inducible), polypeptide 1 (glaucoma 3,	
466	466 859 at	CYP1B1	U03688	primary infantile)	cytochrome P450
				cytochrome P450, subfamily I (dioxin-	
				inducible), polypeptide 1 (glaucoma 3,	
467	467 40071 at	CYP1B1	U03688	primary infantile)	cytochrome P450
468	at	CRLF3	AF046059	cytokine receptor-like factor 3	cytokine receptor related protein 4
469		KIAA0068	D38549	cytoplasmic FMRP interacting protein 1	
				cytoplasmic; Human Ser/Thr protein	
470	1706 at	A-RAF-1	U01337	kinase (A-RAF-1) gene, complete cds.	Ser/Thr protein kinase
471	471 34338 at	CKAP1	D49738	cytoskeleton-associated protein 1	cytoskeleton associated protein
472	472 32529 at	CKAP4	X69910	cytoskeleton-associated protein 4	P63 protein
473	473 40282 s at	DF	M84526	D component of complement (adipsin)	adipsin/complement factor D
474	40877 s at	MN7	AF041080	D15F37 (pseudogene)	
				damage-specific DNA binding protein 2	
475	1243 at	DDB2	U18300	(48kD)	DDBb p48
476		DAZAP2	D31767	DAZ associated protein 2	DAZ associated protein 2
				DEAD/H (Asp-Glu-Ala-Asp/His) box	:
477	37663 at	DDX1	X70649	polypeptide 1	member of DEAD box protein family
				DEAD/H (Asp-Glu-Ala-Asp/His) box	
478	35306_at	DDX15	AB001636	polypeptide 15	ATP-dependent HNA helicase #46
L				DEAD/H (Asp-Glu-Ala-Asp/His) box	-
479	40490_at	DDX21	U41387	polypeptide 21	Gu protein
				DEAD/H (Asp-Glu-Ala-Asp/His) box	:
480	39744_at	DDX3	AF000982	polypeptide 3	dead box, X isoform
				DEAD/H (Asp-Glu-Ala-Asp/His) box	DEAD/H (Asp-Glu-Ala-Asp/His) box
481	34647_at	DDXS	X52104	polypeptide 5 (RNA helicase, 68kD)	polypeptide 5
	$\overline{}$			DEAD/H (Asp-Glu-Ala-Asp/His) box	
				polypeptide 9 (RNA helicase A, nuclear	
482	482 36153 at	6XQQ	L13848	DNA helicase II; leukophysin)	RNA helicase A
483	483 41872 at	DFNA5	AF073308	deafness, autosomal dominant 5	nonsyndromic hearing impairment protein

		נ	>	3	
					ionizing radiation resistance conferring
	1356_at	DAP3	U18321	death associated protein 3	protein
485 391	39114_at	DEPP	AB022718	decidual protein induced by progesterone	DEPP
486 37638_at	38_at	DOCK1	D50857	dedicator of cyto-kinesis 1	DOCK180 protein
487 384	38413 at	DAD1	D15057	defender against cell death 1	DAD-1
				deficient in late-infantile neuronal ceroid	
				lipofuscinosis; Homo sapiens lysosomal	
				pepstatin insensitive protease (CLN2)	
488 328	32824_at	CLN2	AF039704	gene, complete cds.	lysosomal pepstatin insensitive protease
				atocyte homolog, lipid	
489 333	33337_at	DEGS	AF002668		MLD
490 38992_at	992_at	DEK	X64229	DEK oncogene (DNA binding)	putative oncogene
491 37951 at	951 at	DLC1	AF035119	deleted in liver cancer 1	deleted in liver cancer-1
492 33791 at	791 at	DLEU1	Y15227	deleted in lymphocytic leukemia, 1	deleted in lymphocytic leukemia, 1
493 38744 at	744_at	DSS1	N95406	Deleted in split-hand/split-foot 1 region	
_				delta sleep inducing peptide,	
494 366	36629_at	DSIPI	AI635895	immunoreactor	
495 35814_at	814_at	GA17	AF064603	dendritic cell protein	GA17 protein
496 38385 at	385_at	DSTN	S65738	destrin (actin depolymerizing factor)	actin depolymerizing factor
_				development and differentiation enhancing	development and differentiation enhancing development- and differentiation-enhancing
497 394	39410_at	DDEF2	AB007860	factor 2	factor 2
498 390	044 s at	DGKD	D73409	diacylglycerol kinase, delta (130kD)	diacylglycerol kinase delta
499 380	499 38003_s_at	DGKZ	U94905	diacylglycerol kinase, zeta (104kD)	diacylglycerol kinase zeta
500 33	920_at	DIAPH1	AF051782	diaphanous homolog 1 (Drosophila)	diaphanous 1
				diazepam binding inhibitor (GABA	
				receptor modulator, acyl-Coenzyme A	
501 37692_at	692_at	180	AI557240	binding protein)	
_				dihydrolipoamide S-acetyltransferase (E2	
				component of pyruvate dehydrogenase	
502 39041	041_at	DLAT	Y00978	complex)	PDC-E2 precursor (AA -54 to 561)
503 40607	607_at	DPYSL2	U97105	dihydropyrimidinase-like 2	N2A3
504 36	504 36149_at	DPYSL3	D78014	dihydropyrimidinase-like 3	dihydropyrimidinase related protein-3
505 39503_s_	503_s_at	DPYSL4	AB006713	dihydropyrimidinase-like 4	dihydropyrimidinase related protein 4
506 38220_at	1220_at	DPYD	U20938	dihydropyrimidine dehydrogenase	dihydropyrimidine dehydrogenase
507 40	485_at	HSA249128	AA176780	DIPB protein	

(Fig 21)

AB	В		၁	Q	ш
479 at DAB2 U53446		U53446		disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	DOC-2
				mily, member	Line of the contract of the co
DDR1		12081/		disco (Oraccabila) hamalar E	KIAAASS arotoin
510 405/5_at DLG3 ABVIII33		ADOI 1 133			
33753_at DAAM1 AB014566		AB014566		morphogenesis 1	KIAA0666 protein
512 33150_at SAS10 Al126004		Al126004		disrupter of silencing 10	
				dJ635G19.1 (LAMR1 (Laminin Receptor 1 (67kD) (RPSA, 40S Ribosomal Protein SA, P40)) pseudogene); match: cDNAs:	
				Em:M64923 Em:X06406 Em:AF140348	
				Em:02877 Em:L10303 Em:Z22743 Em:D25224 Em:M14199 Em:M27798;	
513 40916_at dJ635G19.1 AL035494		AL035494	- 1	match: ESTs: Em:AA642	dJ635G19.2.1 (novel protein (isoform 1))
				dJ734P14.1 (KRAB box and C2H2 Zinc	
				finger domain protein pseudogene) match: cDNAs: Em:M27878 Em:M29580	
				Em:U27186 Em:D31763 Em:AB007872	
				Em:U09366 Em:U09413 Em:X17617	
				Em:AF011573 Em:AF020591 Em:X78925	
				match: proteins: Sw:P52736 Sw:Q06730	
-				Sw:P51523 Tr:Q14585 Sw:P15620	
				Sw:Q02386 Sw:P51786 Sw:Q99676	
		,		Tr:O60792 Sw:Q03923 Sw:O75820	dJ734P14.2.1 (snRNP (small nuclear
514 38456_s_at dJ734P14.1 AL049650		AL049650		Tr:Q61116 Tr:Q64247	ribonucleoprotein particle) protein B)

ш	dJ734P14.2.1 (snRNP (small nuclear	dJ862K6.2.2 (splicing factor, arginine/serine- rich 6 (SRP55-2)(isoform 2))	dJ862K6.2.2 (splicing factor, arginine/serine- rich 6 (SRP55-2)(isoform 2))	
<u> </u>	dJ734P14.1 (KRAB box and C2H2 Zinc finger domain protein pseudogene) match: cDNAs: Em:M27878 Em:M29580 Em:U27186 Em:D31763 Em:AB007872 Em:U09366 Em:U09413 Em:X17617 Em:U09366 Em:U09413 Em:X77617 Em:C09366 Em:U09413 Em:X78925 match: proteins: Sw:P52736 Sw:Q06730 Sw:P51523 Tr:Q14585 Sw:P15620 Sw:C02386 Sw:P61786 Sw:Q099676 Tr:O60792 Sw:C03923 Sw:O75820 Tr:C061116 Tr:Q64247	dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:P21590 Sw:Q57731 Sw:P40558	dJ862K6.4 (pseudogene similar to part of NBP (Nucleotide Binding Protein)) match: proteins: Sw:P53384 Sw:P52920 Sw:Q57731 Sw:P40558	dJ90L6.1 (RPL15 (60S Ribosomal Protein L15) pseudogene); match: proteins: Sw:O74895 Sw:P51417 Sw:P39030 Sw:O77445 Sw:P54780 Sw:O23515 Sw:O65050 Wp:CE12148 Sw:P30736 Sw:P62018 Sw:P52018 Sw:P52018 Sw:P52018 Sw:P62013 Sw:P52018 Sw:P62013 Sw:P62013 Sw:P037418 Sw:O037418 Sw:O03748 Sw:O037418 Sw:O03748 Sw:O037418 Sw:O03748 Sw:O037418 Sw:O03748 Sw:O03748 Sw:O03748 Sw:O03748 Sw:O03748 Sw:O03748 Sw:O0374 Sw:O
O	AL049650	AL031681	AL031681	297353
В	dJ734P14.1	dJ862K6.4	dJ862K6.4	dJ90L6.1
A.	38455_	35809_g_at	35808_at	518 32433_at
Γ	515	516	517	518

Fig 21

$\vdash$	A	8	O	O	Е
160	34183_at	4C171	AL080169	DKFZP434C171 protein	hypothetical protein
520 4	40801_at	DKFZP434C212	AA643063	DKFZP434C212 protein	
(6)	38400_at	DKFZP434D1335	5 A1920820	u	
522 3	33392_at		AL080155		hypothetical protein
523	39411_at	DKFZP434J214	AL080156		hypothetical protein
524 4	40564_at	_	N42007		
525 3	37000_at	DKFZP564B167	AL035304		hypothetical protein
526 3	33433_at	DKFZP564F0522	2 AL049943		hypothetical protein
527 4	41437_at	DKFZP564F1123 AL080118	AL080118		hypothetical protein
Τ	39442_at	DKFZP564G0222	22 AL080115		hypothetical protein
529 4	40437 at	DKFZP564G2022	AL049944	ui.	hypothetical protein
530	36456_at	DKFZP5641052	AL080063		hypothetical protein
_	38033_at	DKFZP564M1416	16 AL049934	DKFZP564M1416 protein	hypothetical protein
H	36078_at	DKFZP56400423	AL080120	u	hypothetical protein
533	38256_s_at	DKFZP5640092	32 W21827		
	39034_at	DKFZP5640123	AL080122		hypothetical protein
535	41662_at	m	AL050272		hypothetical protein
536	32807_at	4	AF004292	DKFZP566C134 protein	
537	38687_at	6	AL050051	DKFZP566D193 protein	hypothetical protein
538	33776_at	DKFZP566K023	AL050062	DKFZP566K023 protein	hypothetical protein
	41335_at		AL050084	DKFZP56601646 protein	hypothetical protein
	36961_at	DKFZP586A011	AL050286	DKFZP586A011 protein	hypothetical protein
	38717_at	DKFZP586A0522	22 AL050159	DKFZP586A0522 protein	hypothetical protein
542	40831_at	DKFZP586B0923	23 AL050190	DKFZP586B0923 protein	hypothetical protein
543	34821_at	DKFZP586D0623 AL050197	AL050197	DKFZP586D0623 protein	hypothetical protein
544	39986_at	DKFZP586D0919	19 AL050100	DKFZP586D0919 protein	hypothetical protein
545	34269_at	DKFZp586F1019	19 AL050102	DKFZp586F1019 protein	hypothetical protein
546	35736_at	DKFZP586F1918	18 AL050091	DKFZP586F1918 protein	hypothetical protein
547	40832_s_at	DKFZP586G011	AL050126	DKFZP586G011 protein	hypothetical protein
548	36007_at	DKFZP586L151	AL050137	DKFZP586L151 protein	hypothetical protein
	3483	DKFZP58600120	20 AL050157	DKFZP586O0120 protein	hypothetical protein
550	37333_at	DNMT1	X63692	DNA (cytosine-5-)-methyltransferase 1	DNA (cytosine-5-)-methyltransferase
				DNA segment on chromosome X (unique)	
551	40891_f_at	DXS9879E	X92896	9879 expressed sequence	ITBA2 protein
552	34215 at	DXYS155E	L03426	DNA segment on chromosome X and Y (unique) 155 expressed sequence	DNA segment on chromosome X and Y (unique) 155 expressed sequence
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553	1252 at	D5S346	M73547	DNA segment, single copy probe LNS- CAI/LNS-CAII (deleted in polyposis	polyposis locus-encoded protein
_				DNA segment, single copy, probe pH4	DNA segment, single copy, probe pH4
554	37162 at	D10S170	S72869	(transforming sequence, thyroid-1,	(transforming sequence, thyroid-1,
				DnaJ (Hsp40) homolog, subfamily A,	
555	39118 at	DNAJA1	690807	member 1	DNAJ homologue-2
<del></del>				DnaJ (Hsp40) homolog, subfamily A,	•
556	276 at	DNAJA1	L08069	member 1	DNAJ homologue-2
				DnaJ (Hsp40) homolog, subfamily B,	
557	41233_at	DNAJB6	AB014888	member 6	MRJ
				DnaJ (Hsp40) homolog, subfamily B,	
558	35799_at	DNAJB9	AL080081	member 9	hypothetical protein
				DnaJ (Hsp40) homolog, subfamily C,	!
559	36166_at	DNAJC8	AF083190	member 8	SPF31
				docking protein 1, 62kD (downstream of	
560	816 g at	DOK1	U70987	tyrosine kinase 1)	GAP binding protein p62dok
				docking protein 1, 62kD (downstream of	
561	34433_at	DOK1	AF035299	tyrosine kinase 1)	docking protein 1
				dolichyl-phosphate mannosyltransferase	
562	34879 at	DPM1	AF007875	polypeptide 1, catalytic subunit	dolichol monophosphate mannose synthase
563	38957 at	DCAMKL1	AB002367	doublecortin and CaM kinase-like 1	doublecortin and CaM kinase-like 1
		DSCR1	U85267	Down syndrome critical region gene 1	Down syndrome critical region protein 1
565	36088 at	DSCR2	AJ006291	Down syndrome critical region gene 2	leucine rich protein
566	35166 at	DSCR3	D87343	Down syndrome critical region gene 3	DCRA
				down-regulator of transcription 1, TBP-	TATA binding protein-associated
267	32621_at	DR1	M97388	binding (negative cofactor 2)	phosphoprotein
568	37981_at	DBN1	D17530	drebrin 1	drebrin E
				dual specific protein; Homo sapiens	
				tyrosine phosphatase (cdc14B) mRNA,	
569	40920_at	cdc14B	AF023158	complete cds.	tyrosine phosphatase
				dual specificity phosphatase 11	
570	39727_at	DUSP11	AF023917	(RNA/RNP complex 1-interacting)	PIR1
571	38272_at	DUSP14	AF038844	dual specificity phosphatase 14	MKP-1 like protein tyrosine phosphatase
				dual specificity phosphatase 3 (vaccinia	
572	41225_at	DUSP3	AL049417	virus phosphatase VH1-related)	
				1	

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573	41193_at	DUSP6	AB013382	dual specificity phosphatase 6	DOSP6
574	36946 at	DYRK1A	D86550	dual-specificity tyrosine-(Y)- phosphorylation regulated kinase 1A	serine/threonine protein kinase
	1512_at	DYRK1A	D86550	dual-specificity tyrosine-(Y)- phosphorylation regulated kinase 1A	serine/threonine protein kinase
3		מאפאט	V00216	dual-specificity tyrosine-(Y)-	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 isoform 1
0/0	/ou_ai	אייוס	012601	dual-specificity tyrosine-(Y)-	
577	39931_at	DYRK3	Y12735	phosphorylation regulated kinase 3	Dyrk3 protein
578	38368_at	DUT	U31930	dUTP pyrophosphatase	deoxyuridine nucleotidohydrolase
579	38475_at	DCTN2	U50733	dynactin 2 (p50)	dynamitin
580	34891_at	NIA	AI540958	dynein, cytoplasmic, light polypeptide	
581	34829_at	DKC1	U59151	dyskeratosis congenita 1, dyskerin	Cbf5p homolog
	10000	ř.	A CO07874	dystonia 1, torsion (autosomal dominant;	horsinA
7 <u>8</u> 6	32234_at	0111	Arun/0/1	distriction 1 (distrophin-associated	
583	36989 at	DAG1	L19711	dystrogrycair 1 (dystroprim associated dystroprotein 1)	dystroglycan
	ı			dystrophin (muscular dystrophy,	
584	40488_at	DMD	M18533	Duchenne and Becker types)	dystrophin
585	40106_at	E1B-AP5	AJ007509	E1B-55kDa-associated protein 5	E18-55kDa-associated protein
586	33354_at	SMURF2	AA630312	E3 ubiquitin ligase SMURF2	
587	40375 at	EGR3	X63741	early growth response 3	transcription factor
588	36135 at	EBNA18P2	U86602	EBNA1 binding protein 2	nucleolar protein p40
589	37730 at	p100	U22055	EBNA-2 co-activator (100kD)	100 kDa coactivator
590	33254_at	EVIS	AF008915	ecotropic viral integration site 5	EVI-5 homolog
				ectodermal-neural cortex (with BTB-like	
591	39542_at	ENC1	AF059611	domain)	nuclear matrix protein NRP/B
				ectonucleotide	
				pyrophosphatase/phosphodiesterase 2	•
592	41124_r_at	ENPP2	L35594	(autotaxin)	autotaxin
				ectonucleotide	
593	593 41123 s at	ENPP2	L35594	(autotaxin)	autotaxin
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CAN LL	7,000	EGF-containing fibulin-like extracellular	extracellular protein
594	594  32551_at	EFEMPI	1003877	mainx protein i	chiacolaiai Piotoli

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	A	8	ပ	O	Ш
595	36488_at	EGFLS	AB011542	EGF-like-domain, multiple 5	MEGF9
596	40509 at	ETFA	J04058	electron-transfer-flavoprotein, alpha polypeptide (qlutaric aciduria II)	electron transfer flavoprotein, alpha polypeptide
507	36881 at	FTFR	X71129	eta	electron transfer flavoprotein beta subunit
3				actor EF-1-alpha; Human	eukanotic translation elongation factor 1
598	1288 s at	  EEF1A	J04617	complete cds.	alpha 1
		EED	AF080227	embryonic ectoderm development	embryonic ectoderm development protein
				ems1 sequence (mammary tumor and	
009	600 39861 at	EMS1	M98343	(p80/85 src substrate)	amplaxin
				end of last exon based on GENSCAN	
				prediction presumably this gene and	
601	141478 at	dJ477H23.1	AL033538	match: ESTs: Em:AA354647	dJ477H23.1 (novel protein)
				endocytic receptor (macrophage mannose	
602	37408_at	ENDO180	AB014609	receptor family)	KIAA0709 protein
				endosome-associated FYVE-domain	
603	603 37914_at	ENDOFIN	AB002303	protein	endosome-associated FYVE-domain protein
604	604 39010_at	ENSA	AI658639	endosulfine alpha	
				endothelial differentiation,	
605	605 40387 at	EDG2	U80811	lysophosphalidic acid G-protein-coupled receptor, 2	lysophosphatidic acid receptor homolog
90	40074 00	נוטני	A 1005250	endothelial differentiation-related factor 1	endothelial differentiation-related factor 1
3	1001		2000	enhancer of rudimentary homolog	human protein homologous to DROER
607	607 39079_at	ERH	D85758	(Drosophila)	protein
809	608 2035 s at	ENO1	M55914	enolase 1, (alpha)	c-myc binding protein
609	609 34335 at	EFNB2	AI765533	ephrin-B2	
610	37731 at	FPS15	Z29064	epidermal growth factor receptor pathway substrate 15	epidermal growth factor receptor pathway substrate 15
				epidermal growth factor receptor pathway	epidermal growth factor receptor kinase
61	611 1467_at	EPS8	U12535	substrate 8	substrate
612	37762_at	EMP1	Y07909	epithelial membrane protein 1	progression associated protein
613	39631_at	EMP2	U52100	epithelial membrane protein 2	XMP

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				EPM1 disease gene; cysteine protease	
				inhibitor; Human cystatin B gene,	
614	35816_at	cystatin B	U46692	complete cds.	cystatin B
				erythrocyte membrane protein band 4.1-	
615	32585_at	EPB41L2		like 2	protein 4. I -G
616	38375_at	ESD	AF112219	esterase D/formylglutathione hydrolase	esterase D
				estrogen receptor binding site associated,	
617	38283_at	EBAG9	9	antigen, 9	EBAG9
618	37161_at		3	ESTs	
619	40885_s_at			ESTs	
620	33328	C1S	W28612	ESTs	
621	33453_at	ATP6S1	AI400326	ESTs	
622	31801_at		Al808712	ESTs	
623	41598_at		AA890010	ESTs	
				ESTs, Highly similar to RS21_HUMAN	
				40S RIBOSOMAL PROTEIN S21	
624	624 32744_at	RPS21	AI526078	[H.sapiens]	
				ESTs, Moderately similar to	
				ALU8_HUMAN ALU SUBFAMILY SX	
				SEQUENCE CONTAMINATION	
625	39750_at		W61005	WARNING ENTRY [H.sapiens]	
				ESTs, Moderately similar to	-
				GLK5_HUMAN GLUTAMATE	
	·		-	RECEPTOR, IONOTROPIC KAINATE 5	-
626	34906_g_at		AA977136	PRECURSOR [H.sapiens]	
				ESTs, Moderately similar to T46365	
_				hypothetical protein DKFZp434A1518.1	-
627	35787_at		AI986201	[H.sapiens]	
				ESTs, Weakly similar to 0903209A	
628	41463 at		AL042729	peptide PD,basic Pro rich [H.sapiens]	
				ESTs, Weakly similar to N-WASP	
629	41273_at		AL046940	[H.sapiens]	
630	38097_at	PIG8	AF010313	etoposide-induced mRNA	Pig8
3	631 40889 4 24	EEE1 A 1	W28170	eukaryotic translation elongation factor 1	
3	40000 I al	ובברואו	W20170	alpura i	

Fig 21

	A	В	C	O	IJ
				eukaryotic translation elongation factor 1	
632	632 35175_f_at	EEF1A2	X70940	alpha 2	elongation factor 1 alpha-2
Γ				eukaryotic translation elongation factor 1	
633	633 35748_at	EEF182	X60489	beta 2	elongation factor-1-beta
				eukaryotic translation elongation factor 1	
				delta (guanine nucleotide exchange	
634	634 41256_at	EEF10	Z21507	$\neg$	human elongation factor-1-delta
				eukaryotic translation elongation factor 1	
635	1676_s_at	EEF1G	M55409	gamma	pancreatic tumor-related protein
636	36587 at	EEF2	211692	eukaryotic translation elongation factor 2	human elongation factor 2
		FIESA	1 18060		protein synthesis factor
2	bb3_at	EIFIA	L1090U		de la companya de la
638	34278_at	EIF1A	L18960	eukaryotic translation initiation factor 1A	protein synthesis factor
			1	eukaryotic translation initiation factor 2,	eukaryotic translation initiation factor 2,
639	1154_at	EIF2S1	J02645	Subunit 1 (alpha, 35KD )	SUDUINI I (alpha, 30kD)
				eukaryotic translation initiation factor 2B,	eukaryotic translation initiation factor 28,
640	40515_at	EIF2B2	AF035280	subunit 2 (beta, 39kD)	subunit 2 (beta, 39kD)
		00011	10000	eukaryotic translation initiation factor 3,	T.G.E. hata recentor interacting profein 1
8	041 1044 at	E11332	030/04	Subdiff & (Deta, John)	
642	35327 at	EIF3S3	U54559	eukaryone translation illitiation racion 3, subunit 3 (gamma, 40kD)	translation initiation factor eIF3 p40 subunit
				eukaryotic translation initiation factor 3,	
643	32576_at	EIF3S5	U94855	subunit 5 (epsilon, 47kD)	translation initiation factor 3 47 kDa subunit
				eukaryotic translation initiation factor 3,	murine mammary tumor integration site 6
644	38681_at	EIF3S6	U62962	subunit 6 (48kD)	(oncogene homolog)
				eukaryotic translation initiation factor 3,	
645	35298_at	EIF3S7	U54558	subunit 7 (zeta, 66/67kD)	translation initiation factor eIF3 p66 subunit
				eukaryotic translation initiation factor 3,	
646	35323_at	EIF3S9	U78525	subunit 9 (eta, 116kD)	eukaryotic translation initiation factor
				eukaryotic translation initiation factor 4	
647	41785_at	EIF4G2	U73824	gamma, 2	p97
		() ()		eukaryotic translation initiation factor 4	
648	648 33907_at	E1F4G3	AF012072	gamma, 3	eir4Gii

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	٥	R	C	Q	Ш
649	649 1420 s at	EIF4A2		eukaryotic translation initiation factor 4A, isoform 2	eukaryotic initiation factor 4AII
6	27752 at	EIEAE	M15353	enkarvotic translation initiation factor 4E	cap-binding protein
	01105_at			Π	
651	35263_at	EIF4EBP2			
652		EIF5	U49436	ation initiation factor 5	translation initiation factor 5
653	37318 at	ETF1	X81625	eukaryotic translation termination factor 1	C11 protein
				excision repair cross-complementing	excision repair cross-complementing rodent
				ation	repair deficiency, complementation group 3
					(xeroderma pigmentosum group B
654	1885 at	ERCC3 .	M31899	B complementing)	complementing)
				excision repair cross-complementing	
			•	rodent repair deficiency, complementation	
				group 5 (xeroderma pigmentosum,	
				complementation group G (Cockayne	
655	2063_at	ERCC5	L20046	syndrome))	excision repair protein
			,	exons 1-4 beyond this clone; match:	dJ434O14.1 (Hydroxysteroid (11-beta)
929	33734_at	HSD11B1	AL022398	0172 P51975 Q29608	
657	222_at	EXT1	879639	exostoses (multiple) 1	exostoses (multiple) 1
	36526_at	EXTL2	AF000416	exostoses (multiple)-like 2	EXT-like protein 2
629	38809_s_at	EXTL3	AB011091	exostoses (multiple)-like 3	KIAA0519 protein
099	37729_at	XPO1	Y08614	exportin 1 (CRM1 homolog, yeast)	exportin 1
				exportin, tRNA (nuclear export receptor for	
661	38753_at	XPOT	AF039022	(RNAs)	exportin t
				extracellular matrix protein 2, female	
662	39673_i_at	ECM2	AB011792	organ and adipocyte specific	extracellular matrix protein
				extracellular matrix protein 2, female	
663	39674_r_at	ECM2	AB011792	organ and adipocyte specific	extracellular matrix protein
664	664 35226_at	EYA2	U71207	eyes absent homolog 2 (Drosophila)	Eab1
				family with sequence similarity 8, member	-
665	38318_at	FAM8A1	AL050128	Α1	
999	666 31879 at	FUBP3	U69127	far upstream element (FUSE) binding protein 3	FUSE binding protein 3
	10:0:0				

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T	C			larnesyl diphosphate synthase (famesyl	farnesyl diphosphate synthase (farnesyl
					pyrophosphate synthetase, dimethylallyltranstransferase.
722	2722E 24	ENPS	D14697		geranyltranstransferase)
	01050_at			nesyltransferase	
898	668 34848 at	FDFT1	X69141		farnesyl-diphosphate farnesyltransferase
699	1499 at	FNTA	L10413	farnesyltransferase, CAAX box, alpha	farnesyl-protein transferase alpha-subunit
		( ( ( ( ( ( ( ( ( ( ( ( ( ( ( ( ( ( ( (		Fas (TNFRSF6)-associated via death	mediator of receptor induced toxicity
670	38755_at	FAUD	X84/09	domain	וופחומנסן כו נספלינסן ווימפרים
				fasciculation and elongation protein zeta 1	יר נו
671	37743_at	FEZ1	U60060	(zygin I)	FE <b>6</b> 1
Γ				fasciculation and elongation protein zeta 2	
672	38651_at	FEZ2	U60061	(zygin II)	FEZ2
				FAT tumor suppressor homolog 1	
673	40454_at	FAT	X87241	(Drosophila)	homologue of Drosophila Fat protein
Γ				fatty-acid-Coenzyme A ligase, long-chain	
674	40082_at	FACL2	D10040	2	long-chain acyl-CoA synthetase
				fatty-acid-Coenzyme A ligase, long-chain	:
675	33880 at	FACL3	D89053	3	Acyl-CoA synthetase 3
				fatty-acid-Coenzyme A ligase, long-chain	
9/9	33881 at	FACL3	AA977580	3	
677	33360 at	FBXL11	AB023221	F-box and leucine-rich repeat protein 11	KIAA1004 protein
678	37205 at	FBXL7	AB020647	F-box and leucine-rich repeat protein 7	KIAA0840 protein
629	32854 at	FBXW1B	AB014596	F-box and WD-40 domain protein 1B	KIAA0696 protein
989	32169 at	FBX021	AB020682	F-box only protein 21	KIAA0875 protein
681	35337_at	FBXO7	AL050254	F-box only protein 7	hypothetical protein
				FBRNP; heterogeneous ribonucleoprotein homolog; This sequence comes from Fig. 3; D10S102=FBRNP [human, fetal brain,	
682	33817_at	D10S102	S63912		FBRNP
683	683 1877_g_at	niiH	HG1103-HT1103		dinitrogenase reductase
684	684 34678_at	FER1L3	AL096713	fer-1-like 3, myolerlin (C. elegans)	nypotnetical protein
900	2000	CABD1	A1701049	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	
82	32148 at	ונאטניו	21/01043		

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u	ı	Territin neavy chain	fetal Alzheimer antigen	fibrillin	fibroblast activation protein	•	keratinocyte growth factor	fibroblast growth factor receptor 1, isoform 1	precursor: fibroblast growth factor receptor	1. isoform 2 precursor; fibroblast growth	factor receptor 1, isoform 3 precursor;	fibroblast growth factor receptor 1, isoform 4	precursor; fibroblast growth factor receptor	1, isoform 5 precursor; fibroblast growth	factor receptor 1, isoform 6 precursor;	fibroblast growth factor receptor 1, isoform 7	precursor; fibroblast growth factor receptor	1, isoform 8 precursor; fibroblast gro	factor receptor 1, isoform 9 precursor	fibronectin 1, isoform 1 preproprotein;	fibronectin 1, isoform 2 preproprotein	fibronectin precursor	fibronectin leucine rich transmembrane	protein 2	fibulin-1D	UP50	beta-filamin		flavoprotein	Fln29	follistatin isoform FST317 precursor;	Collistatia isoform EST344 precureor
		ferritin, heavy polypeptide 1	fetal Alzheimer antigen	fibrillin 1 (Marfan syndrome)	fibroblast activation protein, alpha	fibroblast growth factor 7 (keratinocyte	growth factor)										fibroblast growth factor receptor 1 (fms-	related tyrosine kinase 2, Pfeitfer	syndrome)		fibronectin 1	fibronectin 1	fibronectin leucine rich transmembrane	protein 2	fibulin 1	fibulin 5	filamin B, beta (actin binding protein 278)	FK506 binding protein 9 (63 kD)	flavin containing monooxygenase 3	FLN29 gene product	follistatin precursor; Human follistatin	
C	٥	L20941	U05237	X63556	U09278		M60828			******									M34641		M10905	X02761		AB007865	U01244	AF093118	AF042166	AA487755	M83772	AB007447		
	מ	TH:	FALZ	FBN1	FAP		FGF7												FGFR1		FN1	FN1		FLRT2	FBLN1	FBLN5	FLNB	FKBP9	FM03	FLN29		i
	A	33943_at	41091 at	7	16		1380_at											•	2057 g at		31720 s at	31719 at		34853_at	38026 at	39038_at	38078 at	698 38761 s at	699 40665 at	700 35254 at		
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Fig 21

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				forkhead (Drosophila)-like 7; FREAC3; Homo sapiens forkhead/winged helix-like	
702	41027 at	FKHL7	AF078096		forkhead/winged helix-like transcription factor 7
703	36319_at	FOXF2	U13220	F2	forkhead protein FREAC-2
704	40570 at	FOX01A	AF032885	forkhead box O1A (rhabdomyosarcoma)	forkhead protein
	34740_at	FOXO3A	AF032886		forkhead protein
	32542_at	FHL1	AF063002	four and a half LIM domains 1	LIM protein SLIMMER
707	38422_s_at	FHL2	U29332	four and a half LIM domains 2	heart protein
8	708 41649 at	FHX	AF038177	FOXJ2 forkhead factor	
18	709 34997_r_at	FZDS	U43318	frizzled homolog 5 (Drosophila)	transmembrane receptor
9	34472_at	FZD6	AB012911	frizzled homolog 6 (Drosophila)	Frizzled-6
=	33222_at	FZD7	AB017365	frizzled homolog 7 (Drosophila)	frizzled-7
12	38923_at	FRG1	L76159	FSHD region gene 1	FSHD region gene 1
13	713 38139_at	FPGT	AF017445	fucose-1-phosphate guanylyttransferase	GDP-L-fucose pyrophosphorylase
14	714 41814_at	FUCA1	M29877	fucosidase, alpha-L- 1, tissue	fucosidase, alpha-L- 1, tissue
				Fukuyama type congenital muscular	
15	715 40022_at	FCMD	AB008226	dystrophy (fukutin)	fukutin
띩	716 32546_at	H	U59309	fumarate hydratase	fumarase precursor
717	36145_at	SIAHBP1	U51586	fuse-binding protein-interacting repressor	siah binding protein 1
1 :		i i	0007		NOT SECULD TO SECULD TO SECULD TO SECULD TO SECULD TO SECULD TO SECULD TO SECULD TO SECULD TO SECULD TO SECULD TO SECULD TO SECURD TO SECULD TO SECURD TO SE
2	718 40480_s_at	TYN	M14333	FIN oncogene related to Sho, Fan, 153	TIN OILCOGRIBE TERRIED TO STO, TOTA, TES
719	2039_s_at	FYN	M14333	FYN oncogene related to SRC, FGR, YES	FYN oncogene related to SRC, FGR, YES FYN oncogene related to SRC, FGR, YES
720	34288_at	RDC1	U67784	G protein-coupled receptor	orphan G protein-coupled receptor
721	37308_at	GPR107	AI888084	G protein-coupled receptor 107	
722	37298_at	GABARAP	AF044671	GABA(A) receptor-associated protein	MM46
723	35785 at	GABABAPL1	W28281	GABA(A) receptor-associated protein like	
l				GABA(A) receptor-associated protein-like	
724	724 35767_at	GABARAPL2	AI565760	2	
725	37825_at	GALK2	M84443	galactokinase 2	galactokinase
128	37742_at	GLB1	M34423	galactosidase, beta 1	galactosidase, beta 1

	A	В.	3	Q	ш
				lase,	
727	37263_at	авн	U55206		human gamma-glutamyl hydrolase
				orotein, alpha 1, 43kD	•
728	32531_at	GJA1	X52947	Ì	connexin 43
				GCN1 general control of amino-acid	
729	36603_at	GCN1L1	D86973	synthesis 1-like 1 (yeast)	
730		GDI2	Y13286	GDP dissociation inhibitor 2	GDP dissociation inhibitor beta
				gene predicted from cDNA with a	gene predicted from cDNA with a complete
731	39386_at	KIAA0110	D14811		coding sequence
				riants near HD	gene with multiple splice variants near HD
732	32180_s_at	RES4-22	AB000461	locus on 4p16.3	locus on 4p16.3
					Bruton's tyrosine kinase-associated protein-
733	466_at	GTF2I	U77948	general transcription factor II, i	135
734	35450 s at	GTF2I	AF015553	general transcription factor II, i	TFII-I protein
				general transcription factor IIA, 2 (12kD	
735	37010_at	GTF2A2	A1203737	subunit)	
				general transcription factor IIA, 2 (12kD	
736	869_at	GTF2A2	U14193	subunit)	transcription factor IIA small 12 kDa subunit
				general transcription factor IIE,	
737	37882_at	GTF2E1	X63468	polypeptide 1 (alpha subunit, 56kD)	TFIIE-alpha
				general transcription factor IIE,	
738	37295_at	GTF2E2	X63469	polypeptide 2 (beta subunit, 34kD)	TFIIE-beta
				general transcription factor IIH,	
739	38782_at	GTF2H1	M95809	polypeptide 1 (62kD subunit)	basic transcription factor 62kD subunit
				general transcription factor IIH,	
740	40754_at	GTF2H3	Z30093	polypeptide 3 (34kD subunit)	basic transcription factor 2, 35 KD subunit
741	36188 at	GTF3A	D32257	general transcription factor IIIA	Xenopus transcription factor IIIA homologue
742		GGPS1	AB019036	geranylgeranyl diphosphate synthase 1	geranylgeranyl pyrophosphate synthase
743	763 at	GMFB	AB001106	glia maturation factor, beta	glia maturation factor
744	39793_at	GBAS	AF029786	glioblastoma amplified sequence	GBAS
L				glucan (1,4-alpha-), branching enzyme 1	
				(glycogen branching enzyme, Andersen	
				disease, glycogen storage disease type	
745	32643_at	GBE1	L07956	V)	1,4-alpha-glucan branching enzyme
746	746 34332_at	GNPI	D31766	glucosamine-6-phosphate isomerase	glucosamine-6-phosphate isomerase

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				glucosaminyl (N-acetyl) transferase 1,	
				core 2 (beta-1,6-N-	
747	38218_at	GCNT1	M97347	acetylglucosaminyltransterase)	Deta-1,6-N-acetyigiucosaminyiiransierase
748	39122_at	GPI	K03515	glucose phosphate isomerase	neuroleukin
	at	GRP58	Z49835	glucose regulated protein, 58kD	protein disulfide isomerase
		GePD	X03674	glucose-6-phosphate dehydrogenase	glucose-6-phosphate dehydrogenase
751		GUSB	M15182	glucuronidase, beta	glucuronidase, beta
_		GLUD1	M20867	glutamate dehydrogenase 1	glutamate dehydrogenase 1
753	35485 at	GRM4	X80818	glutamate receptor, metabotropic 4	metabotropic glutamate receptor type 4
				glutamate-ammonia ligase (glutamine	:
754	40522_at	GLUL	X59834	synthase)	glutamateammonia ligase
				glutamate-cysteine ligase, catalytic	
755	31850_at	GCLC	M90656	subunit	gamma-glutamylcysteine synthetase
				glutamate-cysteine ligase, modifier	gamma-glutamylcysteine synthetase light
756	33163_r_at	GCLM	L35546	subunit	subunit
				glutamic-oxaloacetic transaminase 1,	
757	35343_at	GOT1	M37400	soluble (aspartate aminotransferase 1)	aspartate aminotransferase 1
				glutamic-oxaloacetic transaminase 2,	,
				mitochondrial (aspartate aminotransferase	_
758	758 40764 at	GOT2	M22632	2)	aspartate aminotransferase 2 precursor
759	34719 at	GLS	AB020645	glutaminase	KIAA0838 protein
				glutamine-fructose-6-phosphate	glutamine:fructose-6-phosphate
760	32626 at	GFPT1	M90516	transaminase 1	amidotransferase
				glutamine-fructose-6-phosphate	Glutamine:fructose-6-phosphate
761	39640 at	GFPT2	AB016789	transaminase 2	amidotransferase
762	35300 at	EPRS	X54326	glutamyl-prolyl-tRNA synthetase	glutaminyl-tRNA synthetase
763	34311 at	GLRX	X76648	glutaredoxin (thioltransferase)	glutaredoxin
764	37033 s at	GPX1	X13710	glutathione peroxidase 1	
765	40508 at	GSTA4	AF025887	glutathione S-transferase A4	glutathione S-transferase A4-4
766	38386 r at	GSS	U34683	glutathione synthetase	glutathione synthetase
				glutathione-S-transferase like; glutathione	
767	824_at	GSTTLp28	U90313	transferase omega	glutathione-S-transferase homolog
				glyceraldehyde-3-phosphate	
768	AFFX-HUMGAP(GAPD	)(GAPD	M33197	dehydrogenase	glyceraldehyde-3-phosphate dehydrogenase
-		0	2000	glyceraldehyde-3-phosphate	
769	769 35905_s_at	GAPD	034995	denyarogenase	

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				glyceraldehyde-3-phosphate	
770	AFFX-HUMGAPIGAPD	GAPD	M33197	dehydrogenase	glyceraldehyde-3-phosphate dehydrogenase
77.	30303 31	GNPAT	A.1002190	olyceronephosphate O-acyltrans/erase	dihydroxyacetone phosphate acytransferase
	2000 - at			alycine cleavade system protein H	alveine cleavage system protein H
772	37357 at	GCSH	D00723	(aminomethyl carrier)	(aminomethyl carrier)
773		GLRB	U33267	glycine receptor, beta	glycine receptor beta subunit
774		GSK3B	L33801	glycogen synthase kinase 3 beta	protein kinase
775		GYG	U31525	glycogenin	glycogenin
776		GYG2	U94362	glycogenin 2	glycogenin-2 alpha
777		GPNMB	X76534	glycoprotein (transmembrane) nmb	glycoprotein (transmembrane) nmb
778	778 37251_s_at	GPM6B	AF016004	glycoprotein M6B	
779		AD-017	L13435	glycosyltransferase AD-017	
780	780 36582 g at	GARS	U09510	glycyl-tRNA synthetase	glycyl-tRNA synthetase
781	781 36581 at	GARS	U09510	glycyl-tRNA synthetase	glycyl-tRNA synthetase
782	782 36201 at	GL01	D13315	glyoxalase I	lactoyl glutathione lyase
				glyoxylate reductase/hydroxypyruvate	
783	783 40133 s at	GRHPR	W28944	reductase	
	1				guanine nucleotide binding protein (G
					protein), alpha stimulating activity
					polypeptide 1, isoform alpha-s-2;
					neuroendocrine secretory protein 55;
					guanine nucleotide binding protein (G
					protein), alpha stimulating activity
				•	polypeptide 1, isoform XL-alpha-s; guanine
	-				nucleotide binding protein (G protein), alpha
					stimulating activity polypeptide 1, isoform
784	784 37449 i at	GNAS	X04409	GNAS complex locus	alpha-s-1
785	785 37448 s at	GNAS	X56009	GNAS complex locus	alpha subunit of GsGTP binding protein

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786	786 37450_r_at	GNAS	X04409	GNAS complex locus	guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-2; neuroendocrine secretory protein 55; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform XL-alpha-s; guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1, isoform alpha-s-1
787	37959_at	GGA3	D63876	golgi associated, gamma adaptin ear containing, ARF binding protein 3	ADP-ribosylation factor binding protein 3, isoform short; ADP-ribosylation factor binding protein 3, isoform long
788	788 32713_at	GOLGA1	U51587	χa,	Golgi complex autoantigen golgin-97
790	789 32150_at	GOLGA4	X82834 AF020762	golgi autoantigen, golgin subramily a, 4 dolai phosphoprotein 1	256 KD golgin unknown protein
791	38620 at	GOSR2	AA905543	golgi SNAP receptor complex member 2	
792	34737 at	GOLTC1	AF058718	golgi transport complex 1 (90 kD subunit)	putative 13 S Golgi transport complex 90kD subunit brain-specific isoform
793	793 41767_r_at	KIAA0855	AB020662	golgin-67	KIAA0855 protein
794	36950_at	HSGP25L2G	X90872	gp25L2 protein	
795	36035 at	GPAA1	AB002135	GPAA1P anchor attachment protein 1 homolog (yeast)	glycosylphosphatidylinositol anchor attachment 1 (GPAA1)
796	32595_at	GRSF1	U07231	G-rich RNA sequence binding factor 1	G-rich sequence factor-1
797	39822_s_at	GADD45B	AF078077	growth arrest and DNA-damage-inducible, beta	growth arrest and DNA-damage-inducible protein GADD45beta
798	39821 s at	GADD45B	N95168	growth arrest and DNA-damage-inducible, beta	
799		GAS1	L13698	growth arrest-specific 1	growth arrest-specific 1
800	41839_at	GAS1	L13698	growth arrest-specific 1	growth arrest-specific 1
801	37658_at	GAS6	L13720	growth arrest-specific 6	growth-arrest-specific protein
802	_	GAS6	L13720	growth arrest-specific 6	growth-arrest-specific protein
803	37615_at	GRB10	D86962	growth factor receptor-bound protein 10	growth factor receptor-bound protein 10
804	804 41752_at	GHITM	W28190	growth hormone inducible transmembrane protein	

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	А	В	S	O	U
805	160030_at	GHR	X06562	growth hormone receptor	growth hormone receptor
-	40113_at	GS3955	D87119	GS3955 protein	GS3955
				GTP binding protein overexpressed in	
807	37279_at	GEM	U10550	skeletal muscle	Gem
				guanine nucleotide binding protein (G	
				protein), alpha inhibiting activity	
808	33809_at	GNAI1	AL049933	polypeptide 1	hypothetical protein
				guanine nucleotide binding protein (G	guanine nucleotide binding protein (G
-				protein), alpha inhibiting activity	protein), alpha inhibiting activity polypeptide
808	37307_at	GNAI2	X04828	polypeptide 2	2
				guanine nucleotide binding protein (G	
810	34608 at	GNB2L1	M24194	protein), beta polypeptide 2-like 1	MHC B complex protein 12.3
				guanine nucleotide binding protein (G	
811	35272_at	GNG5	AI541042	protein), gamma 5	
812	37735_at		U31383	guanine nucleotide binding protein 10	G protein gamma-10 subunit
				guanylate binding protein 1, interferon-	
813	35735_at	GBP1	M55542	inducible, 67kD	guanylate binding protein isoform l
814	814 905_at		L76200	guanylate kinase 1	guanylate kinase
815	815 32249_at		M65292	H factor (complement)-like 1	factor H homologue
816	816 32250_at	Ŧ.	X07523	H factor 1 (complement)	complement factor H
				H.sapiens ACTH-R gene for	candidate adrenocorticotropic hormone
817	817 420_at	ACTH-R	X65633	adrenocorticotropic hormone receptor.	receptor
818	818 31673_s_at	cell adhesion regu	gu X65784	H.sapiens CAR gene.	cell matrix adhesion regulator
819	37003 at	CD63; MLA1; ME4	E4X62654	H.sapiens gene for Me491/CD63 antigen. ME491 /CD63 antigen	ME491 /CD63 antigen
6	20070		.h. Y60007	H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form)	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 1
020		5			
821	35125_at	hrp S6	X67309	H.sapiens gene for ribosomal protein S6.	ribosomal protein S6
822	34646_at	rpS7	Z25749	H.sapiens gene for ribosomal protein S7.	ribosomal protein S7
823	823 31510_s_at	hH3.3B	248950	H.sapiens hH3.3B gene for histone H3.3.	histone H3.3

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Artogenase B gene 1.27) (and joined 1.27) (and joined 1.27) (and joined 1.27) (and joined I.27) (and j				4999		
H.sapiens lactate dehydrogenase B gene awon 1 and 2 (EC 1.1.27) (and joined 2.3819_at ldhB	Γ	A	В	ပ	O	ш
12820_g at   1dhB	T				H.sapiens lactate dehydrogenase B gene	
1419					exon 1 and 2 (EC 1.1.1.27) (and joined	-
H.sapiens lactate dehydrogenase B gene	824	33820_g_at	IdhB	X13794	CDS).	lactate dehydrogenase B
Sab	Γ				H.sapiens lactate dehydrogenase B gene	
33819_at         IdhB         X13794         CDS)           34787_at         ORF1         X93209         H.saplens mRNA for NRD1 convertase.           36012_at         PIBF1         Y09631         Complete.           31526_1_at         tre         X63547         213).           40471_at         PxF         Y09048         H.saplens PXMP1 gene.           37038_at         pxF         Y09048         H.saplens PXMP1 gene.           31583_at         pxF         X09048         H.saplens PXMP1 gene.           31583_at         pxF         X09048         H.saplens pxMP1 gene.           31583_at         pxRP         X02419         H.saplens pxRP1 gene.           31583_at         pxRPAR         X67247         S8           31583_at         pxRAP         X62554         protein.           31830_at         pxRAP         X62554	_				exon 1 and 2 (EC 1.1.1.27) (and joined	
34787_at         ORF1         X93209         H.sapiens mRNA for NRD1 convertase.           36012_at         PIBF1         Y09631         complete.           36012_at         Ite         X63547         213).           31526_1at         Ite         X63547         213).           3153_at         PxF         Y09048         H.sapiens mRNA for fre oncogene (clone H.sapiens mRNA for tre oncogene (clone H.sapiens mRNA for machina for treatment in the machina for treatment in the machina for treatment in the machina for machina fo	825	33819 at	ldhB	X13794	CDS).	lactate dehydrogenase B
36012_at         PIBF1         Y09631         H.sapiens mRNA for PIBF1 protein.           31526_f_at         tre         X63547         213           40471_at         PxF         Y09048         H.sapiens PXMP for tre oncogene (clone 14.sapiens PXMP for tre oncogene (clone 14.sapiens PXMP for tre oncogene (clone 15.sapiens PXMP f	928	34787 at	ORF1	X93209	H.sapiens mRNA for NRD1 convertase.	NRD1 convertase
36012_at         PIBF1         Y09631         complete.           31526_1_at         tre         X63547         H.sapiens mRNA for tre oncogene (clone)           31526_1_at         tre         X63547         H.sapiens PXMP1 gene, exon 1 (and H.sapiens PXMP1 gene, exon 1 (and H.sapiens PXMP1 gene, exon 1 (and H.sapiens PXMP1 gene, exon 1 (and H.sapiens PXMP1 gene, exon 1 (and H.sapiens pXMP1 gene, exon 1 (and H.sapiens pXMP1 gene, exon 1 (and H.sapiens pXMP1 gene, exon 1 (and H.sapiens pXMP1 gene, exon 1 (and H.sapiens pXMP1 gene, exon 1 (and H.sapiens pXMP1 gene, exon 1 (and H.sapiens pXMP1 gene, exon 1 (and H.sapiens pXMP1 gene, exon 1 (and H.sapiens pXMP1 gene, exon 1 (and H.sapiens pXMP1 gene, exon 1 (and H.sapiens pXMP1 gene, exon 1 (and H.sapiens pXMP1 gene, exon 1 (and H.sapiens pXMP1 gene, exon 1 (and M.sapiens pXMP1 gene, exon 1 (and H.sapiens pXMP1	Ī				H.sapiens mRNA for PIBF1 protein,	
H. Sapiens mRNA for tre oncogene (clone		36012_at	PIBF1	Y09631	complete.	PIBF1 protein
at bree         X63547         213).           PxF         Y09048         H.sapiens PxF gene.           PXMP1         X83467         H.sapiens PXMP1 gene, exon 1 (and H.sapiens PXMP1 gene, exon 1 (and H.sapiens PXMP1 gene, exon 1 (and H.sapiens PXMP1 gene, exon 1 (and H.sapiens PXMP1 gene, exon 1 (and H.sapiens PXMP1 gene, exon 1 (and H.sapiens PXMP1 gene, exon 1 (and H.sapiens PXMP1 gene, exon 1 (and H.sapiens PXMP1 gene, exon 1 (and H.sapiens PXMP1 gene for ribosomal protein           t         PX82554         H.sapiens SPHAR gene for ryclin-related protein.           t         H2AFL         U90551         H.sapiens SPHAR gene for cyclin-related protein.           t         H2AFL         U90551         H.sapiens SPHAR gene for cyclin-related protein.           t         H2AFL         U90551         H.sapiens SPHAR gene for cyclin-related protein.           t         H2AFL         U90551         H.sapiens SPHAR gene for cyclin-related protein.           t         H2AFL         U90551         H.sapiens SPHAR gene for cyclin-related protein.           t         H2AFL         U90551         H.Sapiens SPHAR gene for cyclin-related protein.           t         H2AFL         U90551         H.Sapiens SPHAR gene for cyclin-related protein.           t         H3FBL         A4049623         H.Zh birding factor.           t         HSPE1         A1912041         10)					H.sapiens mRNA for tre oncogene (clone	
PxF         Y09048         H.sapiens PxF gene.           PXMP1         X83467         joined CDS).           hpS8         X67247         S8.           th sapiens SPHAR gene for ribosomal protein         H.sapiens SPHAR gene for cyclin-related protein.           th SPHAR         X82554         H.sapiens SPHAR gene for cyclin-related protein.           th SPHAR         X82554         H.sapiens SPHAR gene for cyclin-related protein.           th WARL         X02419         H.sapiens syndecan-1 gene (exons 2-5).           th H2AFL         U90551         H.sapiens uPA gene.           th H2AFL         M37583         H.sapiens uPA gene.           th H2AFL         M37583         H.2A histone family, member L.           th H2AFL         A1688098         H2B histone family, member C.           th H4FG         AA255502         H4 histone family, member C.           th H5FA         AA255502         H4 histone family, member G.           th H5PA         AL049996         HOCMA18P protein           th H5PA         AL049996         HDCMA18P protein           th H5PA         AL049996         Ha histone family, member G.           th H5PA         AL049996         Ha histone family, member G.           th H5PA         AL049996         Ha histone family, member G. </td <td>828</td> <td></td> <td>tre</td> <td>X63547</td> <td>213).</td> <td>oncogene</td>	828		tre	X63547	213).	oncogene
H.sapiens PXMP1 gene, exon 1 (and poined CDS).	829	40471_at	PxF	Y09048	H.sapiens PxF gene.	PxF protein
37038_at         PXMP1         X83467         joined CDS).           31583_at         rpS8         x67247         S8           1685_at         SPHAR         x67247         S8           1685_at         SPHAR         x62554         protein.           1685_at         SPHAR         x62554         protein.           1685_at         SPHAR         x62554         protein.           34308_at         HZAFL         U90551         H sapiens syndecan-1 gene (exons 2-5). granter           34308_at         HZAFL         U90551         H sapiens uPA gene.           34308_at         HZAFL         U90551         H sapiens uPA gene.           34308_at         HZAFL         U90551         H sapiens lamily, member L           35337_at         HAZAF         M37583         H2A histone family, member L           40818_at         LOC51580         D14041         H-2K binding factor-2           254_at         HAFG         AA255502         H4 histone family, member L           40818_at         HCDI         AA255502         H4 histone family, member L           35251_at         HCDI         AA255502         H4 histone family           39353_at         HSPE1         AL049996         HOCMA18P protein <td></td> <td></td> <td></td> <td></td> <td>H.sapiens PXMP1 gene, exon 1 (and</td> <td>70kD peroxisomal integral membrane</td>					H.sapiens PXMP1 gene, exon 1 (and	70kD peroxisomal integral membrane
31583_at         pS8         X67247         S8           1685_at         SPHAR         X82554         H.sapiens SPHAR gene for cyclin-related by protein.           1685_at         SPHAR         X82554         protein.           38127_at         syndecan-1         Z48199         H.sapiens SPHAR gene for cyclin-related by protein.           37310_at         uPA         X02419         H.sapiens syndecan-1 gene (exons 2-5). syndecan-1 gene (exons 2-5	830	37038_at	PXMP1	X83467	joined CDS).	protein
31583_at         rpS8         X67247         S8           1685_at         SPHAR         X82554         H.sapiens SPHAR gene for cyclin-related         1685_at           38127_at         Syndecan-1         Z48199         H.sapiens syndecan-1 gene (exons 2-5).         37310_at           37310_at         UPA         WOZ419         H.sapiens syndecan-1 gene (exons 2-5).         183330_at           34308_at         H2AFL         U90551         H.sapiens syndecan-1 gene (exons 2-5).         183330_at           39337_at         H2AFL         U90551         H2A histone lamily, member L         183458_L           39337_at         H2AFL         Al688098         H2B histone lamily, member L         183458_L           40818_at         LOC51580         D14041         H-2K binding factor-2         18353_A           254_at         H3F3A         M11353         H3 histone family, member L         18353_A           39969_at         HCDI         HCMA18P protein         1 (chaperonin)         1 (chaperonin)           39515_at         HCDI         HCMA18P protein         1 (chaperonin)           3953_at         HSPE1         M22362         Ha histone family, member L           3953_at         HSPE1         AL049996         HOCMA18P           HSPD1					H.sapiens rpS8 gene for ribosomal protein	
1685_at         SPHAR         X82554         H.sapiens SPHAR gene for cyclin-related           38127_at         syndecan-1         Z48199         H.sapiens syndecan-1 gene (exons 2-5).           37310_at         uPA         X02419         H.sapiens syndecan-1 gene (exons 2-5).           34308_at         H2AFL         U90551         H2A histone family, member L           39337_at         H2AFZ         M37583         H2A histone family, member L           40818_at         LOC51580         D14041         H-2K binding factor-2           254_at         H3F3A         M11353         H3 histone family, member L           40818_at         LOC51580         D14041         H-2K binding factor-2           254_at         H4FG         AA255502         H4 histone family, member L           39969_at         HCDI protein         HOCMA18P protein           32591_at         HCDI         HCDI protein           39553_at         HSPE1         AL049996         HDCMA18P protein           39553_at         HSPE1         M22382         heat shock 60kD protein 1 (chaperonin)           36514_at         HSPA5         X87949         regulated protein, 78kD)           41510_s_at         HSPA5B         L15189         heat shock 70kD protein 98 (mortalin-2)		31583 at	mS8	X67247	58.	ribosomal protein S8
1685_at         SPHAR         X82554         protein.           38127_at         syndecan-1         Z48199         H.sapiens syndecan-1 gene (exons 2-5).           37310_at         uPA         X02419         H.sapiens uPA gene.           34308_at         HZAFL         U90551         H.sapiens uPA gene.           34308_at         HZAFZ         M37583         H2A histone family, member L           33458_r_at         HZBFL         A1688098         H2A histone family, member L           40818_at         LOC51580         D14041         H-ZK binding factor-2           254_at         H3F3A         M11353         H3 histone family, member L           3969_at         H4FG         AA255502         H4 histone family, member G           35215_at         HCDI         AI194623         HCDI protein           35215_at         HCDI         AI494623         HCDI protein           37720_at         HSPE1         AI049996         HDCMA18P protein         I (chaperonin)           36614_at         HSPA5         X87949         regulated protein, 78kD)					H. sapiens SPHAR gene for cyclin-related	
38127_at         syndecan-1         Z48199         H.sapiens syndecan-1 gene (exons 2-5).           37310_at         uPA         X02419         H.sapiens uPA gene.           34308_at         H2AFL         U90551         H2A histone family, member L           39337_at         H2AFZ         M37583         H2A histone family, member L           40818_at         H2AFZ         A1688098         H2B histone family, member L           254_at         H3F3A         M11353         H3 histone family, member L           254_at         H4FG         AA255502         H4 histone family, member L           39969_at         H4FG         AA255502         H4 histone family, member L           32591_at         HCDI         AL049996         H4 histone family, member L           35215_at         HCDI         AL049996         H4 histone family, member L           35215_at         HCDI         AL049996         HCDI protein           37720_at         HSPD1         AL049996         HDCMA18P protein           37720_at         HSPD1         M22382         heat shock 70kD protein 5 (glucose-regulated protein, 78kD)           36614_at         HSPA5         X87949         regulated protein, 78kD)	832		SPHAR	X82554	protein.	S-phase response (cyclin-related)
38127_at         syndecan-1         248199         H.sapiens syndecan-1 gene (exons 2-5).         33127_at         H2AFL         202419         H sapiens uPA gene.         1           34308_at         H2AFL         U90551         H2A histone family, member L         1           39337_at         H2AFZ         M37583         H2A histone family, member L           33458_r_at         H2BFL         Al688098         H2B histone family, member L           40818_at         LOC51580         D14041         H-2K binding factor-2           254_at         H3F3A         M11353         H3 histone family, member L           3969_at         H4FG         AA255502         H4 histone family, member G           32591_at         HCDI         AL049996         HCDI protein           35215_at         HDCMA18P         AL049996         HDCMA18P protein           35215_at         HDCMA18P         AL049996         HDCMA18P protein           37720_at         HSPD1         M22382         heat shock 70kD protein 1 (chaperonin)           36614_at         HSPA5         X87949         regulated protein, 78kD)						•
37310_at         uPA         X02419         H.sapiens uPA gene.           34308_at         H2AFL         U90551         H2A histone family, member L           39337_at         H2AFZ         M37583         H2A histone family, member Z           33458_r_at         H2BFL         Al688098         H2B histone family, member L           40818_at         LOC51580         D14041         H-2K binding factor-2           254_at         H3F3A         M11353         H3 histone family, member L           3969_at         H4FG         AA255502         H4 histone family, member C           32591_at         HCDI         AI494623         HCDI protein           35215_at         HDCMA18P         AL049996         HDCMA18P protein           35215_at         HDCMA18P         AL049996         HDCMA18P protein           35215_at         HDCMA18P         AL049996         HDCMA18P protein           35215_at         HSPD1         M22382         heat shock 10kD protein 1 (chaperonin)           36614_at         HSPA5         X87949         regulated protein, 78kD)	833	38127_at	syndecan-1	Z48199	H.sapiens syndecan-1 gene (exons 2-5).	syndecan 1
34308_at         H2AFL         U90551         H2A histone family, member L           39337_at         H2AFZ         M37583         H2A histone family, member Z           33458_r_at         H2BFL         Al688098         H2B histone family, member L           40818_at         LOC51580         D14041         H-2K binding factor-2           254_at         H3F3A         M11353         H3 histone, family, member L           3969_at         H4FG         AA255502         H4 histone family, member G           32591_at         HCDI         AA255502         H4 histone family, member G           35215_at         HDCMA18P         AL049996         HCDI protein         (Apack Gold Drotein 1 (chaperonin)           37720_at         HSPD1         M22382         heat shock 70kD protein 5 (glucose-regulated protein, 78kD)           36614_at         HSPA5         X87949         regulated protein, 78kD)	834	37310_at	uPA	X02419	H.sapiens uPA gene.	urokinase-plasminogen activator
39337_at         H2AFZ         M37583         H2A histone family, member Z           33458_r_at         H2BFL         Al688098         H2B histone family, member L           40818_at         LOC51580         D14041         H-2K binding factor-2           254_at         H3F3A         M11353         H3 histone, family, member G           39969_at         H4FG         AA255502         H4 histone family, member G           32591_at         HCDI         AI494623         HCDI protein           35215_at         HDCMA18P         AL049996         HDCMA18P protein           35215_at         HDCMA18P         AL049996         HDCMA18P protein           35215_at         HDCMA18P         AL049996         HDCMA18P protein           35215_at         HSPE1         AI912041         10)           37720_at         HSPD1         M22382         heat shock 60kD protein 1 (chaperonin)           41510_s_at         HSPA5         X87949         regulated protein, 78kD)           A1510_s_at         HSPA9B         L15189         heat shock 70kD protein 9B (mortalin-2)	835	34308_at	HZAFL	U90551	H2A histone family, member L	histone 2A-like protein
3345B r at         H2BFL         Al688098         H2B histone family, member L           4081B_at         LOC51580         D14041         H-2K binding factor-2           254_at         H3F3A         M11353         H3 histone, family 3A           3969_at         H4FG         AA255502         H4 histone family, member G           32591_at         HCDI         AA265502         H4 histone family, member G           35215_at         HCDI         AA265502         H4 bistone family, member G           35215_at         HCDI         AA265502         H4 bistone family, member G           35215_at         HCDI         AA265502         H4 bistone family, member G           35215_at         HCDI         AL049996         HCDI protein           39353_at         HSPE1         AI912041         10)           37720_at         HSPD1         M22382         heat shock 70kD protein 5 (glucose-regulated protein, 78kD)           36614_at         HSPA5         X87949         regulated protein, 78kD)           41510_s_at         HSPA9B         L15189         heat shock 70kD protein 9B (mortalin-2)	836	39337 at	H2AFZ	M37583	H2A histone family, member Z	H2A histone family, member Z
40818_at         LOC51580         D14041         H-2K binding factor-2           254_at         H3F3A         M11353         H3 histone, family 3A           3969_at         H4FG         AA255502         H4 histone family, member G           32591_at         HCDI         AI494623         HCDI protein           35215_at         HDCMA18P         AL049996         HDCMA18P protein           39353_at         HSPE1         AI912041         10)           37720_at         HSPD1         M22382         heat shock 60kD protein 1 (chaperonin)           36614_at         HSPA5         X87949         regulated protein, 78kD)           41510_s_at         HSPA9B         L15189         heat shock 70kD protein 9B (mortalin-2)	837	33458	H2BFL	AI688098	H2B histone family, member L	
254_at         H3F3A         M11353         H3 histone, family 3A           39969_at         H4FG         AA255502         H4 histone family, member G           32591_at         HCDI         AI494623         HCDI protein           35215_at         HDCMA18P         AL049996         HDCMA18P protein           39353_at         HSPE1         AI912041         10)           37720_at         HSPD1         M22382         heat shock 60kD protein 1 (chaperonin)           36614_at         HSPA5         X87949         regulated protein, 78kD)           41510_s_at         HSPA9B         L15189         heat shock 70kD protein 9B (mortalin-2)	838	40818	LOC51580	D14041	H-2K binding factor-2	H-2K binding factor-2
39969_at         H4FG         AA255502         H4 histone family, member G           32591_at         HCDI         AI494623         HCDI protein           35215_at         HDCMA18P         AL04996         HDCMA18P protein           39353_at         HSPE1         AI912041         10)           37720_at         HSPD1         M22382         heat shock 60kD protein 1 (chaperonin)           36614_at         HSPA5         X87949         regulated protein, 78kD)           41510_s_at         HSPA9B         L15189         heat shock 70kD protein 9B (mortalin-2)	839	254 at	H3F3A	M11353	H3 histone, family 3A	H3 histone, family 3A
32591_at         HCDI         A1494623         HCDI protein           35215_at         HDCMA18P         AL04996         HDCMA18P protein           39353_at         HSPE1         A1912041         10)           37720_at         HSPD1         M22382         heat shock 60kD protein 1 (chaperonin)           36614_at         HSPA5         X87949         regulated protein, 78kD)           41510_s_at         HSPA9B         L15189         heat shock 70kD protein 9B (mortalin-2)	840	39969	H4FG	AA255502	H4 histone family, member G	
35215_at         HDCMA18P         AL04996         HDCMA18P protein           39353_at         HSPE1         Al912041         10)           37720_at         HSPD1         M22382         heat shock 60kD protein 1 (chaperonin)           36614_at         HSPA5         X87949         regulated protein, 78kD)           41510_s_at         HSPA9B         L15189         heat shock 70kD protein 9B (mortalin-2)	쭾	32591	HCDI	AI494623	HCDI protein	
39353_at         HSPE1         AI912041         10)           37720_at         HSPD1         M22382         heat shock 60kD protein 1 (chaperonin)           36614_at         HSPA5         X87949         regulated protein, 78kD)           41510_s_at         HSPA9B         L15189         heat shock 70kD protein 9B (mortalin-2)	842	35215	HDCMA18P	AL049996	HDCMA18P protein	hypothetical protein
39353_at         HSPE1         Al912041         10)           37720_at         HSPD1         M22382         heat shock 60kD protein 1 (chaperonin)           36614_at         HSPA5         X87949         regulated protein, 78kD)           41510_s_at         HSPA9B         L15189         heat shock 70kD protein 9B (mortalin-2)					heat shock 10kD protein 1 (chaperonin	
37720_at         HSPD1         M22382         heat shock 60kD protein 1 (chaperonin)           36614_at         HSPA5         X87949         regulated protein, 78kD)           41510_s_at         HSPA9B         L15189         heat shock 70kD protein 9B (mortalin-2)	843	39353_at	HSPE1	AI912041	10)	
HSPA5 X87949 regulated protein, 78kD) HSPA9B L15189 heat shock 70kD protein 9B (mortalin-2)	844	37720 at	HSPD1	M22382	heat shock 60kD protein 1 (chaperonin)	mitochondrial matrix protein
HSPA5 X87949 regulated protein, 78kD) HSPA9B L15189 heat shock 70kD protein 9B (mortalin-2)					heat shock 70kD protein 5 (glucose-	heat shock 70kD protein 5 (glucose-
HSPA9B L15189 heat shock 70kD protein 9B (mortalin-2)	845	36614_at	HSPA5	X87949	regulated protein, 78kD)	regulated protein, 78kU)
	978	41510 c at	HSPA9B	1 15189	heat shock 70kD protein 9B (mortalin-2)	MTHSP75
		11010_3_at	200 1011	22.21		

Γ	<b>V</b>	ď	C	Q	ш
847	at		X15183	heat shock 90kD protein 1, alpha	heat shock 90kD protein 1, alpha
T	at		M16660	heat shock 90kD protein 1, beta	heat shock 90kD protein 1, beta
849	31906_at	HSBP1	AF068754	heat shock factor binding protein 1	neat snock factor binding protein I noor I
0	1769 24		1112595	heat shock protein 75	turnor necrosis factor type i receptor associated protein
	38054 at	HBXIP	AF029890	racting protein	hepatitis B virus X interacting protein
7	Ī			ب	
852	852 38779_r_at	HDGF	D16431		hepatoma-derived GF
853	853 35644_at	HEPH	AB014598	╗	KIAA0698 protein
				progeneous nuclear ribonucleoprotein	
854	38094_at	HNRPAB	M65028	. 1	hnRNP type A/B protein
. 1		9	000001	erogeneous nuclear ribonucleoprotein	hatarorana rihonurlanda AO
CCR	3/334 at	HINAPAO	023003	Т	
				heterogeneous nuclear ribonucleoprotein	
856	34987_s_at	HNRPA1	X79536	A1	hnRNPcore protein A1
					heterogeneous nuclear ribonucleoprotein
				heterogeneous nuclear ribonucleoprotein	A2/B1, isoform A2; heterogeneous nuclear
857	36654 s at	HNRPA2B1	M29065	A2/B1	ribonucleoprotein A2/B1, isoform B1
					heterogeneous nuclear ribonucleoprotein C,
				heterogeneous nuclear ribonucleoprotein	isoform b; heterogeneous nuclear
828	33666 at	HNRPC	M16342	C (C1/C2)	ribonucleoprotein C, isoform a
				heterogeneous nuclear ribonucleoprotein	
_				D (AU-rich element RNA binding protein 1,	
859	38016_at	HNRPD	M94630	37kD)	DNA-binding protein
_				heterogeneous nuclear ribonucleoprotein	
860	33845_at	HNRPH1	W28483	H1 (H)	
_				heterogeneous nuclear ribonucleoprotein	
861	41132_r_at	HNRPH2	U01923	H2 (H')	heterogeneous nuclear ribonucleoprotein H2
	_				heterogeneous nuclear ribonucleoprotein
				heterogeneous nuclear ribonucleoprotein	H3, isoform a; heterogeneous nuclear
862	41283_at	HNRPH3	AF052131	Н3 (2Н9)	nbonucieoprotein n3, isoloriii p
863	863 40836 s at	HNRPH3	W26677	heterogeneous nuclear ribonucleoprotein H3 (2H9)	

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864	39415 · at	HNRPK	X72727	heterogeneous nuclear ribonucleoprotein K	transformation upregulated nuclear protein
	1			heterogeneous nuclear ribonucleoprotein	
865	35201 at	HNRPL	X16135		heterogeneous nuclear ribonucleoprotein L
				heterogeneous nuclear ribonucleoprotein	
998	37717_at	HNRPM	L03532	W	M4 protein
				sterogeneous nuclear ribonucleoprotein	
867	39792_at	HNRPR	AF000364	<b>T</b>	neterogeneous nuclear ribonucleoprotein n
				heterogeneous nuclear ribonucleoprotein	
898	38654 at	HNRPU	X65488	U (scaffold attachment factor A)	hnRNP U protein
698	32818 at	HXB	X78565	hexabrachion (tenascin C, cytotactin)	human tenascin-C
870	39827 at	RTP801	AA522530	HIF-1 responsive RTP801	
				high density lipoprotein binding protein	
871	31504_at	HDLBP	M64098	(vigilin)	high density lipoprotein binding protein
				high-mobility group (nonhistone	3
872	32220_at	HMG1	D63874	chromosomal) protein 1	HMIG-
				high-mobility group (nonhistone	high-mobility group (nonhistone
873	306_s_at	HMG14	J02621	chromosomal) protein 14	chromosomal) protein 14
				high-mobility group (nonhistone	
874	35738_at	HMG17L3	AI347088	chromosomal) protein 17-like 3	-
				high-mobility group (nonhistone	high-mobility group (nonhistone
875	38065_at	HMG2	X62534	chromosomal) protein 2	chromosomal) protein 2
876	38843_at	HMG2L1	AL079310	high-mobility group protein 2-like 1	hypothetical protein
877	35693_at	HPCAL1	AF070616	hippocalcin-like 1	BDP-1 protein
878	1000 at	HINT1	1151004	histidine triad nucleotide binding protein 1	protein kinase C inhibitor
879	34231 at	HBOA	AF074606	histone acetyltransferase	histone acetyltransferase
	41855	HAT1	AF030424	histone acetyltransferase 1	histone acetyltransferase 1
881	38771 at	HDAC1	D50405	histone deacetylase 1	RPD3 protein
882	34368 at	HDAC2	U31814	histone deacetylase 2	transcriptional regulator homolog RPD3
883	883 38271_at	HDAC4	AB006626	histone deacetylase 4	KIAA0288 protein
884	1 39046_at	H2AV	AL049324	histone H2A.F/Z variant	
885	5 39092_at	H2AV	AW007731	histone H2A.F/Z variant	
886		HTATIP2	AF039103	HIV-1 Tat interactive protein 2, 30 kD	Tat-interacting protein TIP30
887		HIS1	AB021179	HMBA-inducible	nevini proteiri



	A	8	၁	O	ш
888	39809_at	HBP1	AF019214	$\neg$	HMG box containing protein 1
				HMG-domain containing protein which is the 57 kd subunit within SWI/SNF-related	
				BAF complexes; contains a proline-rich N-	
				terminus, a kinesin-like coiled-coil region,	
				and a highly acidic c-terminus; Homo	
				sapiens BAF57 (BAF57) gene, complete	
889	33828_at	BAF57	AF035262	$\neg \neg$	BAF57
Γ				HMT1 hnRNP methyltransferase-like 1 (S.	
890	39348_at	HRMT1L1	X99209		arginine methyltransferase
				HMT1 hnRNP methyltransferase-like 2 (S.	
891	32825 at	HRMT1L2	Y10805	cerevisiae)	arginine methyltransferase
Γ				HNRNP Core Protein A1 LIKE	
				pseudogene; match: proteins P04256	
				Q28521 P49312 P09651 P51991 P51992	
892	31463_s_at	dJ256G22.1	AL022097	P51968 P17130 P22626	
				holocytochrome c synthase (cytochrome c	
893	38943_at	HCCS	U36787	heme-lyase)	holocytochrome c-type synthetase
894	39610_at	HOXB2	X16665	homeo box B2	homeo box B2
895	40674_s_at	нохсе	S82986	homeo box C6	homeo box C6
908	38233 at	HOMEB-3	AF093265	Homer neuronal immediate early gene, 3	homer-3
3	00500-at	2 1 1 1 1 1	000000000000000000000000000000000000000		
İ		6	7,5000	Homo sapiens (clone 117252) ubiquinol cytochrome c reductase Rieske iron-	Diacko Fo. S protein
	34401_al	ופרוססט	116767	Homo seniens (clone FFE-7) type [	
				inosine monophosphate dehydrogenase (IMPDH2) gene exons 1-13, complete	inosine monophosphate dehydrogenase type
868	36624_at	IMPDH2	L33842	cds.	
6	27500 24	, XOX	A E017060	Homo sapiens aldehyde oxidase (AOX1)	aldehvde oxidase
660		202	20010	gene, exerted eding complete ed.	
900	900 39740_g_at	NACA	AF054187	nomo sapiens alpira inac illiniva, complete cds.	alpha NAC

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	4	В	O	Q	ш
106	39739 at		AF054187	Homo sapiens alpha NAC mRNA, complete cds.	alpha NAC
206	902 41154 r at	A.	AF102803	Homo sapiens alphaE-catenin (CTNNA1) gene, exon 18 and complete cds.	alphaE-catenin
903	903 41153 f_at			TNNA1)	alphaE-catenin
904	904 39324 at		AL050078	Homo sapiens cDNA FLJ10784 fis, clone NT2RP4000448, highly similar to Homo sapiens mRNA; cDNA DKFZp566G0746	·
905	35310_at		D45288	Homo sapiens cDNA FLJ13267 fis, clone OVARC1000964	
906	35754 at		L40391	Homo sapiens cDNA FLJ13553 fis, clone PLACE1007454	
			10000	Homo sapiens cDNA FLJ14821 fis, clone OVARC1000556, highly similar to RIBOSOMAL PROTEIN S6 KINASE II	
/06 808	33325 at		W28575	Homo sapiens cDNA FLJ25016 fis, clone CBL01574	
606			A1983043	Homo sapiens cDNA FLJ30436 fis, clone BRACE2009037	
910	39162_at		AA156987	Homo sapiens cDNA' FLJ30544 fis, clone BRAWH2001412	
911	41807 at		AL040137	Homo sapiens cDNA FLJ31959 fis, clone NT2RP7007422	
912	38643 at		W87466	Homo sapiens cDNA FLJ33151 fis, clone UTERU2000263	
913	34246 at		AA418437	Homo sapiens cDNA: FLJ21175 fis, clone CAS11071	·
914	914 40813_at		A1768188	Homo sapiens cDNA: FLJ21243 fis, clone COL01164	

Fig 21

A B C   Hemo sapiens CDNA FL/21449 its clone   COLO4483 inghly similar to AF010236     40923_at						
AA290994  W27522  U90909  AI700633  AI700633  AF038185  AF038185  AF038185  AF052138  AF052138  AF052159  AF052159  AF052174  AF052181		A	8		٥	<b>W</b>
AA290994  W27522  U90909  AI700633  AI700633  AF038185  AF038185  AF038185  AF052138  AF052138  AF052159  AF052159  AF052174  AF052181	Γ				Homo sapiens cDNA: FLJ21449 fis, clone	
AA290994  W27522  U90909  AI700633  AI700633  AF038185  AF038185  AF052138  AF052138  AF052159  AF052159  AF052159  AF052174  AF052181					COL04483, highly similar to AF010235	
AA290994 : W27522 U90909 AI700633 AI700633 AF038185 AF038185 AF052138 AF052138 AF052159 AF052159 AF052174 AF070578					Homo sapiens mRNA from chromosome	
W27522 U90909 A1700633 A1700633 A1700633 A1700633 AF038202 AF038202 AF038281 AF035281 AF052159 AF052174 AF052174 AF070578	915	40923_at			5q31-33 region	
W27522 U90909 A1700633 A1700633 A1700633 AF038202 AF038202 AF038281 AF035281 AF052159 AF052174 AF070578 AF052181					Homo sapiens cDNA: FLJ21904 fis, clone	
U90909  AI700633  AI Smooth muscle m S67247  AF038202  AF038202  AF038281  AF038281  AF052138  AF052138  AF052174  AF052174  AF052174  AF052181	916	38993_r_at		W27522	HEP03585	
U90909  A1700633  A1700633  at Smooth muscle m S67247  AF038202  AF038202  AF038202  AF038202  AF038202  AF038202  AF038202  AF038202  AF038202  AF038202  AF038202  AF038201  AF038201  AF038185  AF038211  AF035281  AF035281  AF052181					Homo saniens cDNA: FL.121927 fis. clone	
U90909   AI700633   AI700633   AI700633   AI871359   AF038202   AF038185   AF052138   AF052138   AF052159   AF052174   AF052181				HEP04178, highly similar to HSU90909		
at smooth muscle m S67247  at AI871359  t AF038202  t AF038282  t AF038281  t AF052138  t AF052138  t AF052174  t AF052174	917	38093_at		60606N	Human clone 23722 mRNA sequence	
at S67247  at AIR01359  AF038202  AF038202  AF038185  AF052138  AF052138  AF052159  AF052174  AF052181					Homo sapiens cDNA: FLJ22642 fis, clone	
smooth muscle my S67247  AI871359  AF038202  AF038185  AF052138  AF052138  AF052159  AF052174  AF052174  AF052181	918	34840_at		AI700633	HSI06970	
Al871359 AF038202 AF038185 AF032138 AF052138 AF052138 AF052159 AF052174 AF052174 AF052181					Homo sapiens cDNA: FLJ23324 fis, clone	
Al871359 AR038202 AF038202 AF038185 AF052138 AF052138 AF052159 AF052159 AF052174 AF052181					HEP12482, highly similar to	
Se7247   heavy chain-B (MYH10) mRNA		_			HUMMYOHCB Human nonmuscle myosin smooth r	muscle myosin heavy chain isoform
AIB71359 AF038202 AF038185 AF052138 AF052138 AF052138 AF052159 AF052174 AF052174 AF052174 AF052181	919	32838_at	smooth muscle my	S67247		
AR71359 1 AF038202 8 AF038185 8 AF052138 8 AF007142 8 AF052159 AF052174 AF052174 AF052174 AF052181					Homo sapiens cervical cancer suppressor-	
AF038202 8 AF038185 8 AF052138 8 AF035281 8 AF007142 8 AF052159 8 AF052174 AF052181	920	33737 f_at	,	AI871359	1 mRNA, complete cds	
41663_at       AF038202       \$         36815_at       AF038185       \$         41841_at       AF052138       \$         37794_at       AF035281       \$         38764_at       AF035281       \$         35342_at       AF052159       \$         36758_at       AF052174       \$         41864_at       AF052181       \$					Homo sapiens clone 23570 mRNA	
36815_at AF038185   1	921	41663_at		AF038202	sednence	
36815_at       AF038185       \$         41841_at       AF052138       \$         37794_at       AF035281       \$         38764_at       AF007142       \$         35342_at       AF052159       \$         36758_at       AF052174       \$         41864_at       AF052181       \$					Homo sapiens clone 23700 mRNA	
AF052138 8 8 AF035281 8 AF007142 8 AF052159 8 AF052174 AF052174 AF052181	922	36815_at		AF038185	sednence	
AF052138  AF035281  AF007142  AF052159  AF052174  AF052174  AF052181					Homo sapiens clone 23718 mRNA	
AF035281 8 AF007142 AF052159 AF052174 AF052181 AF052181	923	41841_at		AF052138	sednence	
AF035281  AF007142  AF052159  AF052174  AF052174  AF052181					Homo sapiens clone 23903 mRNA	
AF007142 AF052159 AF052174 AF070578 AF052181	924	37794_at		AF035281	sednence	
AF052159 AF052174 AF070578 AF052181					Homo sapiens clone 23938 mRNA	
AF052159 AF052174 AF070578 AF052181	925	38764_at		AF007142	sednence	
AF052159 AF052174 AF070578 AF052181			-		Homo sapiens clone 24416 mRNA	
AF052174 AF070578 AF052181	926	35342_at		AF052159	sednence	
AF052174 AF070578 AF052181					Homo sapiens clone 24630 mRNA	
AF070578 AF052181	927	31867_at		AF052174	sednence	
AF070578 AF052181					Homo sapiens clone 24674 mRNA	
AF052181	928	36758_at		AF070578	sednence	
AF052181					Homo sapiens clone 24790 mRNA	
	929	41864_at		AF052181	sednence	

38070 at		AL 080234	Homo sapiens clone FBD3 Cri-du-chat critical region mRNA	
			lor A protein mRNA,	
34773_at	TBCA //	AF038952		cofactor A protein
			Homo sapiens cytochrome c oxidase	
			subunit IV precursor (COX4) gene,	
			nuclear gene encoding mitochondrial	
39027 at	COX4	AF017115		cytochrome c oxidase subunit IV precursor
			Homo sapiens D15F37 pseudogene, S4	
933 40878 f at	D15F37	AF041081	allele, mRNA sequence.	
			Homo sapiens deoxycytidylate deaminase	
631 q at	DCTD	L39874	gene, complete cds.	deoxycytidylate deaminase
			ycytidylate deaminase	
630_at	DCTD	L39874	gene, complete cds.	deoxycytidylate deaminase
			Homo sapiens DNA for	
			exon 17 and	
936 33936 at	GALC	D86181		galactocerebrosidase
			Homo sapiens F1Fo-ATPase synthase f	
40134 at	ATP5J2; ATP5JL;	JL; AF047436	subunit mRNA, complete cds.	F1Fo-ATPase synthase f subunit
			Homo sapiens gene for LD78 alpha	
36103_at	SCYA3; LD78ALP D90144	D90144	precursor, complete cds.	LD78 alpha precursor
			Homo sapiens GOS28/P28 protein	
40725_at	GOSR1; P28; GS;	GS2AF047438	mRNA, complete cds.	GOS28/P28 protein
			Homo sapiens GTP binding protein	
38708_at	RAN; TC4; ARA24	A24AF054183	mRNA, complete cds.	GTP binding protein
			Homo sapiens H beta 58 homolog mRNA,	
35790_at	VPS26; HB58; HB	HB AF054179	complete cds.	H beta 58 homolog
			Homo sapiens histone macroH2A1.2	
36576_at	H2AFY; H2A.y; H2AF054174	AF054174	mRNA, complete cds.	histone macroH2A1.2
			Homo sapiens insulin induced protein 1	
35303_at	INSIG1	N96876	(iNSIG1) gene, complete cds.	insulin induced protein 1
			Homo sapiens interferon-gamma receptor	
			alpha chain gene, exon 7 and complete	•
044 11038 c at	lintorforon gamma   110017	1140047	عاد	interferon-gamma receptor alpha chain

		!			
r	A	В	ပ	D	L L
945	895 at	MIF	L19686	Homo sapiens macrophage migration inhibitory factor (MIF) gene, complete cds. macrophage migration inhibitory factor	macrophage migration inhibitory factor
				Homo sapiens mitochondrial proteolipid 68MP homolog mRNA, nuclear gene	
946	38967 at	C14orf2; MP68; PI	P(AF054175	encoding mitochondrial protein, complete cds.	mitochondrial proteolipid 68MP homolog
1	10000		714155	Homo sapiens mRNA for Hmob33 protein, 3' untranslated region	
948	947 31661 at	11132	AJ012755	Homo sapiens mRNA for TL132	TL132 protein
980	38786		AI 079279	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 248114	
3	15 CO (CO)			Homo sapiens mRNA; cDNA	
9	. 00.440		AI 096752	DKFZp434A012 (from clone DKFZp434A012)	
3	33410 at			Homo saniens mRNA: cDNA	
				DKFZp434B102 (from clone	
951	38630 at		AL080192	DKFZp434B102)	
_				Homo sapiens mRNA; cDNA	
				DKFZp434M162 (from clone	
952	952 41529 g_at		W72239	DKFZp434M162)	
				Homo sapiens mRNA; cDNA	
				DKFZp434M245 (from clone	
953	36451 at		AI743299	DKFZp434M245)	
				Homo sapiens mRNA; cDNA	
				DKFZp564A026 (from,clone	:
954	36821_at	DKFZp564A026	AL050367	DKFZp564A026)	hypothetical protein
				Homo sapiens mRNA; cDNA	
				DKFZp564A072 (from clone	
955	37366 at		AL049969	DKFZp564A072)	
				Homo sapiens mRNA; cDNA	
		-		DKFZp564B222 (from clone	-
926	39506 at		AA933984	DKFZp564B222)	
				Homo sapiens mRNA; cDNA	
				DKFZp564D016 (from clone	
957	957 39748_at		AL050021	UKFZp564U016)	

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	<b>∀</b>	80	S		
				Homo sapiens mRNA; cDNA	
				DKFZp564D156 (from clone	
928	38357_at		AL049321	UKFZp364U (36)	
				Homo sapiens mRNA; cDNA	<u> </u>
				UKFZp564E122 (Ifom clone	
929	33716_at		N95443	OKFZp564E122)	T
				Homo sapiens mRNA; cDNA	
				DKFZp564E2222 (from clone	
096	35301 at		AL049941	DKFZp564E2222)	
				Homo sapiens mRNA; cDNA	
				DKFZp564F053 (from clone	•
196	35842 at		AL049265	DKFZp564F053)	
				Homo sapiens mRNA; cDNA	
				DKFZp564F112 (from clone	
362	40552 s at		AL049987	DKFZp564F112)	
				Homo sapiens mRNA; cDNA	
				DKFZp564J0323 (from clone	
963	39170 at		AL049957	DKFZp564J0323)	
				Homo sapiens mRNA; cDNA	
				DKFZp564L0822 (from clone	
964	34303 at		AL049949	DKFZp564L0822)	
	2222			Homo sapiens mRNA; cDNA	
				DKFZp564L222 (from clone	
965	36509 at		AL049998	DKFZp564L222)	
				Homo sapiens mRNA; cDNA	
				DKFZp564P0823 (from clone	
996	40353 at		AL049962	DKFZp564P0823)	
				Homo sapiens mRNA; cDNA	
				DKFZp566J2146 (from clone	
1967	35290 at	_	AL050081	DKFZp566J2146)	
				Homo sapiens mRNA; cDNA	
				DKFZp586B0918 (from clone	
968	38079_at		AL049367	DKFZp586B0918)	
				Homo sapiens mRNA; cDNA	
			_	DKFZp586B1922 (from clone	
696	969 32195 at		AL049450	DKFZp586B1922)	

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35379_at AL049397					Homo sapiens mRNA; cDNA	
39379_at AL049397  37575_at AL050192  34283_at AL080110  39600_at AL080111  36092_at AL080213  35363_at DDX17 AL080113  41013_at AL080114  41690_at AL049471					DKFZp586C1019 (from clone	
35755_at AL050192   34283_at AL050125   34752_at AL080111   1   1   1   1   1   1   1   1   1	2	39379_at		AL049397	DKFZp586C1019)	
34283_at AL050125 C 34283_at AL060110 C 34752_at AL080111 C 34752_at AL080213 C 35187_at AL080213 C 35363_at DDX17 AL080113 C 41690_at AL080114 AL049472					Homo sapiens mRNA; cDNA	
37575_at AL050192 34283_at AL050125 39600_at AL080110 [39103_s_at AL080111 [6] 35187_at AL080216 35363_at DDX17 AL080113 41690_at AL049471 AL04942					DKFZp586C1723 (from clone	
ALOSO125  ALOSO110  ALOSO111  ALOSO213  ALOSO216  ALOSO216  ALOSO113  ALOSO114  ALOSO114  ALOSO114  ALOSO114	371	37575_at		AL050192	DKFZp586C1723)	
ALOSO125 C ALOSO110 C ALOSO111 C C ALOSO111 C C ALOSO111 C C ALOSO213 C C ALOSO216 C C ALOSO216 C C C ALOSO216 C C C C C C C C C C C C C C C C C C C					Homo sapiens mRNA; cDNA	
ALOSO125 C ALOSO110 [ ALOSO111 [ ALOSO111 [ ALOSO111 [ ALOSO111 [ ALOSO113 [ ALOSO113 [ ALOSO113 [ ALOSO114 [					DKFZp586F071 (from clone	
t AL080110 [C AL080111 [C AL080111] [C AL080213 [C AL080213 [C AL080216] [C AL080216] [C AL080113 [C AL080113 [C AL080114 [C AL080114 [C AL080114 [C AL080114 [C AL080114 [C AL080114 [C AL08042 [C AL080114 [C AL080114 [C AL080442 [C AL080114 [C AL080442 [C AL080114 [C AL080442 [C AL080114 [C AL080442 [C AL080114 [C AL080442 [C AL0804442 [C AL080442  [C AL080444 [C AL080444] [C AL080444 [C AL080444] [C AL080444] [C AL080444 [C AL080444 [C AL080444 [C AL080444] [C AL080444 [C AL080444] [C AL080444 [C AL080444] [C AL080444 [C AL080444] [C AL080444] [C AL08	372	34283 at		AL050125	DKFZp586F071)	
ALOBO110 [C ALOB0111 [C ALOB0111] [C ALOB0213 [C ALOB0216] [C ALOB0216] [C ALOB0216] [C ALOB0113 [C ALOB0113 [C ALOB0114] [C ALOB0114] [C ALOB0114 [C ALOB0114] [C ALOB0114] [C ALOB0114 [C ALOB0114] [C ALOB0114] [C ALOB0114 [C ALOB0114] [C ALOB0114] [C ALOB0114 [C ALOB0114] [C ALOB0114] [C ALOB0114 [C ALOB0114] [C ALOB0114] [C ALOB0114] [C ALOB0114] [C ALOB0114 [C ALOB0114] [C ALO	T				Homo sapiens mRNA; cDNA	
ALOBO110   ALOB0111   ALOB0111   ALOB0213   ALOB0216   ALOB0216   ALOB0113   ALOB0114					DKFZp586G1922 (from clone	
at AL080111 [ AL080111 [ I AL080213	973	39600 at		AL080110	DKFZp586G1922)	
at AL080111 [6] AL080213 T AL080216 T AL080113 T AL080114 T AL080114 T AL080114	Γ				Homo sapiens mRNA; cDNA	
at AL080111   R AL080213   AL080216   AL080216   AL080113   AL080114   AL080114   AL080114   AL080114   AL080114   AL08042					DKFZp586G2222 (from clone	
35103_s_at H98552 36092_at AL080213 35187_at AL080216 35363_at DDX17 AL080113 41690_at AL049471	974	34752_at	-	AL080111	DKFZp586G2222)	
35103_s_at H98552 36092_at AL080213 35187_at AL080216 35363_at DDX17 AL080113 41690_at AL049471	Γ				Homo sapiens mRNA; cDNA	
35103_s_at H98552 36092_at AL080213 35187_at AL080216 35363_at DDX17 AL080113 41690_at AL049471					DKFZp586l0523 (from clone	
35187_at AL080213 35363_at DDX17 AL080113 41690_at AL049471	975	39103 s at		H98552	DKFZp58610523)	
35187_at AL080216 35363_at DDX17 AL080113 41013_at AL080114 41690_at AL049471	Γ				Homo sapiens mRNA; cDNA	
35187_at AL080216 35363_at DDX17 AL080113 41013_at AL080114 41690_at AL049471					DKFZp58611823 (from clone	
35363_at DDX17 AL080113 41013_at DDX17 AL080114 41690_at AL049471	926	36092 at		AL080213	DKFZp586l1823)	
35363_at DDX17 AL080216 41013_at AL080114 41690_at AL049471 AL049442		L			Homo sapiens mRNA; cDNA	
35363_at DDX17 AL080113 41013_at AL080114 41690_at AL049471 Al04942					DKFZp586K1123 (from clone	
35363_at DDX17 AL080113 41013_at AL080114 41690_at AL049471 Al049442	12/6	35187 at		AL080216	DKFZp586K1123)	
35363_at DDX17 AL080113 41013_at AL080114 41690_at AL049471 Al049442					Homo sapiens mRNA; cDNA	
35363_at DDX17 AL080113 41013_at AL080114 41690_at AL049471 Al049442					DKFZp586K2322 (from clone	
41013_at AL080114 41690_at AL049471 A0349_at AL049442		35363_at	DDX17	AL080113	DKFZp586K2322) '	
41690_at AL049471 Al04942					Homo sapiens mRNA; cDNA	
41013_at AL080114 41690_at AL049471					DKFZp586M2022 (from clone	
41690_at AL049471	979	41013_at	-	AL080114	DKFZp586M2022)	
AL049471 AL049442					Homo sapiens mRNA; cDNA	
AL049471 AL049442					DKFZp586N012 (from clone	
AI 049442	980	41690 at		AL049471	DKFZp586N012)	
AL 049442					Homo sapiens mRNA; cDNA	
AI 049442		· · · · · ·			DKFZp586N1720 (from clone	
	QR.	40349 at		AI 049442	DKFZp586N1720)	

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	A	a	3	2	
				Homo sapiens mRNA; cDNA	
		-		DKFZp586N1918 (from clone	
982	32672_at		AL049387	DKFZp586N1918)	
				me b5	
983	36668_at	DIA1	M28713		NAUH-cytochrome b5 reductase
Γ				Homo sapiens nucleophosmin	
				phosphoprotein (NPM) gene, 3' flanking	
984	38542 at		U89322	sequence.	
				Homo sapiens p18 protein mRNA,	
985	40587 s at	EEF1E1; P18	AF054186	complete cds.	p18 protein
				Homo sapiens PAC clone RP1-170019	even-skipped homeo box 1 (homolog of
986	41448 at	HOXA4	AC004080	from 7p15-p21, complete sequence.	Drosophila)
				Homo sapiens prion protein (PrP) gene,	•
987	36159 s at	PrP	U29185	complete cds.	prion protein
				Homo sapiens putative dienoyl-CoA	
				isomerase (ECH1) gene, exons 7-10, and	
988	32756 at	ECH1	AF030249	complete cds.	putative dienoyl-CoA isomerase
				Homo sapiens RP58 gene, complete	
686	35824_at	RP58	AJ223321	cDs.	RP58 protein
				Homo sapiens Sec61 gamma mRNA,	
990	39169_at	SEC61G	AF054184	complete cds.	Sec61 gamma
				Homo sapiens signal transducer and	•
				activator of transcription 6 (STAT6) gene,	signal transducer and activator of
991	41222_at	STATE	AF067575	exons 15 through 23 and complete cds.	transcription 6
				Homo sapiens sperm acrosomal protein	•
992	38817_at	SPAG7; ACRP; F\$AF047437	AF047437	mRNA, complete cds.	sperm acrosomal protein
				Homo sapiens splicing factor,	
			00007		
993	36033_at		AL049309	complete cus	
	3	0700	000000	Homo sapiens thymosin beta-10 gene,	thymosin heta-10
994	31481_s_at	IMBBIO	INISCOO	o di la	
		Ç	000	Homo sapiens TIMP gene for tissue	issue inhihitor of metalloproteinases
995	995   1693 s_at	HMF	851110	Innibitor of metalloproteinases, partial cus.	

Γ	A	8	O	Q	3
				Homo sapiens transaldolase-related	
		1		protein gene, exons 3-8 and complete	riotory popular and phonon
966	37311_at	TALDO1; TAL-H;  AF010400	AF010400	cds.	Iransaidolase-related protein
				Homo sapiens translation initiation factor	
997	32229 at	EIF4EL3; 4EHP; 4	P; 4 AF038957	4e mRNA, complete cds.	translation initiation factor 4e
998	998 1323 at	UBB	X04803	Homo sapiens ubiquitin gene.	ubiquitin
999	999 32153 s at	UBB	U49869	Homo sapiens ubiquitin gene.	ubiquitin
8	1000 38372 at		U66042	Homo sapiens unknown mRNA	
				Homo sapiens vacuolar H(+)-ATPase	
1001	1001 38814 at	ATP6V1G1; ATP6	TP6AF038954	subunit mRNA, complete cds.	vacuolar H(+)-ATPase subunit
				Homo sapiens vesicle trafficking protein	
1002	1002 41597 s. at	SEC22L1; SEC22	AF047442	sec22b mRNA, complete cds.	vesicle trafficking protein sec22b
1003	1003 34957_at	X5L Y18504	Y18504	Homo sapiens X5L gene.	XAP-5-like protein
				Homo sapiens, clone IMAGE:3028427,	
1004	1004 38662 at		AL047596	mRNA, partial cds	
				Homo sapiens, clone IMAGE:3140802,	
1005	1005 38312 at		AL050002	mBNA	
				Homo sapiens, clone IMAGE:3855224,	
1006	1006 33388 at		AL080223	mRNA, partial cds	
	1			Homo sapiens, clone IMAGE:4132509,	
1007	1007 38676_at		AA059408	mRNA	
				Homo sapiens, clone IMAGE:4150198,	
1008	1008 40238 at		AI674208	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4182947,	
1009	1009 32119_at		AL049423	mRNA	
				Homo sapiens, clone IMAGE:4183312,	
1010	1010 38650 at	IGFBP5	L27560	mRNA, partial cds	
	1			Homo sapiens, clone IMAGE:4183312,	
101	1011 1396 at	IGFBP5	L27560	mRNA, partial cds	
				Homo sapiens, clone IMAGE:4391536,	
1012	1012 40432_at		AA522891	mRNA	
				Homo sapiens, Similar to RNA helicase-	
		!		related protein, clone MGC:9246	
101	1013 36130_f_at	MI1E	H92331	IMAGE:3892441, MHIVA, complete cus	

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	A	8	O		
				Homo sapiens, Similar to serine (or	
		•	<u>.</u>	cysteine) proteinase inhibitor, clade E	
			<u> </u>	(nexin, plasminogen activator inhibitor	
				type 1), member 2, clone MGC:23129	
-	1014/4104E at	*	AI743134 II	IMAGE:4578406, mRNA, complete cds	
- 1	240_81	-		Homo sapiens, similar to unknown, clone MGC:39325 IMAGE:5440447, mRNA,	
	4045 44500 04	_ <del></del>	U79298		
	000 all			-inducible, endoplasmic	homocysteine-inducible, endoplasmic
				e)	reticulum stress-inducible, ubiquitin-like
	1016 30733 at	HERPUD1	AF055001		domain member 1
	17.50_all			homolog of yeast mutt. gene; Human	
				•	
	1017 525 a at	hPMS1	U13695		postmeiotic segregation 1
	13-6-			homologous to mouse Rsu-1; putative;	
				0	•
	1010 20EAE r at	RSI 1-1	L12535		ras suppressor protein 1
	10407			homologous to mouse Rsu-1; putative;	
				Human HSO-1/HSP-1 innivA, complete	f diatore protein 1
	1019 32544 s at	RSU-1	L12535	cds.	ras suppressor protein i
	1020 39800 s at	HAX1	U68566	HS1 binding protein	HAX-1
		OCAIN .	L 178302	Human 2,4-dienoyl-CoA reductase gene, exon 10 and complete cds.	2,4-dienoyl-CoA reductase
	1021 38104_at	וויייייייייייייייייייייייייייייייייייי	2000	Human alcohol dehydrogenase chi	
				polypeptide (ADH5) gene exons 8-9,	
	1000 27708 r at	ADHS	M81118	complete cds.	alcohol denydrogenase
				Human alcohol dehydrogenase chi	
				polypeptide (ADH5) gene exons 8-9,	
	1023 37707 i at	ADH5	M81118	complete cds.	alcohol denydrogenase
	m-1-1011			Human alpha-1 collagen type IV gene,	
	1024 39333_at	COL4A1	M26576	exon 52.	alpha-1 type IV collagen
	1005 38417 at	AMPD2	M91029	Human AMP deaminase (AMPD2) mRNA	Human AMP deaminase (AMPD2) mRNA. AMP deaminase isoform L splicing variant
				C	V discount
	1026 37747_at	ANX5	U05770	Human annexin V (ANX5) gene, exon 13.	annexin v

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A	B	>			
			e, exons	almodulin	
			exons 7.	to Other Carlo	
	CTSD		3, and 9.	fos FBJ murine osteosarcoma viral	
			sequence).	ncogene homolog	
			Human cellular oncogene c-fos (complete	rios FBJ murine osteosarcoma viral oncogene homolog	
115_s_at				-jun avian sarcoma virus 17 oncogene	
• 000				nomolog Transmin 17 oncorene	
2003 at			le (JUN),	7-jun avian sarcoma viius 17 olicogonio	
895_at	NOC		complete cds, clotte nos-1.	6	
1604_at			Human clone 20009 Hillings 30450100		
			Human clone A9A2BRB5 (CAC)n/(GTG)n		
24 85		-	repeat-containing mRNA		
2 100 at			Human cyclophilin gene for cyclophilin		
23667 at		X52851	(EC 5.2.1.8).	peptidyiprolyt isotilierase	÷
22001 _at			Human cytochrome b5 (CYB5) gene, exon	the months of the	
18450 A at	CYB5	L39945	6 and complete cds.		_
10-10-10-01			Human cytochrome b5 (CYB5) gene, exon	cytochrome b5	
38458 at	CYB5	L39945	6 and complete cus.		
		;	Human dinydrolipoamide deliydrogeriase	dihydrolipoamide dehydrogenase	
36163_at	ı	L13761	gene, excli 14.		_
		079577	exon2 and complete cds.	14-3-3 protein eta chain	-т
1424_s_at		10000	Human DNA sequence from clone 73H22		
			on chromosome 6q23, complete		
	4 172000 1	A1 035699	sednence.	dJ73H22.1 (18P-like protein)	Т
31797_at	1.22HC10	7	Human ENO2 gene for neuron specific		
40193_at	ENO2	X51956	(gamma) enolase.	numan gamina enorase	Т
38326 at	G0S2	M69199	Human GOS2 protein gene, complete cds	G0S2 protein.	
D-07000		V01703	Human gene for alpha-tubulin (b alpha 1)	alpha-tubulin	$\neg$
40567_at	TUBA3; FLJ2511	3701703			
	1028 239_at	A C C C C C C C C C C C C C C C C C C C	CALM1 U12022  CTSD M63138  c-fos V01512 fos V01512  JUN J04111  JUN J04111  JUN J04111  U00946  PPIA X52851  CYB5 L39945  CYB5 L39945  CYB5 L39945  L39945	Human calmodulin (CALMI) gane, exons CALMI   U12022   2,3.4,5 and 6, and complete cds.   CTSD   M63138   Human callular oncogene c-fos (complete cds.   Human callular oncogene (JUN),   Complete cds.   Clone hCJ-1.   Human c-fun proto oncogene (JUN),   Human complete cds.   Human cyclophilin gene for cyclophilin   Human cyclophilin gene for cyclophilin   Human cyclophilin gene, exon   Human cyclophilin gene, exon   Human DNA for 14.3-3 protein eta chain,   Human DNA for 14.3-3 protein eta chain,   Human DNA sequence from clone 73H22 on chromosome 6q23, complete cds.   Human GOS2 protein gene, complete cds.   Human GOS2 protein gene, complete cds.   Human GOS2 protein gene, complete cds.   Human GOS2 protein gene, complete cds.   Human gene for alpha-tubulin (b alpha 1)   Human gene for alpha-tubulin gene for alpha-tubulin gene for alpha-tubulin gene for alpha-tubulin	CALM1   U12022   2,3,4,5 and 6, and complete cds.   CalM1   GALM1   Gane, exons 7.   CalM1   Gane   CalM2   CalM3   Gane   CalM3   CalM3   Gane   CalM3   Gane   CalM3   CalM3   Gane   CalM3   CalM3   Gane   CalM3
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	A	8	C		
10443	1044 39775 at	SERPING1: C1IN	N-X54486		C1 inhibitor
	1- 000			ase B (EC	creatine kinase B
1040	1045 40662 1 at			Γ	
				numan gene for repains Crassociated microtubular aggregate protein p44, exon   hepatitis C-associated microtubular	repatitis C-associated microtubular
1046 3	1046 37641 at	IF144: p44: MTAP4	P4D28915	9 and complete cds.	aggregate protein p44
				Human gene for heterogeneous nuclear	
				ribonucleoprotein (hnRNP) core protein	
1047	1047 40211 at	HNRPA1; HNRNPX12671	X12671		hnrnp a1 protein
				a growth	melanoma growth stimulatory activity
1048 408_at	108_at	MGSA	X54489	Π"	preprotein
				ithine decarboxylase	
1049	1049 36203_at	0001	X16277		ornithine decarboxylase (ODC)
				lsify	
1050	1050 36873 at	VLDLR	D16532		very low density tipoprotein receptor
1051	1051 34759 at		U68494	Human hbc647 mRNA sequence	
				Human hepatic dihydrodiol	
1052	1052 32805 at	AKR1C1; DD1; DI	DtJ U05861	dehydrogenase gene, exon 9.	hepatic dihydrodiol dehydrogenase
				Human HMG-17 gene for non-histone	
1053	1053 41231 f at	HMG17; MGC562 X13546	X13546	chromosomal protein HMG-17.	put. HMG-17 protein
				Human HOX 5.1 gene for HOX 5.1	
1054	1054 38294 at	HOXD4; HOX4; H	H X17360	protein.	hox 5.1 protein
				Human hsc70 gene for 71 kd heat shock	
1055	1055 40637_at	HSP73 HSC70 H	H§Y00371	cognate protein.	/1 Kd neat snock cognate protein
1056	10561232 at	LAMB2	M55210	Human laminin B2 chain gene, exon 28.	laminin B2 chain
				Human lipoprotein-associated coagulation	
				inhibitor (LACI) gene, exon 9 and	Activitation of the second sec
1057	1057 40767_at	TFPI	M59499	complete cds.	ilpoprotein-associated coaguiation initionol
1058	1058 38637 at	XO	L16895	Human lysyl oxidase (LOX) gene, exon 7. Iysyl oxidase	lysyl oxidase
3	n= 10000			Human medium-chain acyl-CoA	
1059	1059 37532_at	MCAD	M91432	dehydrogenase (MCAD) gene, exon 12.	medium-chain acyl-CoA denydrogenase
90,	070 020	MT3: GIE: GIEB	M93311	Human metallothionein-III gene, complete cds.	metallothionein-III
	10/0   al	0 15 1 15 10 10			

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				Human metaxin (MTX) gene, complete	
1061	1061 40890 at	MTX	U46920	cds.	metaxın
				Human mRNA for erythrocyte adducin	
1062	1062 32145 at	ADD1	X58141	alpha subunit.	erythrocyte alpha adducin
-				Human mRNA for general transcription	
1063	37381 g at	TF2B	X59268	factor IIB.	IIB protein
1064	1064 33683 at	TI-227H	D50525	Human mRNA for TI-227H.	
				hancer factor	myocyte-specific enhancer factor 2A, C9
				2A (MEF2A) gene, last coding exon, and	form; myocyte-specific enhancer factor 2A,
1065	1065 41747 s at	MEF2A	U49020	complete cds.	C4 form
				Human NAD(P)H:quinone oxireductase	
1066	1066 38066 at	NOON	M81600	gene, exon 6.	NAD(P)H:quinone oxireductase
				Human natural killer cell enhancing factor	
1067	1067 39729_at	NKEFB	L19185	(NKEFB) mRNA, complete cds.	enhancer protein
				:	##
				Human nonmuscle/smooth muscle alkali	non-muscle myosin light chain; smooth
1068	1068 33994 g at	MLC	M22919	myosin light chain gene, complete cds.	muscle myosin light chain
			-	Human nucleic acid binding protein gene,	
1069	1069 32841_at	ZNF9; DM2; CNB	JB(U19765	complete cds.	nucleic acid binding protein
1070	1070 32590 at	NOL	M60858	Human nucleolin gene, complete cds.	nucleolin
				Human oncoprotein 18 (Op18) gene,	
1071	1071 1782 s at	Op18	M31303	complete cds.	oncoprotein 18
	1			Human prostaglandin D2 synthase gene,	
1072	1072 216_at	PTGDS	M98539	exon 7.	prostaglandin D2 synthase (21kD, brain)
				Human protein phosphatase 2A catalytic	protein phosphatase-2A catalytic subunit-
1073	1073 237 s at	PPP2CA	M60483	subunit-alpha gene, complete cds.	alpha
				Human protein phosphatase inhibitor 2	
				(PPP1R2) gene, exon 6 and complete	
1074	1074 812 at	PPP1R2	U68111	cds.	protein phosphatase inhibitor 2
				Human protein phosphatase inhibitor 2	
				(PPP1R2) gene, exon 6 and complete	
1075	1075 33180_at	PPP1R2	U68111	cds.	protein phosphatase inhibitor 2
40.4	90000		W21884	Human putative ribosomal protein S1	
	10/0/33330_dt		11121004	CAN 1111	

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T				Human receptor tyrosine phosphatase	
				gamma (PTPRG) gene, exon 30 and	
1077	1077 491 at	PTPRG	U46116		receptor tyrosine phosphatase gamma
				Human receptor tyrosine phosphatase	
				gamma (PTPRG) gene, exon 30 and	
1078	1078 492 g at	PTPRG	U46116		receptor tyrosine phosphatase gamma
				Human red cell-type low molecular weight	
				acid phosphatase (ACP1) gene, exon 6	red cell-type fow molecular weight acid
1079	1079 36611 at	ACP1	U25849	and 7, complete cds.	phosphatase
				Human SH3 domain-containing protein	
1080	1080 174_s_at	SH3P18	U61167	SH3P18 mRNA, complete cds	SH3 domain-containing protein SH3P18
				Human spermidine synthase gene,	
1081	1081 241 q at	SRM	M64231	complete cds.	spermidine synthase
				Human sterol carrier protein-X/sterol	
				carrier protein-2 (SCP-X/SCP-2) gene,	
1082	1082 36688_at	SCP-X/SCP-2	U11313	exon 16, and complete cds.	sterol carrier protein-X/sterol carrier protein-2
1083	1083 32587_at	ZFP36L2; BRF2; 1007802	U07802	Human Tis11d gene, complete cds.	Tis11d
1084	1084 31680 at	TOP1P2	M55630	Human topoisomerase I pseudogene 2.	
				Human transformation-related protein	
1085	1085 36446 s at	HMG1L2	L24521	mRNA, 3' end	transformation-related protein
				Human transmembrane protein (CD59)	
1086	1086 39351_at	CD59	M84349	gene, exon 4.	CD59 protein
1087	1087 38727 at	THE1	M23161	Human transposon-like element mRNA	
				Human vascular cell adhesion molecule-1	
1088	1088 41433 at	VCAM1	M73255	(VCAM1) gene, complete CDS.	vascular cell adhesion molecule-1
1089	1089 40121 at	HIP2	U58522	huntingtin interacting protein 2	huntingtin interacting protein
100		НУРН	AB023163	Huntingtin interacting protein H	KIAA0946 protein
1091	1091 40196 at	HYA22	D88153	HYA22 protein	HYA22
				-	
				hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A	enoyl-CoA hydratase/3-hydroxyacyl-CoA
				thiolase/enoyl-Coenzyme A hydratase	dehydrogenase alpha-subunit of trifunctional
1092	1092 36952_at	HADHA	D16480	(trifunctional protein), alpha subunit	protein

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ш	olase bet	oid dehy	269730_2	
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	3-ketoacyl-CoA thiolase beta-subunit of trifunctional protein	hydroxysteroid (17-beta) dehydrogenase 4 17beta-hydroxysteroid dehydrogenase	BC269730_1; BC269730_2; FEN1_HUMAN;	BC269730_4
		lase 4 1	5	
	oenzym ydratas Ibunit	ydroger	own fun hypoth notifs for a containi sontaini al protei al protei al protei al (Z702 egans); ase FEt MF1); C M	
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Δ	coenzym se/3-ket Coenzyn	d (17-be	protein 52 kDa 1s simils 1s simils 1s des 1s des 1s eleg 1s el	ete sed
	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	xysteroi	Hypothetical protein of unknown function: Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypotetical proteins encoded by (Z81122) T13F2.1 [Caenorhabditis elegans] and (Z70271) W08D2.4 [Caenorhabditis elegans] and (Z70271) MATUGRATION FACTOR 1 (MF1); DNase IV, RAD2_HUMAN; Hypothetical human Best's macular dystrophy relatedprotein; Simulated translation extends ORF of previously reported partial coding sequence for Best's macular dystrophy related protein (AF038536); Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1	gene, complete sequence.
	hydro; dehyd thiola: (trifun	hydro	Hypol Hypol hypot hypot fusion encon (Caer WOBI struct FLAF MATI IV, R Best' Simu previ sequ relati	gene
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	D16481	X87176		AC004770
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В	里	HSD17B4		5
-	HADHB	HSD		FEN1
A	at	at		at
	093 39741_at	1094 36626_at		1095 41583_at
	1093	1094		109

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LLIJ.	BC269730 1; BC269730 2; FEN1 HUMAN;	BC269730_4	hypothetical protein CG018	hypothetical protein AF038182
Q	Hypothetical protein of unknown function; Hypothetical 52 kDa protein; Hypothetical protein exhibits similarity to motifs found in (U79010) delta 6 desaturase, a hypothetical cytochrome b5 containing fusion protein, and hypotetical proteins encoded by (Z81122) T13F2.1 [Caenorhabditis elegans] and (Z70271) W08D2.4 [Caenorhabditis elegans]; DNA structure-specific endonuclease FEN1; FLAP ENDONUCLEASE-1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN; Hypothetical human Best's macular dystrophy related protein (AF038536); Homo sequence for Best's macular dystrophy related protein (AF038536); Homo sapiens chromosome 11, BAC CIT-HSP-11 PR (RC269730) containing the hFEN1		hypothetical gene CG018	hypothetical gene supported by AF038182; BC009203
၁		AC004770	U50527	AF038182
8		FEN1	CG018	LOC90355
A		096 34224_at	097 1527 s_at	1098 33466_at
		1096	100	109

Fig 21

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Ξ	R32184_1; R32184_3		hypothetical protein, similar to (AC007017) putative RNA helicase A [Arabidopsis thaliana]			
Q	Hypothetical human protein (partial CDS); CDS constructed from combination of BLASTX, EST matches and Xgrail predictions. N-terminus of protein likely encoded in flanking cosmid R29942. Predicted protein exhibits weak similarity to hypothetical protein PIDIe1226191 (AL021106) from Drosophila melanogaster; Hypothetical human protein most similar to Rat ionotropic glutamate receptor (L34938); CDS constructed primarity from XGRAIL_predictions and BLASTX similarity to (L34938) ionotropic glutamate receptor [Ratus norvegicus] and gil2160125 (U29873) MMDAR-L [Ratus norvegicus]. Also exhibits similarity to PIDIe258718 (Z78413) T01C3.10 [Caenorhabditis elegans]. C-terminus of hypothetical protein is ill-defined at this point; definition will require identification and characterization of appropriate cDNAs; Hypothetical 59.8 kDa human protein; CDS constructed from EST matches and Xgrail predictions. C- terminus of predicted protein not fully confirmed by EST or cDNA coverage. Hypothetical protein exhibits no significant database similarities when queried against R32184_3; R32184_3	hypothetical protein		hypothetical protein	hypothetical protein 23851	hypothetical protein 24636
3	φ	AA015605	AL079292	AF007130	AF035313	A 65 1 3 6 8
α	MGC2436	FLJ20811	LOC54505	LOC54104	LOC56007	LOC55977
V	009 35983 a ta	1100 38440 s at	<u> </u>		103 39517_at	1104 41561 s at
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1105	41128_at	LOC92703	AF070537	hypothetical protein BC013073	
1106	106 38972 at	LOC115207	AF052169	hypothetical protein BC013764	
1107		CGI-57	AF070638	hypothetical protein CGI-57	hypothetical protein CGI-57
1108	108 39960_at		AF091086	hypothetical protein CL640	hypothetical protein CL640
1109	109 38837 at	DJ971N18.2	W26226	hypothetical protein DJ971N18.2	
1110	1110 35142 at	DKFZP564D172	AF070617	hypothetical protein DKFZp564D172	
111	34830_at	DKFZP564K0822	K0822 W25986	hypothetical protein DKFZp564K0822	
1112	31852 at	DKFZP5640043	AL050390	hypothetical protein DKFZp5640043	
1113	1113 33895_at	DKFZP586F1318 AL050373	AL050373	hypothetical protein DKFZP586F1318	hypothetical protein
1114	1114 39692 at	DKFZP586F2423	F2423 AL080209	hypothetical protein DKFZp586F2423	
1115		FLB6421	AI133727	hypothetical protein FLB6421	
1116	1116 36647_at	FLJ10326	AA526812	hypothetical protein FLJ10326	
1117	1117 34804_at	FLJ10618	AL049246	hypothetical protein FLJ10618	
1118	1118 36840_at	FLJ10737	AF052158	hypothetical protein FLJ10737	
1119	1119 35283_at	FLJ10738	H05692	hypothetical protein FLJ10738	
1120	1120 37610_at	FLJ10803	AI765280	hypothetical protein FLJ10803	
1121	1121 33173 q at	FLJ10849	T75292	hypothetical protein FLJ10849	
1122	1122 39923 at	FLJ10971	A1935420	hypothetical protein FLJ10971	
				hypothetical protein FLJ11021 similar to	
1123	1123 38105_at	FLJ11021	W26521	splicing factor, arginine/serine-rich 4	
1124	124 33394_at	FLJ11126	AA034074	hypothetical protein FLJ11126	
1125	1125 35709_at	FLJ11149	AF038172	hypothetical protein FLJ11149	
1126	1126 38141 at	FLJ11193	AF038176	hypothetical protein FLJ11193	
1127	1127 40859 at	FLJ11806	AI561196	hypothetical protein FLJ11806	
1128	1128 41177 at	FLJ12443	AW024285	hypothetical protein FLJ12443	
1129	1129 41434 at	FLJ12552	AF070557	hypothetical protein FLJ12552	hypothetical protein FLJ12552
1130	1130 36580_at	FLJ13910	AL050139	hypothetical protein FLJ13910	hypothetical protein FLJ13910
1131	1131 32222 at	FLJ14639	AA152202	hypothetical protein FLJ14639	
1132	1132 38710 at	FLJ20113	AL096714	hypothetical protein FLJ20113	
1133	1133 38652 at	FLJ20154	AF070644	hypothetical protein FLJ20154	
1134	1134 40868 at	FLJ20274	AA42799	hypothetical protein FLJ20274	
135	1135 34739_at	FLJ20275	W26023	hypothetical protein FLJ20275	
1136	1136 34857_at	FLJ20986	Z24724	hypothetical protein FLJ20986	
1137	1137 32251_at	FLJ21174	AA149307	hypothetical protein FLJ21174	
1138	1138 40615_at	FLJ21439	AA780049	hypothetical protein FLJ21439	
1139	1139 33915_at	FLJ23027	W22655	hypothetical protein FLJ23027	

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AF070596						
Heart   Hear		∢	В			18
HSA01i916	1140	35198_at	LOC57146			hypothetical protein from clone 24/96
HSU79252   U79252   Hypothetical protein HSU79252   HSU79252   MGC14433   U79291   Hypothetical protein MGC2749   AA402538   Hypothetical protein MGC2749   AA402538   Hypothetical protein MGC27840 similar to a mypothetical protein MGC27840 similar to a mypothetical protein MGC3047   MGC3047   AL050202   Hypothetical protein MGC3047   AL050202   Hypothetical protein MGC3047   MGC3047   AL050202   Hypothetical protein MGC3047   MGC3047   MGC3047   MGC3047   MGC3047   MGC3047   MGC3047   MGC3047   MGC3047   MGC3047   MGC3049   MGC3149   U79260   Hypothetical protein MGC3049   MGC3149   WZ6659   Hypothetical protein MGC3041   MGC3084   MGC3084   AL032369   Hypothetical protein MGC3084   HPRT1   M31642   Clesch-Nyhan syndrome)   HPRT1   M31642   Clesch-Nyhan syndrome)   Mypoxia-inducible factor 1, alpha subunit (Casch-Nyhan syndrome)   McC3037   Mypoxia-inducible factor 1, alpha subunit (Casch-Nyhan syndrome)   McC3031   Mypoxia-inducible factor 1, alpha subunit   MC2032   Mypoxia-inducible factor 1, alpha subunit   MC2032   Mypoxia-inducible factor 1, alpha subunit   MC20331   Mypoxia-inducible factor	1141	38483 at	HSA011916		0	hypothetical protein
MGC14433         U79291         hypothetical protein MGC14433           MGC2749         AA402538         hypothetical protein MGC2749           MGC2840         AJ224875         hypothetical protein MGC2840 similar to a putative glucosyttansferase           MGC3047         AL0560202         hypothetical protein MGC3047           MGC3077         Al620381         hypothetical protein MGC3047           MGC3077         Al620381         hypothetical protein MGC3077           MGC3077         AF038186         CG8198           MGC5149         U79260         hypothetical protein MGC8721           MGC90821         MC68729         hypothetical protein MGC8721           MGC90821         AL035369         hypothetical protein MGC8721           MGC90824         AL035369         hypothetical protein MGC8721           MGC9084         AL035369         hypothetical protein MGC8721           MGC9084         AJ012409         hypothetical protein MGC8721           HPRT1         M31642         (Lesch-Nyhan syndrome)           LIVBL         U22431         (Lesch-Nyhan syndrome)           IK         AJ005579         IK cytokine, down-regulator of HLA II           IK         AJ005579         IK cytokine, down-regulator of HLA II           ILVBL         U61263	1142,	11236 at	HSU79252			hypothetical protein HSU79252
MGC2749   AA402538   hypothetical protein MGC2749     MGC2840   AJ224875   putative glucosytransferase   grosytransferase   MGC3047     MGC3047   AI620381   hypothetical protein MGC3047     MGC3047   AI620381   hypothetical protein MGC3047     MGC3047   AI620381   hypothetical protein MGC3047     MGC3149   U79260   hypothetical protein MGC8721     MGC8721   W26659   hypothetical protein MGC8721     MGC9724   AU025369   hypothetical protein MGC9084     MY014   AW024812   hypothetical protein MGC9084     MY014   AW024812   hypothetical protein MGC9084     MY014   AW024812   hypothetical protein MGC9084     HF11   M31642   (Lesch-Nyhan syndrome)     HF71   M31642   (Lesch-Nyhan syndrome)     IGFBP4   U20982   gene, promoter and complete cds.     IK   S74221   IK cytokine, down-regulator of HLA II     ILVBL   U61263   ivmediate early protein     ICRP   M62831   immediate early protein     IGRB   immediate early protein     IGRB   immediate early brotein	1143	38443_at	MGC14433		hypothetical protein MGC14433	
MGC2840	1144	39811 at	MGC2749		hypothetical protein MGC2749	
MGC2840					similar to a	
MGC3047   AL050202   hypothetical protein MGC3077   MGC3077   Al620381   hypothetical protein MGC4276 similar to hypothetical protein MGC4276 similar to hypothetical protein MGC4276 similar to hypothetical protein MGC4278 similar to CG8198   MGC5149   U79260   hypothetical protein MGC8721   MGC5149   MGC5084   AL035369   hypothetical protein MGC9084   AL035369   hypothetical protein MGC9084   AU035369   hypothetical protein MGC9084   hypothetical protein MGC9084   AU035369   hypothetical protein MGC9084   h	1145	32051 at	MGC2840			glucosyltransferase
MGC3077         Al620381         hypothetical protein MGC3077           MGC4276         AF038186         CG8198           MGC5149         U79260         hypothetical protein MGC5149           MGC8721         W26659         hypothetical protein MGC9084         h           MGC9084         AL035369         hypothetical protein MGC9084         h           MY014         AW024812         hypothetical protein MGC9084         h           MY014         AW024812         hypothetical protein MGC9084         h           MY014         AW024812         hypothetical protein MGC9084         h           HPRT1         M31642         hypothetical protein MGC9084         h           HPRT1         M31642         (Lesch-Nyhan syndrome)         h           HPRT1         M31642         (Lesch-Nyhan syndrome)         h           HPRT1         M31642         (Lesch-Nyhan syndrome)         h           HR         U20982         gne. promote and corp. HLA II         l           IK         S74221         IK cytokine, down-regulator of HLA II         l           ILVBL         U61263         iNR (bacterial acetolactate synthase)-like         l           IER3         S81914         immediate early response 3         immunoqlobulin (CD79A) bi	1146	35219_at	MGC3047		hypothetical protein MGC3047	
MGC4276         AF038186         CG8198         CG8198           MGC5149         U79260         hypothetical protein MGC5149         CG8198           MGC8721         W26659         hypothetical protein MGC8721         F           MGC9084         AL035369         hypothetical protein MGC9084         F           MY014         AW024812         hypothetical protein MGC9084         F           MY014         AW024812         hypothetical protein MGC9084         F           HPRT1         AJ012409         hypothetical protein MGC9084         F           HPRT1         M31642         (Lesch-Nyhan syndrome)         H           HIF1A         U22431         (basic helix-loop-helix transcription factor)         H           IK         AJ008579         IK cytokine, down-regulator of HLA II         IK           IK         S74221         IK cytokine, down-regulator of HLA II         IK cytokine, down-regulator of HLA II           ILVBL         U61263         INB (bacterial acetolactate synthase)-like         IR cytokine, down-regulator of HLA II           IER3         S81914         Immediate early protein         Immediate early protein           IGBP1         Y08915         Immediate early response 3           IGBP1         Immediate early protein	1147	11696_at	MGC3077			
MGC4276         AF038186         CG8198         CG8198         CG8199         CG8149         CG8149         CG8149         CG8149         CG8149         CG8149         CG8149         CG8198         CG8121         CG81223         CG8121         CG82323         CG82323         CG82323         CG82431         CG82431         CG82431         CG82431         CG82431         CG824-Nyhan syndrome)         CG82431         CG8241         CG8241         CG8241         CG8241         CG8241         CG8241         CG7241         CG7						hypothetical protein MGC4276 similar to
MGC5149         U79260         hypothetical protein MGC5149           MGC8721         W26659         hypothetical protein MGC8721         If           MGC9084         AL035369         hypothetical protein MGC9084         If           MY014         AW024812         hypothetical protein MGC9084         If           HPRT1         M31642         (Lesch-Nyhan syndrome)         If           HPRT1         M31642         (Lesch-Nyhan syndrome)         If           LESch-Nyhan syndrome)         hypothetical protein Tanscription factor)         If           LESch-Nyhan syndrome)         If         Clesch-Nyhan syndrome)         If           LESch-Nyhan syndrome)         If         Clesch-Nyhan syndrome)         If           LESch-Nyhan syndrome         If         Clesch-Nyhan syndrome         If           LESch-Nyhan syndrome         If         If         If           LESch-Nyhan syndrome         If         If         If           IK         AJ005579         IK cytokine, down-regu	1148	41147_at	MGC4276		CG8198	CG8198
MGC8721         W26659         hypothetical protein MGC8721         Item           MGC9084         AL035369         hypothetical protein MGC9084         Item           MY014         AW024812         hypothetical protein MGC9084         Item           YR-29         AJ012409         hypothetical protein My014         Item           YR-29         AJ012409         hypothetical protein My014         Item           HPRT1         M31642         Lesch-Nyhan syndrome)         Itemscription factor Item           HPRT1         M31642         (Lesch-Nyhan syndrome)         Itemscription factor Item           HPRT1         M31642         (Lesch-Nyhan syndrome)         Itemscription factor Item           HPRT1         M31642         (Lesch-Nyhan syndrome)         Itemscription factor Item           HET4         U22431         (basic helix-loop-helix transcription factor)         Item           IK         AJ005579         Itemother and complete cds.         Item           ILVBL         U61263         Item         Item           ILVBL         U61263         Item         Item           IER3         S81914         Immediate early protein           ICBP1         Y08915         Immunodlobulin (CD79A) binding protein 1	1149	37242_at	MGC5149		hypothetical protein MGC5149	
MGC9084         AL035369         hypothetical protein MGC9084         Ith           MY014         AW024812         hypothetical protein My014         Ith           YR-29         AJ012409         hypothetical protein My014         Ith           YR-29         AJ012409         hypothetical protein My014         Ith           HPRT1         M31642         (Lesch-Nyhan syndrome)         Ith           Lesch-Nyhan syndrome)         Ith         (Lesch-Nyhan syndrome)         Ith           LO22431         (Lesch-Nyhan syndrome)         Ith           NG2431         (basic helix-loop-helix transcription factor)         Ith           IGFBP4         U20982         gene, promoter and complete cds.           IK         AJ005579         IK cytokine, down-regulator of HLA II           IK         S74221         IK cytokine, down-regulator of HLA II           ILVBL         U61263         INB (bacterial acetolactate synthase)-like           IER3         S81914         Immediate early protein           ICBP1         Y08915         Immediate early response 3           Immunoqlobulin (CD79A) binding protein 1	1150	36975 at	MGC8721	W26659	hypothetical protein MGC8721	
MY014   AW024812   hypothetical protein My014	1151	35677 at	MGC9084	AL035369	hypothetical protein MGC9084	hypothetical protein
YR-29	1152	32504 at	MY014	AW024812	hypothetical protein My014	
hypoxanthine phosphoribosyltransferase 1  (Lesch-Nyhan syndrome)  HIF1A  U22431  (Lesch-Nyhan syndrome)  hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) I (BEBP4)  (GFBP4)  1153	38106 at	YR-29	AJ012409	hypothetical protein YR-29	hypothetical protein	
hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) (basic helix-loop-helix transcription factor) (BF binding protein-4; Human insulin-like growth factor binding protein-4 (IGFBP4) (IGFBP4 Growth factor binding protein-4 (IGFBP4) (IK AJ005579 IK cytokine, down-regulator of HLA II IK S74221 IK cytokine, down-regulator of HLA II IK Gytokine, down-regulator of HLA II IK Gytoki	1154	37640 at	HPRT1	M31642	hypoxanthine phosphoribosyttransferase 1 (Lesch-Nyhan syndrome)	hypoxanthine phosphoribosyltransferase 1
HIF1A   U22431   (basic helix-loop-helix transcription factor)					hypoxia-inducible factor 1, alpha subunit	
IGF binding protein-4; Human insulin-like growth factor binding protein-4 (IGFBP4) IGFBP4 U20982 gene, promoter and complete cds. IK AJ005579 IK cytokine, down-regulator of HLA II IK S74221 IK cytokine, down-regulator of HLA II ILVBL U61263 IVB (bacterial acetolactate synthase)-like ETR101 M62831 immediate early protein IER3 S81914 immediate early response 3 immunoqlobulin (CD79A) binding protein 1	1155	တ	HIF1A	U22431	(basic helix-loop-helix transcription factor)	hypoxia-inducible factor 1 alpha
IGFB74 O20962 gene, promoter and complete cas.  IK AJ005579 IK cytokine, down-regulator of HLA II  ILVBL U61263 iv B (bacterial acetolactate synthase)-like  ETR101 M62831 immediate early protein  IER3 S81914 immediate early response 3  immunoqlobulin (CD79A) binding protein 1			, (		IGF binding protein-4; Human insulin-like growth factor binding protein-4 (IGFBP4)	insulin-like arouth factor hinding protein-4
IK S74221 IK cytokine, down-regulator of HLA II ILVBL U61263 IVB (bacterial acetolactate synthase)-like ETR101 M62831 immediate early protein IER3 S81914 immediate early response 3 immunoqlobulin (CD79A) binding protein 1	1156	39781_at	IGFBP4	020982	gene, promoter and complete cus.	Der protein
IK S74221 IK cytokine, down-regulator of nLA ii  ILVBL U61263 ivB (bacterial acetolactate synthase)-like  ETR101 M62831 immediate early protein  IER3 S81914 immediate early response 3  IGBP1 Y08915 immunoqlobulin (CD79A) binding protein 1	1157	38046_at	¥	AJ005579	IN CYTORITIE, GOWII-TEGUIATOR OF THE STATE O	
ILVBL U61263 ivB (bacterial acetolactate synthase)-like ETR101 M62831 immediate early protein IER3 S81914 immediate early response 3 immunoqlobulin (CD79A) binding protein 1	158	218_at	¥	S74221	IK cytokine, down-regulator of HLA II	INTACION
ETR101 M62831 immediate early protein IER3 S81914 immediate early response 3 IGBP1 Y08915 immunoqlobulin (CD79A) binding protein 1	1159	37690_at	ILVBL	U61263	iNB (bacterial acetolactate synthase)-like	acetolactate synthase homolog
IER3 S81914 immediate early response 3 (GD79A) binding protein 1	1160	36097_at	ETR101	M62831	immediate early protein	immediate early protein
1GBP1 Y08915	1161	1237_at	IER3	S81914	immediate early response 3	immediate early response 3, isoform short; immediate early response 3, isoform long
	1162	34391_at	IGBP1	Y08915	immunoglobulin (CD79A) binding protein 1	alpha 4 protein

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				perfamily containing	
1163	38636_at	ISLR	AB003184		ISLH
				IMP (inosine monophosphate)	IMP (inosine monophosphate)
1164	1164 40695_at	IMPDH1	J05272		dehydrogenase 1
1165		IBTK	AL050018		hypothetical protein
				nant	inhibitor of DNA binding 1, dominant
1166	1166 36617 at	01	X77956		negative helix-loop-helix protein
				inhibitor of DNA binding 2, dominant	
1167	1167 41215 s at	ID2	D13891		Id-2H
				inhibitor of kappa light polypeptide gene	
1168	1168 34344 at	IKBKAP	AF044195	associated protein	IkappaB kinase complex associated protein
				inner membrane protein, mitochondrial	
1169	1169 37659 at	IMMI	L42572		transmembrane protein
					human type 1 inositol 1,4,5-trisphosphate
11170	1170 755 at	ITPR1	D26070	inositol 1,4,5-triphosphate receptor, type 1	receptor
					human type 1 inositol 1,4,5-trisphosphate
11171	1171 32778 at	ITPR1	D26070	inositol 1,4,5-triphosphate receptor, type 1	receptor
1172	1172 36154 at	IHPK1	D87452	inositol hexaphosphate kinase 1	KIAA0263 protein
					lithium-sensitive myo-inositol
11173	1173 32697 at	IMPA1	AF042729	inositol(myo)-1(or 4)-monophosphatase 1	monophosphatase A1
					•
1174	1174 36496_at	IMPA2	AF014398	inositol(myo)-1(or 4)-monophosphatase 2 myo-inositol monophosphatase 2	myo-inositol monophosphatase 2
1175	1175 35833_at	LOC51141	AL080184	insulin induced protein 2	
1176	1176 41049 at	IRS1	S62539	insulin receptor substrate 1	insulin receptor substrate-1
1177	1177 851 s at	IRS1	S62539	insulin receptor substrate 1	insulin receptor substrate-1
				insulin-like growth factor 1 (somatomedin	
1178	1178 38737 at	1GF1	X57025	(0)	insulin-like growth factor I
				insulin-like growth factor 1 (somatomedin	
1175	1179 1501 at	IGF1	X57025	(2)	insulin-like growth factor I
1180	160027 s at	IGF2R	Y00285	insulin-like growth factor 2 receptor	insulin-like growth factor 2 receptor
				insulin-like growth factor binding protein 2	insulin-like growth factor binding protein 2 insulin-like growth factor binding protein 2
118	1181 40422_at	IGFBP2	X16302	(36kD)	(36kD)
,	1707 0	KGEBDA	MEDAUS	insulin-like growth factor binding protein 4	insulin-like growth factor binding protein 4 linsulin-like growth factor binding protein 4
α -	118211/3/ S.at	Gror4	INIOZ400	insuliting grown many branch	6

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	A	മ	C	O	บ
1183	1183 2062 at	(GFBP7	L19182	insulin-like growth factor binding protein 7	
3	·.I	176.84	1 20021	integral membrane protein 1	integral membrane protein 1
201	1184 37991_at	I MI	L3030 I	וויפקימו וויפיווסימוס בייסימיי	
	_ <del>-</del>			integral membrane protein; swiss-prot accession: O04901; may play role in cell	
1185	1185 37326 at	A4	U93305	differentiation in intestinal epithelium	LIM domain only 6
1186	1186 41163 at	P24B	AL109672	integral type I protein	p24B protein
					integrin beta 1 isoform 1A precursor; integrin
					beta 1 isoform 1B precursor; integrin beta 1
					isoform 1C-1 precursor, integrin beta 1
				integrin beta 1 subunit precursor; Human	isoform 1D precursor; integrin beta 1 isoform
1187	1187 32808_at	ITGB1; CD29; FN X07979	87670X	mRNA for integrin beta 1 subunit.	1C-2 precursor
				integrin cytoplasmic domain-associated	integrin cytoplasmic domain associated
1188	1188 1195 s_at	ICAP-1A	AF012024	protein 1	protein
1189	1189 120 at	ITGA1	X68742	integrin, alpha 1	
1190	37484 at	ITGA1	X68742	integrin, alpha 1	
1191	191 36892 at	ITGA7	AF032108	integrin, alpha 7	integrin alpha-7
				integrin, alpha V (vitronectin receptor,	integrin, alpha V (vitronectin receptor, alpha
1192	1192 39071 at	ITGAV	M14648	alpha polypeptide, antigen CD51)	polypeptide, antigen CD51)
1193	193 39754 at	ITGB5	X53002	integrin, beta 5	
1194	1194 2058 s at	ITGB5	M35011	integrin, beta 5	integrin, beta 5
	1			integrin, beta-like 1 (with EGF-like repeat	
1195	1195 40681 at	ITGBL1	AB008375	domains)	osteoblast specific cysteine-rich protein
1196	1196 35365 at	봇	U40282	integrin-linked kinase	integrin-linked kinase
				interacts with adenovirus E3-14.7KDa, a	
				TNF-alpha cytolysis antagonist; leucine	
				zipper protein; alternatively translated;	
				long form; interacts with adenovirus E3-	
	_			14.7KDa, a TNF-alpha cytolysis	
				antagonist; leucine zipper protein;	
				alternatively translated; short form; Homo	
	•		i d	sapiens FIP2 alternatively translated	
119,	1197 41743_!_at	OPIN, NAP, FIF,	FZAFU61034	India, complete cas.	1116

	₫	В	O	Q	Ш
T				interacts with adenovirus E3-14.7KDa, a	
				TNF-alpha cytolysis antagonist; leucine	
				zipper protein; alternatively translated;	
				long form; interacts with adenovirus E3-	
				14.7KDa, a TNF-alpha cytolysis	
				antagonist; leucine zipper protein;	
_				alternatively translated; short form; Homo	
1198	1198 41742 s at	OPTN; NRP; FIP2	P2/AF061034	mRNA, complete cds.	FIP2
				interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 1
1199	1199 676 q at	IIFITM1	J04164	1 (9-27)	(9-27)
	-6-			interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 1
1200	1200 675 at	IFITM1	J04164	1 (9-27)	(9-27)
				interferon induced transmembrane protein	interferon induced transmembrane protein interferon induced transmembrane protein 3
1201	1201 41745 at	IFITM3	X57352	3 (1-8U)	(1-8U)
1202 1456	1456 s at	IF116	M63838		interferon-gamma induced protein
1203	╢ؾ	IFI30	J03909		interferon, gamma-inducible protein 30
1204	1204 39728 at	IF130	103909		interferon, gamma-inducible protein 30
					interferon-induced protein with
1205	1205 32814 at	FIT	M24594	tetratricopeptide repeats 1	tetratricopeptide repeats 1
				interferon-related developmental regulator	
1206	1206 37679 at	IFRD1	Y10313		PC4 protein
1207	1207 1368 at	IL1R1	M27492	interleukin 1 receptor, type l	interleukin 1 receptor, type l
1208	1208 33228 g at	IL10RB	AI984234	interleukin 10 receptor, beta	
1209	33227_at	IL10RB	Al984234	interleukin 10 receptor, beta	
1210	1210 38969_at	11.27	A1828168	interleukin 27	
1211	1211 38299_at	IL6	X04430	interleukin 6 (interferon, beta 2)	interleukin 6 (interferon, beta 2)
1212	1212 35372 r at	11.8	M17017	interleukin 8	interleukin 8
				interleukin enhancer binding factor 2,	
1213	1213 36189 at	ILF2	U10323	45kD	NF45 protein
1214	1214 36030 at	DKFZP58612223	AL080214	intermediate filament-like MGC:2625	hypothetical protein
1215	1215 35776 at	ITSN1	AF064243	intersectin 1 (SH3 domain protein)	intersectin short form
1216	1216 41431 at	ΞĊΚ	AB023153	intestinal cell kinase	KIAA0936 protein
		0	75000	IQ motif containing GTPase activating	res GTPase-activating-like protein
121/	121 / 1825_at	IGGAPT	L330/3	Diotem 1	ומי כוו מים תפונגתווים וווים ליכיכוו

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-	¥	В	3	(TOUN) F SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	
218	1218 39023 at	IDH1	AF020038	soluble	NADP-dependent isocitrate dehydrogenase
	5-0-000		0000	increte dehydronensee 3 (NAD+) beta	
1219	1219 40112 at	ПНЗВ	AA522698	וצטכווומום חפוואחוספרוומום בייניים	NAD+-specific isocitrate dehydrogenase
	400040111 0 00	IDH3B	U49283	fa	beta precursor
221	) to	KIAA1162	AL021396	UJA1	hypothetical protein
201		dJ196E23.1	Z97632	isoform 2 match: protein Q99991	compesiii-like receptor o
1223		IARS	U04953	isoleucine-tHNA synthetase	Soledayin the symmetry
1224	1224 36985 at	IDI.	X17025	elta isomerase	isopentenyl-diphosphate delta isomerase
		FNO	AEDRADRA	isoprenylcysteine carboxyl methyltransferase	prenylcysteine carboxyl methyltransferase
1225	1225 41 / /5_at	2			
1226	1226 34877_at	JAK1	AL039831	Janus Kinase 1 (a protein tyrosine ninase)	IMA protein
1227	1227 34318 at	JM4	AJ005896	JM4 protein	isiasa ta IAZE1
1228	1228 40957 at	JJAZ1	D63881	joined to JAZF1	John Barrier 10 State 11
1229	1229 41250 at	JTV1	U24169	JTV1 gene	31 V-1
1230	1230 41483 s at	QNOC	X56681	jun D proto-oncogene	Juno protein
1231	1231 1612 s at	QNOC	X56681	jun D proto-oncogene	Jund protein
1232	1232 40464 g at	KPNB2	U70322	karyopherin (importin) beta 2	Transporting profession 5
1233	1233 39028 at	KPNB3	Y08890	karyopherin (importin) beta 3	Ran_Gir biliding protein 5
1232	1234 35725 at	KPNA3	D89618	karyopherin alpha 3 (importin alpha 4)	Karyopnerin ampir 3
1 5	1035 32487 c at	KPNA4	AB002533	karyopherin alpha 4 (importin alpha 3)	Cip.
3	20-10-10			katanin p60 (ATPase-containing) subunit	
1936	1236,32708 g at	KATNA1	AI191768	A1	
	-6-22			KDEL (Lys-Asp-Glu-Leu) endoplasmic	L
1237	1237 37386 i at	KDELR1	X55885	reticulum protein retention receptor 1	NUEL receptor
	11			KDEL (Lys-Asp-Glu-Leu) endoplasmic	KDEL receptor 2
1238	1238 39080_at	KDELR2	M88458	KDFI (I vs-Asp-Glu-Leu) endoplasmic	
- 2	00700	KOEI B3	Al 035081	reticulum protein retention receptor 3	hypothetical protein
	1239 33402 at	ABOSE180	AR026190	Kelch motif containing protein	Kelch motif containing protein
124	1240 37 50_al	KRTHB6	X99142	keratin, hair, basic, 6 (monilethrix)	type II intermediate filament of hair keratin
	05050	000	Meedo	KH domain containing, RNA binding,	p62
124	1242 39346_at	KHUHBS I	W166 1 00		

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						L
KIAA0099         D13634         KIAA0002 gene product           KIAA0022         D14664         KIAA0022 gene product           KIAA0022         D14664         KIAA0022 gene product           KIAA0032         D31887         KIAA0032 protein           KIAA0062         D38521         KIAA0037 protein           KIAA0097         D43848         KIAA0097 protein           KIAA0097         D43848         KIAA0097 gene product           KIAA0097         D43848         KIAA0097 gene product           KIAA0100         D43848         KIAA0097 gene product           KIAA0110         D43849         KIAA0198 close product           KIAA0111         D43847         KIAA0198 protein           KIAA0112         D43847         KIAA0110 gene product           KIAA012         D50928         KIAA0113 gene product           KIAA013         D50928         KIAA0136 protein           KIAA0152         D63877         KIAA0170 gene product           KIAA0113         D63877         KIAA0170 gene product           KIAA0114         D63877         KIAA0170 gene product           KIAA01152         D63877         KIAA0170 gene product           KIAA01162         D63926         KIAA0170 gene product	_	⋖	ω	ပ	Ü	IJ
KIAA0022         D14664         KIAA0022 gene product           KIAA0033         D26067         KIAA0033 prolein           KIAA0062         D33621         KIAA0032 prolein           KIAA0096         D43826         KIAA0077 prolein           KIAA0097         D43848         KIAA0097 gene product           KIAA0097         D43948         KIAA0097 gene product           KIAA0098         D43948         KIAA0098 is a human countenpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified.           KIAA0190         D43948         KIAA0098 is a human countenpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified.           KIAA0190         D43948         KIAA0098 is a human countenpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified.           KIAA0110         D43940         KIAA0098 is a human countenpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified.           KIAA0110         D43947         KIAA0109 gene product           KIAA0111         D21853         KIAA0110 gene product           KIAA0112         D5091         KIAA0113 gene product           KIAA0113         D50928         KIAA0130 protein           KIAA0112         D50928         KIAA0130 protein           KIAA0112         D50928         KIAA0112 protein	1243	32679 at	KIAA0009	D13634	KIAA0009 gene product	KIAA0009 gene product
KIAA0033         D26067         KIAA0033 protein           KIAA0062         D31887         KIAA0062 protein           KIAA0096         D43636         KIAA0096 protein           KIAA0097         D43638         KIAA0096 protein           KIAA0097         D43848         KIAA0098 protein           KIAA0097         D43848         KIAA0098 protein           KIAA0097         D43848         KIAA0098 protein           KIAA0098         D43848         KIAA0098 protein           KIAA0102         D43848         KIAA0098 protein           KIAA0102         D14658         KIAA0108 protein           KIAA0102         D14658         KIAA0102 gene product           KIAA01102         D14658         KIAA01102 gene product           KIAA01103         D63877         KIAA01102 gene product           KIAA0	1244	34760 at	KIAA0022	D14664	KIAA0022 gene product	KIAA0022 gene product
KIAA0062         D31887         KIAA0062 protein           KIAA0077         D38521         KIAA0097 protein           KIAA0096         D43636         KIAA0096 protein           KIAA0097         D43948         KIAA0097 gene product           KIAA0097         D43948         KIAA0097 gene product           KIAA0098         Pannan counterpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified.           Ha01413         CDA3950         Ha01413 cDNA clone for KIAA0098 has a 2-bp insertion between 736-73 of the sequence of KIAA0098 protein, partial cds. If KIAA0110           KIAA0110         D43947         KIAA0102 gene product           KIAA0111         D21853         KIAA0102 gene product           KIAA0136         D50926         KIAA0113 gene product           KIAA0131         D50928         KIAA0132 gene product           KIAA0132         D63477         KIAA0132 protein           KIAA0136         D50928         KIAA0152 protein           KIAA0157         D79996         KIAA0157 protein           KIAA0172         D79996         KIAA0173 gene product           KIAA0174         D79996         KIAA0173 gene product           KIAA0174         D79996         KIAA0157 protein           KIAA0191         D80006         KIAA0173 gene pro	1245	at	KIAA0033	D26067	KIAA0033 protein	
KIAA0096         D43636         KIAA0096 protein           KIAA0096         D43636         KIAA0096 protein           KIAA0097         D43948         KIAA0096 protein           KIAA0097         D43948         KIAA0096 protein           KIAA0097         D43948         KIAA0098 c a human counterpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified.           KIAA0109         D43947         MA0133 c DNA clone for KIAA0098 has a sequence of KIAA0098 protein. Partial cds. It kIAA0111           KIAA0102         D14658         KIAA0100 gene product           KIAA0111         D21853         KIAA0100 gene product           KIAA0112         D50911         KIAA0138 protein           KIAA0138         D50928         KIAA0138 protein           KIAA0139         D63877         KIAA0133 protein           KIAA0157         D63877         KIAA0132 protein           KIAA0157         D63877         KIAA0132 protein           KIAA0157         D79996         KIAA0172 protein           KIAA0174         D80000         KIAA0173 protein           KIAA0174         D80000         KIAA0174 pene product           KIAA0174         D80000         KIAA0174 pene product           KIAA0174         D80000         KIAA0174 pene product	1246		KIAA0062	D31887	KIAA0062 protein	
KIAA0096         D43636         KIAA0096 protein           KIAA0097         D43948         KIAA0097 gene product           KIAA0097         D43948         KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified. hao1413 cDNA clone for KIAA0098 has a 2-bp insertion between 736-737 of the sequence of KIAA0098; Homo sapiens           KIAA0102         D43947         KIAA0102 gene product         PKIAA0098           KIAA0121         D21853         KIAA0110 gene product         PKIAA0121 gene product           KIAA0122         D50911         KIAA0111 gene product         PKIAA0121           KIAA0138         D50926         KIAA0112 gene product         PKIAA0136           KIAA0152         D63477         KIAA0152 gene product         PKIAA0152           KIAA0153         D63477         KIAA0152 gene product         PKIAA0152           KIAA0154         D63877         KIAA0152 gene product         KIAA0152           KIAA0157         D63877         KIAA0152 gene product         KIAA0174           KIAA0174         D79992         KIAA0175 protein         KIAA0176           KIAA0174         D79995         KIAA0179 gene product         KIAA0179 protein           KIAA0191         D83776         KIAA0179 gene product         KIAA0191           KIAA0191	1247		KIAA0077	D38521	KIAA0077 protein	
KIAA0097         D43948         KIAA0097 gene product         M           KIAA0097         D43948         KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified. ha01413 cDN4 clone for KIAA0088 has a 2-bp insertion between 736-737 of the sequence of KIAA0098. Homo sapiens           KIAA0102         D43950         mRNNA for KIAA0098 protein, partial cds. b KIAA0112         MAA0102         b MAA0102	1248	37718 at	KIAA0096	D43636	KIAA0096 protein	
KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene. Start codon is not identified.	1249	37293_at	KIAA0097	D43948	KIAA0097 gene product	KIAA0097 protein
Mouse chaperonin containing TCP-1   gene. Start codon is not identified.					KIAA0098 is a human counterpart of	
Start codon is not identified.		•			mouse chaperonin containing TCP-1	
National					gene. Start codon is not identified.	
S-bp insertion between 736-737 of the sequence of KIAA0098   Puserion between 736-737 of the sequence of KIAA0098; Homo sapiens   KIAA0100   Duay 17   Color				ha01413 cDNA clone for KIAA0098 has a		
KIAA009B         D43950         mRNA for KIAA009B; Homo sapiens           KIAA0100         D43947         KIAA0100 gene product           KIAA0102         D14658         KIAA0102 gene product           KIAA0111         D21853         KIAA0102 gene product           KIAA0121         D50911         KIAA011 gene product           KIAA0136         D50926         KIAA012 gene product           KIAA0138         D50928         KIAA0138 gene product           KIAA0143         D63477         KIAA0138 gene product           KIAA0152         D63477         KIAA0143 protein           KIAA0152         D63877         KIAA0157 gene product           KIAA0174         D79996         KIAA0172 protein           KIAA0174         D79996         KIAA0174 gene product           KIAA0191         D80001         KIAA0199 protein           KIAA0193         D80006         KIAA0199 protein           KIAA0195         D83776         KIAA0195 gene product           KIAA0196         D83779         KIAA0195 gene product           KIAA0196         D83779         KIAA0195 gene product           KIAA022         D86957         KIAA0195 gene product           KIAA0225         D86978         KIAA0225 protein					2-bp insertion between 736-737 of the	
KIAA0109B         D43950         mRINA for KIAA0109 protein, partial cds.         Individed for KIAA0100 gene product           KIAA0102         D14658         KIAA0102 gene product         Individed for for for for for for for for for for					sequence of KIAA0098.; Homo sapiens	
KIAA0100         D43947         KIAA0100 gene product           KIAA0102         D14658         KIAA0102 gene product           KIAA0121         D21853         KIAA0111 gene product           KIAA0121         D50911         KIAA0121 gene product           KIAA0138         D50928         KIAA0138 gene product           KIAA0143         D63477         KIAA0138 gene product           KIAA0152         D63477         KIAA0143 protein           KIAA0152         D63877         KIAA0152 gene product           KIAA0170         D79994         KIAA0172 protein           KIAA0172         D79996         KIAA0174 gene product           KIAA0174         D79996         KIAA0174 gene product           KIAA0191         D80006         KIAA0179 protein           KIAA0193         D83776         KIAA0191 protein           KIAA0195         D83779         KIAA0195 gene product           KIAA0196         D83779         KIAA0195 gene product           KIAA0196         D83779         KIAA0195 gene product           KIAA0202         D83779         KIAA0196 gene product           KIAA0202         D86957         KIAA0202 protein           KIAA0217         D86978         KIAA0225 protein	1250		KIAA0098	D43950	mRNA for KIAA0098 protein, partial cds.	KIAA0098 protein
KIAA0102         D14658         KIAA0102 gene product           KIAA0111         D21853         KIAA0111 gene product           KIAA0121         D50911         KIAA0121 gene product           KIAA0136         D50926         KIAA0136 protein           KIAA0138         D50928         KIAA0138 gene product           KIAA0143         D63477         KIAA0132 gene product           KIAA0152         D63877         KIAA0152 gene product           KIAA0170         D79994         KIAA0172 protein           KIAA0172         D79996         KIAA0174 gene product           KIAA0174         D79996         KIAA0179 protein           KIAA0191         D80001         KIAA0179 protein           KIAA0193         D83776         KIAA0191 protein           KIAA0195         D83779         KIAA0195 gene product           KIAA0196         D83779         KIAA0195 gene product           KIAA0196         D83779         KIAA0195 gene product           KIAA0202         D83779         KIAA0195 gene product           KIAA0202         D883779         KIAA0195 gene product           KIAA0202         D86957         KIAA0202 protein           KIAA0225         D86978         KIAA0225 protein	1251	39783 at	KIAA0100	D43947	KIAA0100 gene product	KIAA0100 protein
KIAA0111         D21853         KIAA0111 gene product           KIAA0121         D50911         KIAA0121 gene product           KIAA0136         D50926         KIAA0136 protein           KIAA0138         D50928         KIAA0138 gene product           KIAA0143         D63477         KIAA0143 protein           KIAA0152         D63477         KIAA0152 gene product           KIAA0170         D79992         KIAA0175 protein           KIAA0172         D79994         KIAA0174 gene product           KIAA0174         D79996         KIAA0174 gene product           KIAA0179         D80001         KIAA0179 protein           KIAA0191         D80006         KIAA0194 protein           KIAA0193         D83776         KIAA0195 gene product           KIAA0196         D83779         KIAA0195 gene product           KIAA0196         D83779         KIAA0195 gene product           KIAA0202         D83780         KIAA0195 gene product           KIAA0202         D86957         KIAA0202 protein           KIAA0225         D86978         KIAA0225 protein	1252	37359 at	KIAA0102	D14658	KIAA0102 gene product	KIAA0102 gene product
KIAA0121         D50911         KIAA0121 gene product           KIAA0136         D50926         KIAA0136 protein           KIAA0138         D50928         KIAA0138 gene product           KIAA0143         D63477         KIAA0143 protein           KIAA0152         D63486         KIAA0152 gene product           KIAA0170         D79992         KIAA0170 gene product           KIAA0172         D79994         KIAA0172 protein           KIAA0174         D79996         KIAA0174 gene product           KIAA0179         D80001         KIAA0179 protein           KIAA0191         D80006         KIAA0199 protein           KIAA0193         D83776         KIAA0191 protein           KIAA0195         D83779         KIAA0195 gene product           KIAA0196         D83779         KIAA0195 gene product           KIAA0196         D83779         KIAA0195 gene product           KIAA0202         D86957         KIAA0196 gene product           KIAA0202         D86957         KIAA0202 protein	1253	38031 at	KIAA0111	D21853	KIAA0111 gene product	KiAA0111 gene product
KIAA0136         D50926         KIAA0136 protein           KIAA0138         D50928         KIAA0138 gene product           KIAA0143         D63477         KIAA0143 protein           KIAA0152         D63486         KIAA0152 gene product           KIAA0170         D79992         KIAA0170 gene product           KIAA0172         D79994         KIAA0172 protein           KIAA0174         D79996         KIAA0174 gene product           KIAA0179         D80001         KIAA0179 protein           KIAA0191         D80006         KIAA0191 protein           KIAA0193         D83776         KIAA0193 gene product           KIAA0195         D83779         KIAA0195 gene product           KIAA0196         D83780         KIAA0195 gene product           KIAA0196         D83780         KIAA0195 gene product           KIAA0202         D86957         KIAA0202 protein           KIAA0225         D86978         KIAA0225 protein	1254	40279 at	KIAA0121	D50911	KIAA0121 gene product	KIAA0121 protein
KIAA0138         D50928         KIAA0138 gene product           KIAA0143         D63477         KIAA0143 protein           KIAA0152         D63486         KIAA0152 gene product           KIAA0170         D79992         KIAA0170 gene product           KIAA0172         D79996         KIAA0172 protein           KIAA0174         D79996         KIAA0174 gene product           KIAA0179         D80001         KIAA0179 protein           KIAA0191         D80006         KIAA0194 protein           KIAA0193         D83776         KIAA0193 gene product           KIAA0195         D83779         KIAA0195 gene product           KIAA0196         D83780         KIAA0195 gene product           KIAA0202         D83780         KIAA0195 gene product           KIAA0202         D86957         KIAA0202 protein           KIAA0225         D86978         KIAA0225 protein	1255	36845 at	KIAA0136	D50926	KIAA0136 protein	
KIAA0143         D63477         KIAA0143 protein           KIAA0152         D63486         KIAA0152 gene product           KIAA0170         D79992         KIAA0170 gene product           KIAA0172         D79996         KIAA0172 protein           KIAA0174         D79996         KIAA0174 gene product           KIAA0179         D80001         KIAA0179 protein           KIAA0191         D80006         KIAA0199 protein           KIAA0193         D83776         KIAA0191 protein           KIAA0195         D83779         KIAA0195 gene product           KIAA0196         D83780         KIAA0195 gene product           KIAA0196         D83780         KIAA0196 gene product           KIAA0202         D83780         KIAA0196 gene product           KIAA0202         D86957         KIAA0202 protein           KIAA0225         D86978         KIAA0225 protein	1256	32099 at	KIAA0138	D50928	KIAA0138 gene product	KIAA0138 gene product
KİAA0152         D63486         KİAA0152 gene product           KİAA0157         D63877         KİAA0157 protein           1         KİAA0170         D79992         KİAA0170 gene product           KİAA0172         D79996         KİAA0172 protein           KİAA0174         D79996         KİAA0174 gene product           KİAA0184         D80001         KİAA0179 protein           KİAA0191         D83776         KİAA0191 protein           KİAA0193         D83777         KİAA0193 gene product           KİAA0196         D83779         KİAA0195 gene product           KİAA0196         D83780         KİAA0196 gene product           KİAA0202         D86957         KİAA0196 gene product           KİAA0202         D86957         KİAA0202 protein           KİAA0225         D86978         KİAA0225 protein	1257	38472 at	KIAA0143	D63477	KIAA0143 protein	
KIAA0157         D63877         KIAA0157 protein           t         KIAA0170         D79992         KIAA0170 gene product           KIAA0172         D79994         KIAA0172 protein           KIAA0174         D79996         KIAA0174 gene product           KIAA0179         D80001         KIAA0179 protein           KIAA0191         D83776         KIAA0191 protein           KIAA0193         D83777         KIAA0193 gene product           KIAA0196         D83779         KIAA0195 gene product           KIAA0196         D83780         KIAA0196 gene product           KIAA0202         D86957         KIAA0202 protein           KIAA0217         D86957         KIAA0217 protein           KIAA0225         D86978         KIAA0225 protein	1258	41728 at	KIAA0152	D63486	KIAA0152 gene product	KIAA0152 gene product
(1)         KIAA0170         D79992         KIAA0170 gene product           (1)         KIAA0172         D79994         KIAA0172 protein           (1)         KIAA0174         D79996         KIAA0174 gene product           (1)         KIAA0179         D80001         KIAA0179 protein           (1)         KIAA0191         D83776         KIAA0191 protein           (1)         KIAA0193         D83777         KIAA0193 gene product           (1)         KIAA0196         D83779         KIAA0195 gene product           (1)         KIAA0196         D83780         KIAA0196 gene product           (1)         KIAA0202         D86957         KIAA0202 protein           (1)         KIAA0217         KIAA0218         KIAA0217           (1)         KIAA0225         KIAA0225 protein	1259	37642 at	KIAA0157	D63877	KIAA0157 protein	KIAA0157 protein
KIAA0172         D79994         KIAA0172 protein           KIAA0174         D79996         KIAA0174 gene product           KIAA0179         D80001         KIAA0179 protein           KIAA0184         D80006         KIAA0184 protein           KIAA0191         D83776         KIAA0191 protein           KIAA0195         D83777         KIAA0195 gene product           KIAA0196         D83779         KIAA0195 gene product           KIAA0196         D83780         KIAA0196 gene product           KIAA0202         D86957         KIAA0202 protein           KIAA0217         D86971         KIAA0225 protein           KIAA0225         D86978         KIAA0225 protein	1260	32661_s_at	KIAA0170	D79992	KIAA0170 gene product	KIAA0170 gene product
KIAA0174         D79996         KIAA0174 gene product           KIAA0179         D80001         KIAA0179 protein           KIAA0184         D80006         KIAA0184 protein           KIAA0191         D83776         KIAA0191 protein           KIAA0193         D83777         KIAA0193 gene product           KIAA0196         D83779         KIAA0195 gene product           KIAA0196         D83780         KIAA0196 gene product           KIAA0202         D86957         KIAA0202 protein           KIAA0217         D86971         KIAA0217 protein           KIAA0225         D86978         KIAA0225 protein	1261	37225_at	KIAA0172	D79994	KIAA0172 protein	
KIAA0179         D80001         KIAA0179 protein           KIAA0184         D80006         KIAA0184 protein           KIAA0191         D83776         KIAA0191 protein           KIAA0193         D83777         KIAA0195 gene product           KIAA0196         D83779         KIAA0195 gene product           KIAA0196         D83780         KIAA0196 gene product           KIAA0202         D86957         KIAA0202 protein           KIAA0217         D86971         KIAA0225 protein	1262	36942_at	KIAA0174	D79996	KIAA0174 gene product	KIAA0174 gene product
KIAA0184         D80006         KIAA0184 protein           KIAA0191         D83776         KIAA0191 protein           KIAA0193         D83777         KIAA0193 gene product           KIAA0196         D83779         KIAA0195 gene product           KIAA0196         D83780         KIAA0196 gene product           KIAA0202         D86957         KIAA0202 protein           KIAA0217         D86971         KIAA0225 protein	1263	31863_at	KIAA0179	D80001	KIAA0179 protein	
KIAA0191         D83776         KIAA0191 protein           KIAA0193         D83777         KIAA0193 gene product           KIAA0195         D83779         KIAA0195 gene product           KIAA0196         D83780         KIAA0196 gene product           KIAA0202         D86957         KIAA0202 protein           KIAA0217         D86971         KIAA0217 protein           KIAA0225         D86978         KIAA0225 protein	1264	37734_at	KIAA0184	D80006	KIAA0184 protein	
KIAA0193         D83777         KIAA0193 gene product           KIAA0195         D83779         KIAA0195 gene product           KIAA0196         D83780         KIAA0196 gene product           KIAA0202         D86957         KIAA0202 protein           KIAA0217         D86971         KIAA0217 protein           KIAA0225         D86978         KIAA0225 protein	1265	41669 at	KIAA0191	D83776	KIAA0191 protein	
KIAA0195         D83779         KIAA0195 gene product           KIAA0196         D83780         KIAA0196 gene product           KIAA0202         D86957         KIAA0202 protein           KIAA0217         D86971         KIAA0217 protein           KIAA0225         D86978         KIAA0225 protein	1266	36192 at	KIAA0193	D83777	KIAA0193 gene product	KIAA0193 gene product
KIAA0196         D83780         KIAA0196 gene product           KIAA0202         D86957         KIAA0202 protein           KIAA0217         D86971         KIAA0217 protein           KIAA0225         D86978         KIAA0225 protein	1267	38056 at	KIAA0195	D83779	KIAA0195 gene product	KIAA0195 gene product
KIAA0202 D86957 KIAA0217 D86971 KIAA0225 D86978	1268	38419 at	KIAA0196	D83780	KIAA0196 gene product	KIAA0196 gene product
KIAA0217 D86971 KIAA0225 D86978	1269	38067_at	KIAA0202	D86957	KIAA0202 protein	
38728 at KIAA0225 D86978	1270	32586_at	KIAA0217	D86971	KIAA0217 protein	
	1271	38728	KIAA0225	D86978	KIAA0225 protein	

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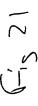
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	A	æ	ی	1	
1272 40	40971_at	KIAA0229	D86982	KIAA0229 protein	
12733	1273 37748 at	KIAA0232	D86985	KIAA0232 gene product	KIAA0232 protein
1274 3	38892 at	KIAA0240	D87077	KIAA0240 protein	
1275 40765	0765 at	KIAA0251	D87438	KIAA0251 protein	
12764	1276 41634 at	KIAA0256	D87445	KIAA0256 gene product	KIAA0256 protein
12773	36971_at	KIAA0257	D87446	KIAA0257 protein	
12783	32237 at	KIAA0265	D87454	KIAA0265 protein	
12793	39405 at	KIAA0266	D87455	KIAA0266 gene product	KIAA0266 gene product
12803	1280 35039 at	KIAA0276	D87466	KIAA0276 protein	
1281 38592	8592 s at	KIAA0284	AI828210	KIAA0284 protein	
1282 41381	1381_at	KIAA0308	AB002306	KIAA0308 protein	
1283 37943	17943 at	KIAA0321	AB002319	KIAA0321 protein	
1284 32592	32592 at	KIAA0323	AB002321	KIAA0323 protein	
1285 39797	39797 at	KIAA0349	AB002347	KIAA0349 protein	
1286 34661		KIAA0350	AB002348	KIAA0350 protein	KIAA0350 protein
1287 3		KIAA0355	AB002353	KIAA0355 gene product	KIAA0355 gene product
12883	1288 32223 at	KIAA0365	AB002363	KIAA0365 gene product	
1289	1289 33442 at	KIAA0367	AB002365	KIAA0367 protein	
1290	1290 35830_at	KIAA0370	AB002368	KIAA0370 protein	
1291	1291 40517_at	KIAA0372	AB002370	KIAA0372 gene product	KIAA0372 gene product
1292	1292 34837 at	KIAA0376	AB002374	KIAA0376 protein	
12937	1293 41457 at	KIAA0423	AB007883	KIAA0423 protein	
1294	1294 35167 at	KIAA0433	AB007893	KIAA0433 protein	KIAA0433 protein
1295	1295 33340 at	KIAA0438	AB007898	KIAA0438 gene product	KIAA0438 gene product
1296	1296 40805 at	KIAA0440	AB007900	KIAA0440 protein	KIAA0440 protein
1297	1297 32091 at	KIAA0446	AB007915	KIAA0446 gene product	KIAA0446 protein
1298	1298 41243 at	KIAA0447	AB007916	KIAA0447 gene product	KIAA0447 protein
1299	1299 32206 at	KIAA0451	AB007920	KIAA0451 gene product	KIAA0451 protein
1300	1300 36069 at	SRGAP2	AB007925	KIAA0456 protein	KIAA0456 protein
1301	1301 37230 at	KIAA0469	AB007938	KIAA0469 gene product	KIAA0469 protein
1302	1302 33893 r at	KIAA0470	AB007939	KIAA0470 gene product	KIAA0470 protein
1303	1303 34445 at	KIAA0471	AB007940	KIAA0471 gene product	KIAA0471 protein
1304	1304 35318 at	KIAA0475	AB007944	KIAA0475 gene product	KIAA0475 protein
1305	1305 35786_at	KIAA0476	AB007945	KIAA0476 gene product	KIAA0476 protein
1306	1306 35762_at	KIAA0483	AB007952	KIAA0483 protein	KIAA0483 protein
1307	1307 41830_at	KIAA0494	AB007963	KIAA0494 gene product	KIAA0494 protein

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1308 35534 at	KIAA0514	AB011086	KIAA0514 gene product	
1309 38724_at	KIAA0515	AB011087	KIAA0515 protein	KIAA0515 protein
34192	KIAA0532	AB011104	KIAA0532 protein	KIAA0532 protein
1311 33787_at .	KIAA0537	AB011109	KIAA0537 gene product	KIAA0537 protein
1312 35184_at	KIAA0546	AB011118	KIAA0546 protein	KIAA0546 protein
1313 31849_at	KIAA0564	AB011136	KIAA0564 protein	KIAA0564 protein
1314 39434 at	KIAA0592	AB011164	KIAA0592 protein	KIAA0592 protein
1315 41379_at	KIAA0594	AB011166	KIAA0594 protein	KIAA0594 protein
1316 32866_at	KIAA0605	AB011177	KIAA0605 gene product	KIAA0605 protein
1317 39852 at	KIAA0610	AB011182	KIAA0610 protein	KIAA0610 protein
318 40160 at	KIAA0618	AL080109	KIAA0618 gene product	hypothetical protein
319 40083 at	KIAA0625	AB014525	KIAA0625 protein	KIAA0625 protein
1320 33241 at	KIAA0626	AB014526	KIAA0626 gene product	KIAA0626 protein
	KIAA0630	AB014530	KIAA0630 protein	KIAA0630 protein
	KIAA0648	AB014548	KIAA0648 protein	KIAA0648 protein
38082	KIAA0650	AB014550	KIAA0650 protein	KIAA0650 protein
1324 39117_at	KIAA0662	AB014562	KIAA0662 gene product	KIAA0662 protein
4117	KIAA0663	AB014563	KIAA0663 gene product	KIAA0663 protein
1326 31826_at	KIAA0674	AB014574	KIAA0674 protein	KIAA0674 protein
1327 39403_at	KIAA0678	AB014578	KIAA0678 protein	KIAA0678 protein
1328 39519_at	KIAA0692	AB014592	KIAA0692 protein	KIAA0692 protein
1329 39380 at	KIAA0697	AB014597	KIAA0697 protein	KIAA0697 protein
	KIAA0700	AB014600	KIAA0700 protein	KIAA0700 protein
	KIAA0716	AB018259	KIAA0716 gene product	KIAA0716 protein
1332 33835_at	KIAA0721	AB018264	KIAA0721 protein	KIAA0721 protein
1333 35177_at	KIAA0725	AB018268	KIAA0725 protein	KIAA0725 protein
1334 41218_at	KIAA0729	AB018272	KIAA0729 protein	KIAA0729 protein
1335 38694_at	KIAA0738	AB018281	KIAA0738 gene product	KIAA0738 protein
1336 39771_at	KIAA0740	AB018283	KIAA0740 gene product	KIAA0740 protein
1337 41585 at	KIAA0746	AB018289	KIAA0746 protein	KIAA0746 protein
1338 38424 at	KIAA0747	AB018290	KIAA0747 protein	KIAA0747 protein
1339 40848 g_at	KIAA0750	AB018293	KIAA0750 gene product	KIAA0750 protein
1340 32224_at	KIAA0769	AB018312	KIAA0769 gene product	KIAA0769 protein
1341 36474_at	KIAA0776	AB018319	KIAA0776 protein	KIAA0776 protein
1342 33251_at	KIAA0779	AB018322	KIAA0779 protein	KIAA0779 protein
1343 35999_r_at	KIAA0781	AB018324	KIAA0781 protein	KiAA0781 protein

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1344   11224_at	_	_
KIAA0788		
KIAA0995   A   KIAA0810   A   KIAA0810   A   KIAA0810   A   KIAA0811   A   KIAA0811   A   KIAA0811   A   KIAA0811   A   KIAA0811   A   KIAA0811   A   KIAA0811   A   KIAA0903   A   KIAA0903   A   KIAA0931   A   KIAA0931   A   KIAA0931   A   KIAA0931   A   KIAA0931   A   KIAA0931   A   KIAA0931   A   KIAA0931   A   KIAA0931   A   KIAA0931   A   KIAA0931   A   KIAA0931   A   KIAA0931   A   KIAA0931   A   KIAA0931   A   KIAA0932   A   KIAA0933   A   KIAA0993   A   KIAA0993   A   KIAA0993   A   KIAA0993   A   KIAA0993   A   KIAA0993   A   KIAA0993   A   KIAA09999   A   KIAA09999		KIAAU/88 protein
KIAA0802		KIAA0795 protein
KIAA0810	18345 KIAA0802 protein	KIAA0802 protein
KIAA0826		KIAA0810 protein
KIAA0830		KIAA0826 protein
KIAA0831		KIAA0830 protein
KIAA0841		KIAA0831 protein
KIAA0843		KIAA0841 protein
KIAA0854	)20650 KIAA0843 protein	KIAA0843 protein
at KIAA0984  at KIAA0877  at KIAA0878  at KIAA0893  at KIAA0903  at KIAA0911  at KIAA0911  at KIAA0937  at KIAA0947  at KIAA0947  at KIAA0987  at KIAA0982  at KIAA0993  at KIAA0993  at KIAA0993  at KIAA0993  at KIAA0993  at KIAA0993  at KIAA0993  at KIAA0993  at KIAA0999		KIAA0854 protein
at KIAA0877  at KIAA0878  at KIAA0893  at KIAA0903  at KIAA0901  at KIAA0916  at KIAA0937  at KIAA0937  at KIAA0947  at KIAA0970  at KIAA0981  at KIAA0993  at KIAA0993  at KIAA0993  at KIAA0993  at KIAA0993  at KIAA0993  at KIAA0993  at KIAA0993  at KIAA0999		KIAA0864 protein
at KIAA0878		KIAA0877 protein
at KIAA0882		KIAA0878 protein
KIAA0993		KIAA0882 protein
KIAA0903		KIAA0893 protein
41421_at KIAA0909	320710 KIAA0903 protein	KIAA0903 protein
41498_at KIAA0911 / 39777_at KIAA0916 / 32735_at KIAA0931 / 33408_at KIAA0934 / 35369_at KIAA0937 / 32735_at KIAA0937 / 35794_at KIAA0942 / 41595_at KIAA0947 / 38649_at KIAA0981 / 32085_at KIAA0981 / 32085_at KIAA0981 / 32085_at KIAA0999 / 34751_at KIAA0999 / 34808_at KIAA0999	020716 KIAA0909 protein	KIAA0909 protein
39777_at KIAA0916 // 32735_at KIAA0931 // 33408_at KIAA0934 // 35369_at KIAA0937 // 32235_at KIAA0938 // 32740_at KIAA0942 // 35794_at KIAA0947 // 38649_at KIAA0978 // 32085_at KIAA0981 // 32085_at KIAA0981 // 34306_at KIAA0993 // 34808_at KIAA0999	020718 KIAA0911 protein	KIAA0911 protein
32735_at KIAA0931 / 33408_at KIAA0934 / 35369_at KIAA0937 / 32235_at KIAA0938 / 32740_at KIAA0942 / 41595_at KIAA0947 / 38649_at KIAA0978 / 32085_at KIAA0981 / 32085_at KIAA0981 / 32085_at KIAA0981 / 32769_at KIAA0993 / 34808_at KIAA0999		protein associated with Myc
33408_at KIAA0934	023148 KIAA0931 protein	KIAA0931 protein
35369_at KIAA0937 / 33235_at KIAA0937 / 32740_at Rab11-FIP2 / 35794_at KIAA0947 / 41595_at KIAA0978 / 32085_at KIAA0981 / 35199_at KIAA0993 / 32769_at KIAA0993 / 34751_at KIAA0999	023151 KIAA0934 protein	KIAA0934 protein
33235_at KIAA0938 / 32740_at Rab11-FIP2 / 35794_at KIAA0947 / 41595_at KIAA0970 / 34396_at KIAA0978 / 32085_at KIAA0993 / 32769_at KIAA0993 / 34751_at KIAA0999	023154 KIAA0937 protein	KIAA0937 protein
32740_at Rab11-FIP2	023155 KIAA0938 protein	KIAA0938 protein
35794_at KIAA0942 41595_at KIAA0947 41595_at KIAA0970 34396_at KIAA0978 32085_at KIAA0982 415459_at KIAA0993 34751_at KIAA0999 KIAA0899		KIAA0941 protein
41595_at KIAA0947 38649_at KIAA0970 34396_at KIAA0981 35199_at KIAA0982 32769_at KIAA0993 34751_at KIAA0999		KIAA0942 protein
38649_at KIAA0970 34396_at KIAA0981 32085_at KIAA0981 35199_at KIAA0993 32769_at KIAA0993 34751_at KIAA0999		KIAA0947 protein
34396_at KIAA0978 32085_at KIAA0981 35199_at KIAA0982 32769_at KIAA0993 34751_at KIAA0999		KIAA0970 protein
32085_at KIAA0981 35199_at KIAA0982 32769_at KIAA0993 34751_at KIAA0997 34808_at KIAA0999		KIAA0978 protein
35199_at KIAA0982 32769_at KIAA0993 34751_at KIAA0997 KIAA0999	-	KIAA0981 protein
32769_at KIAA0993 34751_at KIAA0997 34808_at KIAA0999	023199 KIAA0982 protein	KIAA0982 protein
at KIAA0997		KIAA0993 protein
at KIAA0999		
		KIAA0999 protein
1378 36002 at KIAA1012 AB023229		KIAA1012 protein
1379 35802 at KIAA1014 AB023231	3023231 KIAA1014 protein	KIAA1014 protein



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1380 39615	at	KIAA1026	AB028949	KIAA1026 protein	KIAA1026 protein
1381 34089 at	at	KIAA1030	AB028953	KIAA1030 protein	KIAA1030 protein
1382 41651	at	KIAA1033	AB028956	KIAA1033 protein	KIAA1033 protein
1383 41708 at	at	KIAA1034	AB028957	KIAA1034 protein	KIAA1034 protein
1384 35163 at	at	KIAA1041	AB028964	KIAA1041 protein	KIAA1041 protein
1385 38778_at	at	KIAA1046	AB028969	KIAA1046 protein	KIAA1046 protein
1386 41268 q	g at	KIAA1049	AB028972	KIAA1049 protein	KIAA1049 protein
1387 40855 at		KIAA1053	AB028976	KIAA1053 protein	KIAA1053 protein
1388 39400 at	at	KIAA1055	AB028978	KIAA1055 protein	KIAA1055 protein
1389 33877	sat	KIAA1067	AB028990	KIAA1067 protein	KIAA1067 protein
390 34688 at	3 at	KIAA1078	AB029001	KIAA1078 protein	KIAA 1078 protein
1391 33924 at	at	KIAA1091	AB029014	KIAA1091 protein	KIAA1091 protein
1392 32508 at	at	KIAA1096	AL096857	KIAA1096 protein	hypothetical protein
1393 41179 at	at	KIAA1100	AB029023	KIAA1100 protein	KIAA1100 protein
1394 34839_at	9 at	KIAA1104	AB029027	KIAA1104 protein	KIAA1104 protein
1395 33457 at	7 at	RAP140	AB029028	KIAA1105 protein	KIAA1105 protein
1396 36814_at	4 at	KIAA1109	AB029032	KIAA1109 protein	KIAA1109 protein
1397 34274 at	4_at	KIAA1116	AB029039	KIAA1116 protein	KIAA1116 protein
1398 37617	7 at	KIAA1128	U90912	KIAA1128 protein	-
1399 33358 at	8 at	KIAA1157	W29087	KIAA1157 protein	
1400 40308_at	8 at	KIAA1240	A1830496	KIAA1240 protein	
1401 33811	1 at	KIAA1254	AI761567	KIAA1254 protein	
1402 38674 at	4 at	KIAA1354	AA115140	KIAA1354 protein	
1403 32730 at	0 at	KIAA1750	AL080059	KIAA1750 protein	
1404 32171_at	1 at	KIAA1856	AL080102	KIAA1856 protein	hypothetical protein
1405 39897 at	7_at	KIAA1966	N36997	KIAA1966 protein	
1406 32846_s_at	6 s at	KTN1	D13629	kinectin 1 (kinesin recéptor)	kinectin 1
1407 39057_at	7_at	KNS2	L04733	kinesin 2 (60-70kD)	kinesin light chain
1408 32079 at	9 at	KIF13B	AB014539	kinesin family member 13B	KIAA0639 protein
1409 33345_at	5 at	KIF3C	AF035621	kinesin family member 3C	kinesin-related protein
1410 34294	4 at	KIFC3	AL041493	kinesin family member C3	
1411 41474		KIF2	Y08319	kinesin heavy chain member 2	kinesin-2
1412 40779		KIFAP3	U59919	kinesin-associated protein 3	SMAP
1413 34216	6 at	KLF7	AA478904	Kruppel-like factor 7 (ubiquitous)	
1414 38768 at	t a	НАПНЯС	X96752	L-3-hydroxyacyl-Coenzyme A dehydrodenase, short chain	3-hydroxyacyl-CoA dehydrogenase
1414 3016	o al	201001	70000		

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	A	В	ပ	Ŋ	ש
1415	41485_at	LDHA	X02152	lactate dehydrogenase A	lactate dehydrogenase A
1416	1416 288 s_at	LBR	125931	lamin B receptor	lamin B receptor
				laminin receptor 1 (67kD, ribosomal	
1417	1417 256 s at	LAMR1	M14199	protein SA)	laminin receptor 1
1418 37671	37671 at	LAMA4	S78569	laminin, alpha 4	laminin alpha 4 chain
1419 581	581 at	LAMB1	M61916	laminin, beta 1	laminin B1
				LanC lantibiotic synthetase component C-	
1420	1420 39441 at	LANCL1	Y11395	like 1 (bacterial)	lanthionine synthetase C-like protein 1
				latent transforming growth factor beta	latent transforming growth factor beta
1421	1421 1495 at	LTBP1	M34057	binding protein 1	binding protein 1 precursor
				latent transforming growth factor beta	
1422	1422 37906 at	LTBP2	237976	binding protein 2	LTBP-2 precursor
				lectin, galactoside-binding, soluble, 1	
1423	1423 33412 at	LGALS1	AI535946	(galectin 1)	
				lectin, galactoside-binding, soluble, 3	
1424	1424 35367_at	LGALS3	AB006780	(galectin 3)	galectin-3
				lectin, galactoside-binding, soluble, 3	,
1425	1425 37754_at	LGALS3BP	L13210	binding protein	Mac-2 binding protein
				lectin, galactoside-binding, soluble, 8	
1426	1426 1846_at	LGALS8	L78132	(galectin 8)	prostate carcinoma tumor antigen
1427	1427 34267 r at	LEPR	U50748	leptin receptor	leptin receptor
1428	1428 33830 at	HSOBRGRP	AW026535	leptin receptor gene-related protein	
1429	33829_at	HSOBRGRP	Y12670	leptin receptor gene-related protein	leptin receptor gene-related protein
1430	1430 38985 at	I EPBOTI 1	AF063605	leptin receptor overlapping transcript-like 1 brain my047 protein	brain my047 protein
	15-0000			leucine rich repeat (in FLII) interacting	
1431	1431 41320_s_at	LRRFIP1	U69609	protein 1	transcription repressor
				-	
1432	1432 39967_at	LDOC1	AB019527	leucine zipper, down-regulated in cancer 1	
1433	1433 41754 at	LRPPRC	M92439	leucine-rich PPR-motif containing	leucine-rich PPR-motif containing protein
1434	1434 37470 at	LAIR1	AF013249	leukocyte-associated Ig-like receptor 1	leukocyte-associated Ig-like receptor-1
1435	1435 38081 at	LTA4H	J03459	leukotriene A4 hydrolase	leukotriene A4 hydrolase
1436	1436 36062 at	LPXN	AF062075	leupaxin	leupaxin
				libtest16.A02.r bvnorm Homo sapiens	
1437	1437 35278_at	RPS29	AI541542	cUNA 5, mKNA sequence.	
1438	1438 39687_at	E46L	AI524873	like mouse brain protein £46	

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E46L	Γ	٨	B	O		Ľ
E46L	130	30686 g at	l	AL050282		ypothetical protein
KIDINS220   W27233   Substance of 220 kDa	2	39000_y_a	746	A1 050282		lypothetical protein
KIDINS220   W27233   Substance of 220 kDa     SOCS5   AB014571   Cytokine signalling 5     TC10   AL043108   likely ortholog of mouse TC10-alpha     TC10   AL043108   likely ortholog of mouse TRR-containing,     TSBP   D63875   SH2-binding phosphoprotein   Rely ortholog of mouse TRR-containing,     TSBP   D63875   SH2-binding phosphoprotein   Rely ortholog of mouse TRR-containing,     TSBP   D63875   SH2-binding phosphoprotein   Rely ortholog of mouse TRR-containing,     CSTF2T   AB014589   Rely ortholog of mouse Variant   Rely ortholog of mouse Variant   Rely ortholog of mouse Variant   Rely ortholog of mouse Variant   Rely ortholog of May a Polyadenylation protein CSTF-64   Rely ortholog of May a Polyadenylation protein CSTF-64   Rely ortholog of May a Polyadenylated   LIM and Senescent cell antigen-like   LIM and Senescent cell antigen-like   LIM and SH3 protein 1   LIM domain kinase 2   LIM domain kinase 2   LIM domain kinase 2   LIM domain kinase 2   LIM domain kinase 2   LIM domain himsen   LIM domain kinase 2   LIM domain himsen   LIM domain himsen   LIM domain kinase 2   LIM domain kinase 3   LIM domain kinase 3   LIM domain kinase 4   LIM domain kinase 6   LIM domain kinase 6   LIM domain kinase 6   LIM domain kinase 6   LIM domain kinase 7   LIM domain kinase 8   LIM domain kinase 8   LIM domain kinase 8   LIM domain kinase 8   LIM domain kinase 9   LIM domain kinase 8   LIM domain kinase 9   LIM domain kinase 9   LIM domain kinase 9   LIM domain kinase 8   LIM domain kinase 9   LIM domain kinase 8   LIM domain kinase 8   LIM domain kinase 8   LIM domain kinase 9   LI	3	39685_at	בלסר	שרמסקקק	-interacting	
SOCS5 AB014571 cytokine signalling 5  SOCS5 AB014571 cytokine signalling 5  TC10 AL043108 likely ortholog of mouse TC10-alpha likely ortholog of mouse TRR-containing, PD63875 SH2-binding phosphoprotein likely ortholog of mouse variant likely orthologon limited lipoma HMGIC fusion partner-like 2 lipoma HMGIC fusion partner-like 2 lipoma HMGIC fusion partner-like 2 lipoma HMGIC fusion partner-like 2 lipoma HMGIC fusion partner-like 2 lipoma HMGIC fusion partner-like 2 lipoma HMGIC fusion partner-like 2 lipoma HMGIC fusion partner-like 2 lipoma HMGIC fusion partner-like 2 lipoma furn; Homo sapiens glycogen complete cds.	141	30163 at	KIDINS220	W27233	substance of 220 kDa	
SOCS5   AB014571   Cytokine signalling 5   TC10   AL043108   likely ortholog of mouse TC10-alpha   likely ortholog of mouse TPR-containing,   TSBP   D63875   SH2-binding phosphoprotein   Meley ortholog of mouse variant   D63875   SH2-binding phosphoprotein   Meley ortholog of mouse variant   D63875   SH2-binding phosphoprotein   Meley ortholog of mouse variant   D63875   LIM and senescent cell antigen-like   LIMS1   D45906   LIM and SH3 protein   LIMO4   U24576   LIM domain kinase 2   LIM domain kinase 2   LIM domain kinase 2   LIM domain only 4   AB007890   limkain b1   Meley   LIM domain only 4   AB007890   limkain b1   LIPA   X76488   esterase (Wolman disease)   AB0010   Meley   Mi5856   LIPA   Mi5856   LIPA   LIPA   D80010   Mipin 1   LIPA   LIPA   D80010   LIPA   LIPA   LIPA   LIPA   LIPA   LIPA   LIPA   LIPA   LIPA   LIPA   LIPA   LIPA   LIPA   LIPA   LIPA   LIPA   LIPA   D80010   LIPA   LIP		m - 001 60			e suppressors of	
TC10	442	32669 at	SOCS5	AB014571	-	(IAA0671 protein
Ilkely ortholog of mouse TPR-containing, SH2-binding phosphoprotein   SH2-binding phosphoprotein   SH2-binding phosphoprotein   SH2-binding phosphoprotein   SH2-binding phosphoprotein   SH2-binding phosphoprotein   SH2-binding phosphoprotein   SH2-binding phosphoprotein   SH2-binding phosphoprotein   SH2-binding phosphoprotein   SH2-binding phosphoprotein   SH2-binding phosphoprotein   SH2-binding phosphorylase   SH2	443	40555 at	TC10	AL043108	likely ortholog of mouse TC10-alpha	
TSBP D63875 SH2-binding phosphoprotein  (CSTF2T AB014589 polyadenylation protein CSTF-64 likely ortholog of rat golgi stacking protein likely ortholog of rat golgi stacking protein CSTF-64 likely ortholog of rat golgi stacking protein likely ortholog of rat golgi stacking protein likely ortholog of rat golgi stacking protein likely ortholog of rat golgi stacking protein likely ortholog of rat golgi stacking protein likely ortholog GRASP55 LIM and senescent cell antigen-like lim and SH3 protein 1 LIM LASP1 X82456 LIM domains that LIMAZ D45906 LIM domain kinase 2 LIM domain only 4 LIMO4 AB007890 limkain b1 lilikain b1 limkain b1 limkain b1 lilikain b1 limkain b1 li	}					
CSTF2T AB014589 polyadenylation protein CSTF-64 polyadenylation protein CSTF-64 likely ortholog of rat golgi stacking protein likely ortholog of rat golgi stacking protein bordon call antigen-like to LIM and senescent cell antigen-like to LIM and SH3 protein 1 lim and SH3 protein 1 lim and SH3 protein 1 lim and SH3 protein 1 lim and SH3 protein 1 lim and SH3 protein 1 lim and SH3 protein 1 lim and SH3 protein 1 lim and SH3 protein 1 lim and SH3 protein 1 lim and SH3 protein lim and	444	40844 at	TSBP	D63875		KIAA0155 gene product
CSTF2T AB014589 polyadenylation protein CSTF-64 likely ortholog of rat golgi stacking protein likely ortholog of rat golgi stacking protein homolog GRASP55 LIM and senescent cell antigen-like domains 1 LIMS1 X82456 LIM and SH3 protein 1 LIMS2 D45906 LIM domain kinase 2 LIM domain kinase 2 LIM domain nohly 4 LIMO4 U24576 LIM domain only 4 LIMO4 AB007890 limkain b1 lipase A, lysosomal acid, cholesterol lipase A, lysosomal acid, cholesterol esterase (Wolman disease)  It LIPA X76488 esterase (Wolman disease)  It LIPA D80010 lipin 1 lipoma HMGIC fusion partner-like 2 lipoprotein lipase LIV-1 D41060 LIV-1 protein, estrogen regulated liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and phosphorylase Complete cds.		-				
Ikely ortholog of rat golgi stacking protein homolog GRASP55	445	41248 at	CSTF2T	AB014589		KIAA0689 protein
GRASP55   AA447263   homolog GRASP55		20.31.1			likely ortholog of rat golgi stacking protein	
LIMS1   U09284   domains 1   LIMS1   U09284   domains 1   LASP1   X82456   LIM and SH3 protein 1   LIMK2   D45906   LIM domain kinase 2   LIM domain kinase 2   LIM domain nolly 4   LIM domain nolly 4   LIM domain nolly 4   LIM domain nolly 4   LIM domain nolly 4   LIM domain nolly 4   LIM domain nolly 4   LIM domain nolly 4   LIM domain nolly 4   LIM domain nolly 4   LIM domain nolly 4   LIMB   L	776	35805 at	GRASP55	AA447263	homolog GRASP55	
LIMS1   U09284   domains 1   LASP1   X82456   LIM and SH3 protein 1   LASP1   X82456   LIM domain kinase 2   LIM domain kinase 2   LIM domain only 4   LMO4   U24576   LIM domain only 4	ŕļ.	5000			cell antigen-like	•
LASP1         X82456         LIM and SH3 protein 1         I           LIMC2         D45906         LIM domain kinase 2         I           LMO4         U24576         LIM domain only 4         I           LMO4         AB007890         Imkain b1         I           LIPA         X7648B         esterase (Wolman disease)         I           LIPA         X7648B         esterase (Wolman disease)         I           LHFPL2         D86961         Iipon 1         I           LIV-1         U41060         IIV-1 protein, estrogen regulated         IIV-1 protein, estrogen regulated           LIV-1         U41060         IIV-1 protein, estrogen regulated         IIV-1 protein, estrogen regulated           PYGI         AF04679B         complete cds.	447	139232 at	LIMS1	U09284		PINCH protein
LIMK2   D45906   LIM domain kinase 2			LASP1	X82456		LIM and SH3 domain protein
LMO4   U24576   LIM domain only 4   LMO4   AB007890   Imkain b1   Impase A, Ivsosomal acid, cholesterol   Iipase A, Ivsosomal acid, cholesterol   Iipase A, Ivsosomal acid, cholesterol   LIPA   X76488   esterase (Wolman disease)   LPIN1   D80010   Iipin 1   Iipoma HMGIC fusion partner-like 2   LPL   M15856   Iipoprotein lipase   LIV-1   U41060   LIV-1 protein, estrogen regulated   LIV-1   U41060   LIV-1 protein, estrogen regulated   Iiver form; Homo sapiens glycogen   pyGI   AF046798   complete cds.		20017	LIMKS	D45906		LIMK-2
LIPA X76488 inpase A, lysosomal acid, cholesterol lipase A, lysosomal acid, cholesterol sterase (Wolman disease)  LIPA X76488 esterase (Wolman disease)  LPIN1 D80010 lipin 1 lipoma HMGIC fusion partner-like 2  LPL M15856 lipoprotein lipase  LIV-1 U41060 LIV-1 protein, estrogen regulated liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and phosphorylase (PYGL) gene, exon 20 and phosphorylase (PYGL) gene, exon 20 and complete cds.	֓֞֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	1 300 1 / at	MOA	U24576		breast tumor autoantigen
LIPA X76488 esterase (Wolman disease)  LIPA X76488 esterase (Wolman disease)  LPIN1 D80010 lipin 1  LHFPL2 D86961 lipoma HMGIC fusion partner-like 2  LPL M15856 lipoprotein lipase  LIV-1 U41060 LIV-1 protein, estrogen regulated liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and phosphorylase (PYGL) gene, exon 20 and phosple cds.	5 1	1 21036 c at	KAP	AB007890		KIAA0430 protein
LIPA X76488 esterase (Wolman disease)  LPIN1 D80010 lipin 1 LHFPL2 D86961 lipoma HMGIC fusion partner-like 2 LPL M15856 lipoprotein lipase LIV-1 U41060 LIV-1 protein, estrogen regulated liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and PYGL AF046798 complete cds.	2	101300_s_a	5		lipase A, lysosomal acid, cholesterol	
LPIN1         D80010         lipin 1           LHFPL2         D86961         lipoma HMGIC fusion partner-like 2           LPL         M15856         lipoprotein lipase           LIV-1         U41060         LIV-1 protein, estrogen regulated liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and phosphorylase (PYGL) gene, exon 20 and complete cds.	145	2 38745 at	LIPA	X76488	esterase (Wolman disease)	lysosomal acid lipase
LHFPL2         D86961         lipoma HMGIC fusion partner-like 2           LPL         M15856         lipoprotein lipase           LIV-1         U41060         LIV-1 protein, estrogen regulated           liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and phosphorylase (PYGL) gene, exon 20 and complete cds.	45	338098 at	LPIN1	D80010	lipin 1	
LPL M15856 lipoprotein lipase LIV-1 U41060 LIV-1 protein, estrogen regulated liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and PYGL AF046798 complete cds.	1	4 37542 at	LHFPL2	D86961	lipoma HMGIC fusion partner-like 2	
LIV-1 U41060 LIV-1 protein, estrogen regulated iver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and PYGL AF046798 complete cds.		5 41209 at	LPL	M15856	lipoprotein lipase	lipoprotein lipase precursor
liver form; Homo sapiens glycogen phosphorylase (PYGL) gene, exon 20 and PYGL AF046798 complete cds.	15	61798 at	LIV-1	U41060	LIV-1 protein, estrogen regulated	estrogen regulated LIV-1 protein
phosphorylase (PYGL) gene, exon 20 and PYGL AF046798 complete cds.	2				liver form; Homo sapiens glycogen	
PYGL AF046798 complete cds.					phosphorylase (PYGL) gene, exon 20 and	
	145	7 37215 at	PYGL	AF046798	complete cds.	glycogen pnospnorylase

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				long tailed isoform; individual exons 6-14	
				are afternative exons any of which can be	
				spliced out of the mRNA.; putative; long	
				tailed isoform; putative; long tailed	
				isoform; hemopoietic variant; putative;	
				long tailed isoform; epithelial form;	
				putative; Human cell surface glycoprotein	,
1458	1458 40493 at	CD44	L05424		cell surface glycoprotein CD44
				low density lipoprotein-related protein-	
				associated protein 1 (alpha-2-	
				macroglobulin receptor-associated protein alpha-2-macroglobulin receptor-associated	alpha-2-macroglobulin receptor-associated
1459	1459 36194 at	LRPAP1	M63959	1)	protein
				low molecular mass ubiquinone-binding	
1460	1460 34400_at	QP-C	AI540957	protein (9.5kD)	
1461	1461 37025 at	PIG7	AL120815	LPS-induced TNF-alpha factor	
1462	1462 39017 at	LSM1	AJ238094	Lsm1 protein	Lsm1 protein
1463	1463 38038 at	LUM	U21128	lumican	lumican
1464	1464 38115 at	FUS1	AF055479	lung cancer candidate	lung cancer candidate FUS1
1465	1465 39428 at	LNK	AF055581	otein	adaptor protein Lnk
1466	1466 39396_at	LYPLA1	AF081281		lysophospholipase
1467	1467 33788 at	LYSAL1	AB002390	lysosomal apyrase-like 1	lysosomal apyrase-like 1
,		- ONA	104182	Vsosomal-associated membrane protein 1 (vsosomal membrane divcoprotein-1	Nsosomal membrane alvcoprotein-1
1408	1408 39/36 1 at	- Lainit	204105	lysosolitai-associated including process	3-16
1469	1469 38403_at	LAMP2	X77196	lysosomal-associated membrane protein 2 lysosome-associated membrane protein-2	lysosome-associated membrane protein-2
1470	1470 38402 at	LAMP2	U36336	lysosomal-associated membrane protein 2	lysosomal-associated membrane protein 2 lysosome-associated membrane protein-2b
	ļ.			lysosomal-associated protein	lysosomal-associated protein
1471	1471 39019 at	LAPTM4A	D14696	transmembrane 4 alpha	transmembrane 4 alpha
1472	1472 33127_at	LOXL2	U89942	lysyl oxidase-like 2	lysyl oxidase-related protein
1473	34336_at	KARS	D32053	lysyl-tRNA synthetase	Lysyl tRNA Synthetase
1474	1474 32832_at	MAEA	AF084928	$\neg$	erythroblast macrophage protein EMP
1,4	147E 36174 at	MACMABCKS	X70326	macrophage myristoylated alanine-rich C kinase substrate	macrophage myristoylated alanine-rich C kinase substrate
*	301/4 at	CHOLDINOVINI	N 0350		

	B MADH2	C U68018	D MAD, mothers against decapentaplegic homolog 2 (Drosophila) MAD, mothers against decapentaplegic	E mad protein homolog
MADH3		U68019	homolog 3 (Drosophila) MAD, mothers against decapentaplegic	mad protein homolog
MADH3 MADH4	3	U68019 1144378	homolog 3 (Drosophila) MAD, mothers against decapentaplegic homolog 4 (Drosophila)	mag protein normong  Dpc4
MADHS		U59913	MAD, mothers against decapentaplegic homolog 5 (Drosophila)	Smad5
MADH6	9	AF035528	MAD, mothers against decapentaplegic homolog 6 (Drosophila)	Smad6
MADH7	4	AF010193	MAD, mothers against decapentaplegic homolog 7 (Drosophila)	MAD-related gene SMAD7
HLA-A		D32129	major histocompatibility complex, class I, A	HLA-A26
HLA-DMB	OMB	U15085	major histocompatibility complex, class II, DM beta	HLA-DMB
H A	HLA-DPB1	M83664	major histocompatibility complex, class II, DP beta 1	HLA-DPB1
₹	HLA-DPB1	M83664	major histocompatibility complex, class II, DP beta 1	HLA-DPB1
HLA-DRA	DRA	J00194	major histocompatibility complex, class II, DR alpha	major histocompatibility complex, class II, DR alpha precursor
Ą	HLA-DRB1	M16941	major histocompatibility complex, class II, DR beta 1	
HLALS	S	AF031469	major histocompatibility complex, class I- like sequence	MHC class I-related protein 1 isoform D
CD 4		U47924	major receptor for HIV-1; member of immunoglobulin supergene family; T cell surface glycoprotein T4	protein 'A', isoform 1
MDH1	<b>-</b>	D55654	malate dehydrogenase 1, NAD (soluble)	cytosolic malate dehydrogenase
ME1	-	U43944	malic enzyme 1, NADP(+)-dependent, cytosolic	cytosolic NADP(+)-dependent malic enzyme

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				malic enzyme 2, NAD(+)-dependent,	mitochondrial NAD(P)+ -dependent malic
1493	1493 36599 at	ME2	M55905		enzyme
1494	1494 36673 at	MPI	X76057		phosphomannose isomerase
				ase-interacting serine/threonine	
1495	1495 35299 at	MKNK1	AB000409	kinase 1	MNK1
				MAP/microtubule affinity-regulating kinase	
1496	1496 40826 at	MARK3	M80359		protein p78
				MAPK-activated protein kinase; PRK;	
				Homo sapiens mitogen activated protein	
				kinase activated protein kinase gene,	mitogen activated protein kinase activated
1497	1497 41506_at	MAPKAPKS; PRA AF032437	AF032437	complete cds.	protein kinase
		_		match proteins: Sw:P04040 Sw:P04762	
				Sw:P24270 Tr:O62839 Sw:P00432	
				Sw:P17336 Tr:P90682 Tr:Q27487	
				Sw:O61235 Tr:O18193 Tr:O77229	
				Tr:Q49133 Sw:P26901 Sw:P55306	
				Sw:P30263 Tr:P95631 Sw:P44390	
				Tr:Q27710 Sw:Q96528 Sw:O13289	
				Sw:P07820 Sw:P30265 Sw:P77872	
				Tr:Q59602 Tr:P77924 Sw:Q59170	
				Sw:P15202 Tr:Q59296 Tr:O33613	
				Sw:Q92405 Sw:Q59635 Sw:P81138	
1498	1498 37009 at	CAT	AL035079	match ESTs: W94164 N28621	dJ53C18.1 (Catalase)
				match to ESTs AA316181	
				(NID:g3165221), AA032221	
				(NID:g1502183), and Al167942	
	-			(NID:g3701112); H_RG041D11.1; Homo	
				sapiens BAC clone CTB-41D11 from	six transmembrane epithelial antigen of the
149	1499 40297_at	WUGSC:H_RG04 AC005053	4 AC005053	7q21, complete sequence.	prostate

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A	В	O	Q	Ш
500 34860_g_at E	BCG1	7 7 7 8 8 8 8 8 9 9 9	match: cDNAs X67055 X14690 D89287 X70393 S82800 X16260 M18192 Y11283 D38535 D38595 match: proteins Q06033 P97280 O54882 O35802 Q61704 Q14624 P79263 Q63416 O42141 P19823 O02668 Q61703 P97279 Q29052	match: cDNAs X67055 X14690 D89287 X70393 S82800 X16260 M18192 Y11283 D38535 D38595 match: proteins Q06033 P97280 O54882 O35802 Q61704 Q14624 P79263 Q63416 Q42141 P19823 O02668 hepatocellular carcinoma associated protein; Q61703 P97279 Q29052 breast cancer associated gene 1
		<del></del>	match: cDNAs: Em:AL050345 match: ESTs: Em:AA304885 Em:AA447346 Em:AA314213 Em:AA209368	
			Em:AA209372 Em:T84723 Em:H23039 Em:AA542125 Em:W41686	
501 35336_at	HS508115A	AL021707	Em:AA384854 Em:AA492678	chromosome 22 open reading frame 2
	dJ1033B10.1	AL031228	match: protein 015214	BING4
	dJ1033B10.1	AL031228	match: protein O15214	BING4
	dJ886K2.1	AL031295	match: protein SPTREMBL; Q14241	UDP-galactose-4-epimerase
			match: proteins CE02000 O59733	
			CE01999; supported by FGENES and	
1505 38072_at	dJ465N24.1	AL031432	GENSCAN	hypothetical protein dJ465N24.2.1
			match: proteins O15037 CE16881	
			supported by GENSCAN possibly this	
			partial gene and dJ281H8.1 are part of	dJ281H8.2 (PUTATIVE novel protein similar
1506 32478_f_at	dJ281H8.1	AL031133	one gene	to KIAA0323 and worm C30F12.1)
	dJ281H8.1	AL031133	one gene	

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507	1507 39759_at	dJ51J12.1	P C C C C C C C C C C C C C C C C C C C	match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstram; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.	dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKQ-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein QKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein QKI-77 (isoform 2))
	39760_at	ძJ51J12.1	AL031781	match: proteins O42476 Q94539; match: protein O88972; match: cDNA AF091047; owing to a different in-frame ORF, the translation of the last coding exon (8 C-terminal amino-acids) differs from that in mouse and is terminated more upstream; match: protein Q61110; Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse OKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.	dJ51J12.1 (human ortholog of zebrafish Quaking protein homolog ZKG-1 (isoform 1)); dJ51J12.1.2 (human ortholog of mouse KH Domain RNA Binding protein GKI-7B (isoform 2)); dJ51J12.1.3 (human ortholog of mouse KH Domain RNA Binding protein GKI-77 (isoform 3))
1509	1509 32573_at	COX6A	AL021546	match: proteins P13182 P12074 P10818 P43024 Q02221 P07471 P10817 P43023 P13182 O13085 O13082	cytochrome c oxidase subunit Vla polypeptide 1



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1510 33443 at HSF2 Z99129		299129		match: proteins P38533 Q03933 P38530 P41154 Q00613 P38529 P38531 Q63717 P38532 Q99472	heat shock transcription factor 2
			1		
				match: proteins Q14189 P15924 Q03001 pozads Pozads P97394: Human DNA	
				sequence from clone 512B11 on	
				chromosome 6p24-25. Contains the	
				s, STSs	
1511 36133 at dJ512B11.1 AL031058		AL031058		_	dJ512B11.1 (Desmoplakin I (DPI))
				match: proteins Q14209 Q16254 O35261	
				O00716 Q61501 Q90977 Q01094	
1512 37043 at E2F-2 AL021154		AL021154		٦	E2F transcription factor 2
			i	match: proteins Q15774; match: protein	
				Q01968 P32019; Homo sapiens DNA	
				sequence from PAC 454M7 on	
				chromosome Xq25-26.3. Contains the	•
				OCRL1 gene for Lowe Oculocerebrorenal  dJ454M7.1.2 (Lowe Oculocerebrorenal	dJ454M7.1.2 (Lowe Oculocerebrorenal
				Syndrome protein OCRL-1. Contains	Syndrome protein OCRL-1) (isoform 2);
				ESTs, STSs and GSSs, complete	dJ454M7.1.1 (Lowe Oculocerebrorenal
1513/41227 at OCRL1   AL022162		AL022162		sednence.	Syndrome protein OCRL-1) (isoform 1)
					dJ341E18.1 (Serine/Threonine Protein
	_			match: proteins Q62726 P20793 Q04859	Kinase (presumptive isolog of Rat protein
1514 38990 at   dJ341E18.1   AL031178		AL031178		Q39423 P43294 O49669	Q62726))

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1515	1515 34782_at	ICMOMUL	AL021938	match: proteins Q92833 Q62315; protein Q92833 has a different stop codon 19 aa further downstream because it jumps frame twice, circumventing the stopcodon in this entry. This could be due to a sequence error in the cDNA sequence; Homo sapiens DNA sequence from PAC 232K4 on chromosome 6p22.3. Contains the JUMONJI gene for a hypothetical 141.7 kD protein. Contains ESTs, STSs, a CA repeat polymorphism and genomic marker D6S260', complete sequence.	dJ232K4.1 (hypothetical 141.7 kD protein JUMONJI)
1516	1516 37350 at	dJ889N15.1	AL031177	664 1939 3907 522 0040 S	dJ889N15.1 (novel protein similar to X. laevis Cortical Thymocyte Marker CTX)
1517	1517 39738_at	APOL2	Z82215	П	apolipoprotein L
1518	1518 31824 at	ME1	AL049699	match: proteins: Sw:P06801 Sw:P28227 Sw:Q29558 Sw:P13697 Sw:P40927 Sw:Q16798 Tr:Q16797 Sw:P48163	dJ747H23.1 (malic enzyme 1, soluble (NADP-dependent malic enzyme, malate oxidoreductase, EC 1.1.1.40))
1519	1519 32766 at	OTK27 SSFA1	283840	match: proteins: Sw:P12956	non-histone chromosome protein 2 (S. cerevisiae)-like 1
				match: proteins: Sw:P17861 Tr:O35426; Human DNA sequence from clone CTA- 292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete	
1520	1520 39756_g_at	XBP1	Z93930	sequence.	(TREB5))

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	<b>T</b>			match: proteins: Sw:P17861 Tr:O35426; Human DNA sequence from clone CTA- 292E10 on chromosome 22q11-12 Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island, complete	bK292E10.1 (X-box binding protein 1
1521	1521 39755_at	XBP1	Z93930	_	(TREB5))
		,		match: proteins: Sw:P26038 Tr:O35763 Sw:P26041 Sw:P26042 Sw:P26044 Sw:P35241 Sw:P26043 Sw:P15311 Sw:P31976 Sw:P26040 Tr:Q26520 Tr:Q24788 Tr:Q24796 Tr:Q94815; Human DNA sequence from clone 376D21 on chromosome Xq11.1-12 Contains the	
			·	(er nd,	dJ376D21.1 (Moesin (Membrane-organizing
152	1522 40771_at	MSN	Z98946	complete sequence.	Extension Spike protein//
152	1523 31722 at	яргз	AL022326	match: proteins: Sw:P39023 Sw:O16797 Sw:P21531 Sw:P39872 Sw:P27659 Sw:Q92901 Sw:P49149 Sw:P22738 Sw:P35684 Sw:P17094 Wp:CE05598	ribosomal protein L3
	5			match: proteins: Sw;P50550 Sw:009181 Tr:062622 Sw:P40984 Sw:P50623 Tr:Q42551 Tr:024240 Tr:Q42973 Sw:P52478 Sw:Q02159 Sw:P15732	
152	1524 33136_at	UBE21	AL031714	Sw:O00102 Tr:O76542 Sw:P27949 Sw:P49427 Tr:O17424 Sw:P25867 Sw:P52490	C358B7.1 (ubiquitin-conjugating enzyme E2I (homologous to yeast UBC9))
152	1525 36607_at	bK250D10.3	299716	match: proteins: Sw:Q12772 Sw:Q60429 Sw:P36956 Sw:Q60416 Tr:O15352	septin 3
152	1526 38399_at	SNRPB2	AL034428	match: proteins: Sw:Q28038 Sw:Q16674 Tr:P97591 Sw:Q61865	Small nuclear riborructeoprotein porypeprate
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				match: proteins: Tr.O54791 Sw.Q90595 Sw.Q61827 Sw.Q90596 Tr.O54790 Tr.O15525 Sw.Q90889 Tr.O73679 Tr.O75444 Sw.P54844 Sw.P54843	chromosome 22 onen reading frame 5
1527 36711		HSSO6A UKFZPS ALOZ1977	AL021977	29	chromobox homolog 6
2261	1528 3936 I_at		ALCCOCCO		
					dJ738P15.2 (CD39-like 2 (a nucleoside
15293	1529 39876 at	dJ738P15.1	AL035252		phosphatase))
				match: proteins: Tr:094136 Sw:Q99798	
					dJ347H13.1 (aconitase 2, mitochondrial
				<u>~</u>	(Aconitate Hydratase, EC 4.2.1.3, Citrate
1530	1530 37189 at	ACO2	AL023553	Sw:P19414 Tr:O75944 Sw:O13966	Hydrolyase))
				match: proteins: Tr:P70386 Sw:Q02527	
1531	1531 41235 at	TAXREB67 TXRE	E AL022312	Sw:Q10470 Sw:Q09327	activating transcription factor 4
3					dJ117516.1 (Ras inhibitor JC265 (Ras
				match: proteins: Tr:Q00425 Sw:Q13671	association (RaIGDS/AF-6) domain
1532	1532 36550 at	dJ1175l6.1	AL049538	Tr:O15010 Tr:P97680	containing protein))
				match: proteins: Tr:Q14621 Tr:Q64012	•
				Sw:P07910 Sw:P19600 Tr:O60812	RNA-binding protein (autoantigenic) long
1533	1533 39368 at	P542	AL031668	Sw:Q14011 Sw:P26686	isoform
	-			match: proteins: Tr:Q9Y3M0 Tr:Q9WU14	
1534	1534 33821 at	dJ483K16.1	AL034374	Sw:P39540 Tr:Q9Y396	dJ483K16.1.1 (novel protein (isoform 1))
1535	1535 39029 at	G10	U11861	maternal G10 transcript	maternal G10 transcript
1536	1536 35145 at	MNT	X96401	MAX binding protein	ROX protein
	m=0: 100				MAX interacting protein 1, isoform a; MAX
1537	1537 39072 at	MXII	L07648	MAX interacting protein 1	interacting protein 1, isoform b
3	21000				MAX interacting protein 1, isoform a; MAX
1538	1538 654 at	MXI1	L07648	MAX interacting protein 1	interacting protein 1, isoform b
				MCM2 minichromosome maintenance	
1539	1539 35312 at	MCM2	D21063	deficient 2, mitotin (S. cerevisiae)	
				MCM3 minichromosome maintenance	
				deficient 3 (S. cerevisiae) associated	Z A A O C C C C C C C C C C C C C C C C C
1540	1540 40469_at	MCM3AP	AB011144	protein	NIAMON 2 PIOTEIN

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				MCM6 minichromosome maintenance	
7	1541 40417 pt	MCM6	D84557		HsMcm6
7	10 - 11 - at			sloid ecotropic viral integration	
542	1542 41388 at	MEIS2	AF017418		homeobox protein MEIS2
				Meis1, myeloid ecotropic viral integration	-
1543	1543 37486 f at	MEIS3	U68385	site 1 homolog 3 (mouse)	Meis1-related protein 2
				mel transforming oncogene (derived from	
1544	1544 35340 at	MEL	AI819948	cell line NK14)- RAB8 homolog	
				melanoma antigen, family A, 2, copy a;	•
				similar to GenBank Accession Number	
1545	1545 36500 at	MAGEA2A	AF027974	L18920	melanoma antigen family Aza
1546	1546 41139 at	MAGED1	W26633	metanoma antigen, family D, 1	
1547	1547 39327 at	D2S448	D86983	Melanoma associated gene	
				membrane cofactor protein (CD46,	membrane colactor protein (CD46,
				trophoblast-lymphocyte cross-reactive	trophoblast-lymphocyte cross-reactive
1548	1548 38441 s at	MCP	X59408	antigen)	antigen)
2				membrane component, chromosome 11,	
15.40	1540 39471 at	M11S1	Z48042	surface marker 1	GPI-anchored protein p137
3	11			membrane component, chromosome 17,	
				surface marker 2 (ovarian carcinoma	membrane component, chromosome 17,
1550	1550 33444 at	M17S2	D30756	antigen CA125)	surface marker 2
3	15-			membrane metallo-endopeptidase	
				(neutral endopeptidase, enkephalinase,	aspilasachae elleten
1551	1551 1389 at	MME	J03779	CALLA, CD10)	membrane metallo-endopephoase
				mesenchyme homeo box 2 (growth arrest-	
1552	1552 40399 r at	MEOX2	AI743406	specific homeo box)	
				Met at bp 326 also used as initiation	
				codon in vitro; Met at bp 248 also used as	
			-	initiation codon in vitro; Homo sapiens	
		-		porin (por) mRNA, complete cds and	•
1553	1553 37697 s at	por	L08666	truncated cds.	porin
		MPPF1	AI743654	metallo phosphoesterase	
3	140547-3-41				

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				Material (MT). like gene. H sanjens	
				neardocene for metallothionein and	
1555	1555 31075 at		X55503		metallothionein
1556	1556 39081 at	MT2A	AI547258	metallothionein 2A	
1557	1557 38945 at	MTE1	X78710	anscription factor 1	metal-regulatory transcription factor
155g	1558 1643 g at	MTA1	U35113		metastasis associated protein
1550	1550 35642 at	MTX2	AF053551		metaxin 2
3	12.000				
1560	1560 39342_at	MARS	X94754	0	yeast methionyl-tRNA synthetase homolog
1561	1561 37619 at	METAP1	D42084		
1562	41828_at	MBD1	Y10746		methyl-CpG binding protein
1563	33905_at	MBD2	AF072242		methyl-CpG binding protein MBU2
1564	1564 34386_at	MBD4	AF072250	methyl-CpG binding domain protein 4	methyl-CpG binding protein MBD4
					-
					methylene tetrahydrofolate dehydrogenase
				dehydrogenase (NAD+ dependent),	(NAD+ dependent), methenyltetrahydrofolate
1565	1565 40074 at	MTHFD2	X16396	methenyltetrahydrofolate cyclohydrolase	cyclohydrolase, precursor
				methylenetetrahydrofolate dehydrogenase methylenetetrahydrofolate dehydrogenase	methylenetetrahydrofolate dehydrogenase
				(NADP+ dependent),	(NADP+ dependent),
				methenvitetrahydrofolate cyclohydrolase,	methenyitetrahydrofolate cyclohydrolase,
1566	1566 674 g at	MTHFD1	J04031	formyltetrahydrofolate synthetase	formyltetrahydrofolate synthetase
1567	1567 40105 at	MUT	M65131	methylmalonyl Coenzyme A mutase	methylmalonyl-CoA mutase
				MHC class I chain-related gene B; cDNA	
				sequence deposited under GenBank	
				Accession Number X91625; Human MHC	
				class I molecule (MICB) gene, complete	
1568	1568 35937 at	MICB	U65416	cds.	MHC class I molecule
1569	1569 36535 at	MFAP1	U04209	microfibrillar-associated protein 1	associated microfibrillar protein
				microphthalmia-associated transcription	A-type microphthalmia associated
1570	1570 38228 g at	MITE	AB006909	factor	transcription factor
1571	1571 820 at	MGST2	U77604	microsomal glutathione S-transferase 2	microsomal glutathione S-transferase 2
1572	1572 38704 at	MACF1	AB007934	microtubule-actin crosslinking factor 1	KIAA0465 protein
157	1573 35917 at	MAP1A	W26631	microtubule-associated protein 1A	
1574		MAP4	W28892	microtubule-associated protein 4	

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		740004	1124166	microtubule-associated protein, RP/EB	EB1
12/21	15/5 33456_at	MARINE	054100	ciated proteins 1A/1B	
1576	1576 30370 at	MAP1A/1BLC3	W28807		
212	1577 34296 at	MID1	AF041210	pitz/BBB syndrome)	midline 1 fetal kidney isoform 3
1578	1578 34403 at	MFGE8	U58516	otein	BA46
2	B-00110			mitochondrial ATP synthase regulatory	
1579	1579 40027 at	ATPW	W52999		
1580	37174 at	MRPL19	D14660	6	mitochondrial ribosomal protein L19
1581	1581 37726 at	MRPL3	X06323		mitochondrial ribosomal protein L3
1582	39717 d at	MRPL33	AI597616		
1583	3222	MRPS18B	AL050361	mitochondrial ribosomal protein S18B	mitochondrial ribosomal protein S18B
1584	1584 38899 s at	MEN1	U95822		putative transmembrane GTPase
1585	1585 34369 at	MFN2	D86987	mitofusin 2	KIAA0214 protein
1586	36577 at	Migs	224725	lucible 2	mitogen inducible gene mig-2
1587	1587 37733 at	MAPK14	L35263	rotein kinase 14	CSaids binding protein
1588	1588 36926 at	MAPK6	X80692		p97mapk
15.89	1589 38431 at	MAPK9	U09759	mitogen-activated protein kinase 9	protein kinase
1590	1590 1238 at	MAPK9	U09759	mitogen-activated protein kinase 9	protein kinase
1591	1591 1130 at	MAP2K1	L11284	-	mitogen-activated protein kinase kinase i
				mitogen-activated protein kinase kinase	a property county between the contract of the county county county between the county of the county
1592	1592 1327_s_at	MAP3K5	U67156	kinase 5	mitogen-activated Kiliase Kiliase Kiliase S
				mitogen-activated protein kinase kinase	
1593	1593 36905 at	MAP3K7	AB009356	kinase 7	TGF-beta activated kinase 1a
				mitogen-activated protein kinase kinase	•
1594	1594 38980 at	MAP3K7IP2	AB018276	kinase 7 interacting protein 2	KIAA0733 protein
				mitogen-activated protein kinase kinase	•
1595	1595 35694 at	MAP4K4	AB014587	kinase kinase 4	KIAA0687 protein
				mitogen-activated protein kinase-activated	
1596	1596 36179 at	MAPKAPK2	U12779	protein kinase 2	MAP kinase activated protein kinase 2
				mitogen-activated protein kinase-activated	
1597	1597 1637 at	<b>MAPKAPK3</b>	U09578	protein kinase 3	MAPKAP kinase
1598	1598 41220 at	MSF	AB023208	MLL septin-like fusion	KiAA0991 protein
1590	1599 38437 at	MLN51	X80199	MLN51 protein	MLN51 protein

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w		MMS19 (MET18 S. cerevisiae)-like			monoamine oxidase A		monoamine oxidase B	monocyte to macrophage differentiation-	associated, precursor	MORF-related gene X	•	M phase phosphoprotein 10	muscleblind (Drosophila)-IIKe	musculin	mutL homolog 3	•	mutS homolog 2	G/T mismatch binding protein	protein zero related protein	myeloid cell leukemia sequence 1 (BCL2-	related)	myeloid cell leukemia sequence 1 (BCL2-	related)	myeloid/lymphoid or mixed-lineage leukemia	(trithorax homolog, Drosophila); translocated	to, 2	DEXI	myh-1c	KIAA0727 protein	myosin-IC		myosin regulatory light chain	KIAA0799 protein	Imvosin, light polypeptide, regulatory, non-
		2														er,			_							$\neg$					/a	hain		aca recording
٥	MMS19-liké (MET18 homolog, S.	cerevisiae)	modulator of apoptosis 1	monoamine oxidase A	monoamine oxidase A	monoamine oxidase A	monoamine oxidase B	monocyte to macrophage differentiation-	associated	MORF-related gene X	M-phase phosphoprotein 10 (U3 small	nucleolar ribonucleoprotein)	muscleblind-like (Drosophila	musculin (activated B-cell factor-1)	mutL homolog 3 (E. coli)	mutS homolog 2, colon cancer,	nonpolyposis type 1 (E. coli)	mutS homolog 6 (E. coli)	myelin protein zero-like 1	myeloid cell leukemia sequence 1 (BCL2-	related)	myeloid cell leukemia sequence 1 (BCL2-	related)	myeloid/lymphoid or mixed-lineage	leukemia (trithorax homolog, Drosophila);	translocated to, 2	MYLE protein	myosin IB	myosin ID	myosin IE	myosin light chain 1 slow a	myosin regulatory light chain	myosin X	missin light polymentide regulatory non-
-	MMS	cere	pou	mon	mon	mon	mon	mom	asso	WO	M-p	nuci	mns	snu	mut	mut	non	mut	mye	mye	rela	m/e	rela	m W	len	trar	MY	m	Ē	m V	JE.	ξE	ξ	-
O		AF007151	A1670788	AA420624	M68840	AA420624	M69177		X85750	D14812		X98494	AB007888	AF087036	L40399		U03911	U28946	AF087020		L08246		L08246			L13773	AF108145	AJ001381	AB018270	U14391	AI127424	U26162	AB018342	
B		MMS19L	MAP-1				MAOR		MMD	MRGX		MPHOSPH10	MBNL	MSC	MLH3		MSH2	MSH6	MPZL1		MCI 1		MCI 1			MLLT2	MYLE	MYO1B	MYO1D	MYO1E	MLC1SA	MLC-B	MYO10	
4		73 at	at	a at	at				65 at	161 at	4	797 at	306 at	192 at	384 at		at	03 s at			146 at	5	7 21	11		037 at					**	187 at	362 at	
	+	1600 35273	1601 34767	1602 41771	1603 41772 at	604 417	1605 37628 at	200	1606 37565 at	1607 40861		1608 33797	1609 34306 at	1610 35992 at	1611 31884 at		1612 860 at	1613 2003 s	1614 33769		1615 33146 at	21	1616 277	10101		1617 39037	1618 41637	1619 41439	1620 35729	1621 37631	1622 38251 at	1623 41187 at	1624 35362	

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1627	39707_at	MTMR4	AB014547		KIAA0647 protein
1628	1628 38035 at	MTMR6	AF072928		myotubularin related protein 6
1629	1629 39607 at	MTMR8	AL080178		hypothetical protein
1630	1630 36692 at	MTMR8	AF052099	myotubularin related protein 8	
				ein kinase C	
1631	1631 32434_at	MARCKS	D10522	-	80K-L protein
1632	1632 39267 at	AGM1	AF102265	N-acetylglucosamine-phosphate mutase	N-acetylglucosamine-phosphate mutase
				N-acylsphingosine amidohydrolase (acid	
1633	1633 36938_at	ASAH	U70063	ceramidase)	acid ceramidase
				N-acylsphingosine amidohydrolase (acid	
1634 461	461_at	ASAH	U70063	ceramidase)	acid ceramidase
				NADH dehydrogenase (ubiquinone) 1	
1635	1635 36169_at	NDUFA1	N47307	alpha subcomplex, 1 (7.5KD, MWPE)	
		1	1	NADH dehydrogenase (ubiquinone) 1	NAUH-ubiquinone oxidoreduciase subunit Cit
1636	1636 40546_s_at	NDUFA2	AF04/185	alpha subcomplex, z (8kD, 58)	000
				NADH dehydrogenase (ubiquinone) 1	NAUPH:ubiquinone oxidoreductase subunit
1637	1637 38462_at	NDUFA5	U64028	alpha subcomplex, 5 (13kD, B13)	B13
				NADH dehydrogenase (ubiquinone) 1	
1638	1638 32752 at	NDUFA7	W72440	alpha subcomplex, 7 (14.5kD, B14.5a)	
				NADH dehydrogenase (ubiquinone) 1 beta	
1639	38605_at	NDUFB1	Al345944	subcomplex, 1 (7kD, MNLL)	
				NADH dehydrogenase (ubiquinone) 1 beta	
1640	1640 38981_at	NDUFB3	AA203354	subcomplex, 3 (12kD, B12)	
				NADH dehydrogenase (ubiquinone) 1 beta	NADH dehydrogenase (ubiquinone) 1 beta NADH-ubiquinone oxidoreductase subunit Cl
1641	1641 32232 at	NDUFBS	AF047181	subcomplex, 5 (16kD, SGDH)	SGDH
				NADH dehydrogenase (ubiquinone) 1 beta	
1642	1642 32774_at	NDUFB8	AI541050	subcomplex, 8 (19kD, ASHI)	
				NADH dehydrogenase (ubiquinone) 1,	
1643	38485 at	NDUFC1	AA760866	subcomplex unknown, 1 (6kD, KFYI)	
				NADH dehydrogenase (ubiquinone) Fe-S	
				protein 1 (75kD) (NADH-coenzyme Q	75 kDa subunit NADH dehydrogenase
1644	1644 38395 at	NDUFS1	X61100	reductase)	precursor
				NADH dehydrogenase (ubiquinone) Fe-S	
	1	(		protein 4 (18kU) (NAUH-coenzyme C	
1645	1645 38695_at	NDUFS4	AA203303	(reductase)	

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	⋖	8	S	ח	
				NADH dehydrogenase (ubiquinone) Fe-S	
	10000	000	A 15.44236	protein 5 (15kD) (NADH-coenzyme Q	
040	1040 30000 at	NDOL33	00014014	MADE Johndrogese (uhiguinone)	
647	1647134893 at	NDUFV2	AI557064	flavoprotein 2 (24kD)	
	50000			natriuretic peptide receptor C/guanylate	
				cyclase C (atrionatriuretic peptide receptor	
648	1648 34519_at	NPR3	M59305		atrial natriuretic peptide clearance receptor
649	1649 34234 f at	NKTR	AI688640	natural killer-tumor recognition sequence	
920	1650 41795 at	NCK1	X17576	NCK adaptor protein 1	NCK adaptor protein 1
651	1651 33357 at	NCKAP1	AB011159	in 1	KIAA0587 protein
652	1652 36073 at	NDN	U35139·	necdin homolog (mouse)	NECDIN related protein
653	1653 34202 at	DKFZP566B0846	AL050071	nectin 3	hypothetical protein
654	1654 34264_at	NESCA	AB026894	nesca protein	NESCA
655	1655 38719 at	NSF	U03985	N-ethylmaleimide-sensitive factor	N-ethylmaleimide-sensitive factor
1656	1656 39356 at	NEDD4L	AB007899	developmentally down-regulated 4-like	ubiquitin-protein ligase NEDD4-like
				neural precursor cell expressed,	neural precursor cell expressed,
1657	1657 40281 at	NEDDS	D63878	developmentally down-regulated 5	developmentally down-regulated 5
				neural precursor cell expressed,	
1658	1658 1695_at	NEDD8	D23662	developmentally down-regulated 8	ubiquitin-like protein
				neuroblastoma, suppression of	neuroblastoma, suppression of
1659	37005 at	NBL1	D28124	tumorigenicity 1	tumorigenicity 1
1660	1660 31896 at	NAG	AL050281	neuroblastoma-amplitied protein	hypothetical protein
1661	1661 37286 at	NRCAM	AB002341	neuronal cell adhesion molecule	neuronal cell adhesion molecule
				neutral sphingomyelinase (N-SMase)	
1662	1662 37673_at	NSMAF	X96586	activation associated factor	FAN protein
				NGFI-A binding protein 1 (EGR1 binding	
1663	1663 38692_at	NAB1	AF045451	protein 1)	transcriptional regulatory protein p54
1664	34835 at	NCSTN	D87442	nicastrin	
1665	37032	NNMT	U08021	nicotinamide N-methyltransferase	nicotinamide N-methyltransferase
1666	1666 41709 at	LNN	1140490	nicotinamide nucleotide transhydrogenase	nicotinamide nucleotide transhydrogenase nicotinamide nucleotide transhydrogenase
	1667 35366 at	CIN	M30269	nidogen (enactin)	nidogen
198		NID2	D86425	nidogen 2	osteonidogen
	m_00		) 22		

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	A	В	ပ	٥	w
1669 37047	1 ~1	1	AF002020	Niemann-Pick disease, type C1	Niemann-Pick C disease protein
1670 980 at	380_at	NPC1	AF002020	Niemann-Pick disease, type C1	Niemann-Pick C disease protein
1671	1671 39345_at		AI525834	Niemann-Pick disease, type C2	
1672	1672 35153_at	NBS1	AF058696	Nijmegen breakage syndrome 1 (nibrin)	cell cycle regulatory protein p95
				NIMA (never in mitosis gene a)-related	
1673 36047	36047_at	NEK1	AL050385	kinase 1	
1674	1674 35843 at	Nek8	L40402	NIMA-related kinase Nek8	
1675	1675 40866_at	NIPSNAP1	AJ001258	nipsnap homolog 1 (C. elegans)	NIPSNAP1 protein
1676	1676 33916_at	NISCH	AB023192	nischarin	KIAA0975 protein
1677	39165_at	NIFU	U47101	nitrogen fixation cluster-like	NifU-like protein
1678	1678 36472_at	IWN	U32849	N-myc (and STAT) interactor	Nai
1679	36933_at	NDRG1	D87953	N-myc downstream regulated gene 1	RTP
1680	1680 41656 at	NMT2	AF043325	N-myristoyltransferase 2	N-myristoyltransferase 2
				non-canonical ubquitin conjugating	
1681	1681 39040_at	NCUBE1	W28360	enzyme 1	
				non-canonical ubquitin conjugating	
1682	1682 39039_s_at	NCUBE1	AI557497	enzyme 1	
				non-metastatic cells 1, protein (NM23A)	
1683	1683 1521_at	NME1	X17620	expressed in	Nm23 protein
		-		non-metastatic cells 2, protein (NM23B)	
1684	1684 33415_at	NME2	X58965	expressed in	NM23-H2 protein
				non-metastatic cells 2, protein (NM23B)	
1685	1685 1980_s_at	NME2	X58965	expressed in	NM23-H2 protein
				non-POU domain containing, octamer-	
1686	1686 38527_at	ONON	U02493	binding	54 kDa protein
1687	38750_at	NOTCH3	N97669	Notch homolog 3 (Drosophila)	Notch3
1688	1688 34781_at	WS-3	D84145	novel RGD-containing protein	novel RGD-containing protein
1689	40122_at	NSAP1	AF037448	NS1-associated protein 1	Gry-rbp
1690	1690 33752_at	NS1-BP	AB020657	NS1-binding protein	KIAA0850 protein
				N-sulfoglucosamine sulfohydrolase	
1691	1691 35626_at	SGSH	U30894	(sulfamidase)	N-sulphoglucosamine sulphohydrolase
1692	1692 37352_at	SP100	M60618	nuclear antigen Sp100	nuclear autoantigen
1693	37353_g_at_	SP100	M60618	nuclear antigen Sp100	nuclear autoantigen
1694	1694 40901_at	GS2NA	U17989	nuclear autoantigen	GS2NA
1605	1605 32780 at	NCBD2	A A 1 4 9 4 2 8	nuclear cap binding protein subunit 2,	
020	32703_al	INCOR 2	02464100	Cana	

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				listribution gene C homolog (A.	nuclear distribution gene C (A.nidulans)
1696	1696 35836_at	NUDC	AB019408		nomolog
1697	1697 39782 at	C1D	X95592	nuclear DNA-binding protein	C1D protein
1698		NDP52	U22897	nuclear domain 10 protein	NDP52
	0	o longing	824017	unclear factor (anthroid-derived 2)-like 2	CFZ
000 6601	000_dl	וארבברב			CCAAT/enhancer binding protein (C/EBP),
1700	1700 38354 at	CEBPB: LAP: CRI	RIX52560		beta
				lls,	nuclear factor of activated T-cells,
1701	1701 40822 at	NFATC3	L41067	cytoplasmic, calcineurin-dependent 3	cytoplasmic, calcineurin-dependent 3
				qe	:
1702	1702 38438_at	NFKB1	M58603	7	nuclear factor kappa-B DNA binding subunit
				eptide	
1703	1703 1377_at	NFKB1	M58603	gene enhancer in B-cells 1 (p105)	nuclear factor kappa-B DNA binding subunit
				nuclear factor of kappa light polypeptide	nuclear factor of kappa light polypeptide
1704	1704 1461 at	NFKBIA	M69043		gene enhancer in B-cells inhibitor, alpha
1705	1705 37544 at	NFIL3	X64318		nuclear factor, interleukin 3 regulated
1706	1706 38648 at	CIZ	U80760	nuclear matrix transcription factor 4	CAGH1 alternate open reading frame
				nuclear phosphoprotein similar to S.	
1707	1707 40816_at	PWP1	L07758	cerevisiae PWP1	IEF SSP 9502
1708	1708 34312_at	NCOA2	AI040324	nuclear receptor coactivator 2	
1709	1709 33381_at	NCOA3	AF012108	nuclear receptor coactivator 3	Amplified in Breast Cancer
1719	1710 39174 at	NCOA4	X77548	nuclear receptor coactivator 4	Ret fused gene
1711	1711 40088_at	NRIP1	X84373	nuclear receptor interacting protein 1	nuclear factor RIP140
				nuclear receptor subfamily 2, group F,	
1712	1712 39397_at	NR2F2	M64497	member 2	apolipoprotein Al regulatory protein-1
L				nuclear receptor subfamily 3, group C,	nuclear receptor subfamily 3, group C,
1713	1713 36690 at	NR3C1	M10901	member 1	member 1
1714	1714 35302 at	NXF1	AJ132712	nuclear RNA export factor 1	nuclear RNA export factor 1
1715	37928_at	NFYB	AA621555	nuclear transcription factor Y, beta	
L				nuclear transcription factor, X-box binding	
1716	1716 34667_at	NFX1	U15306		NFX1
		į		nuclear, Homo sapiens tyrosine	
	1717 33413_at	PRL-1	AF051160	phosphatase (PRL-1) gene, complete cds. lyrosine phosphatase	lyrosine pnospnatase

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	A	מצ	3		
17183	1718 32340 c at	NSEP1	M85234	nuclease sensitive element binding protein	nuclease sensitive element binding protein-1
17193	1719 35643 at	NUCR2	X76732	nucleobindin 2	NEFA protein
2	m=0100				
17203	1720[36597 at	NOLC1	D21262	nucleolar and coiled-body phosphprotein 1 ORF	)RF
17213	721 37520 at	HSA6591	AJ006591	nucleolar cysteine-rich protein	cysteine-rich protein
17223	722 36930 at	HUMAUANTIG	L05425		nucleolar GTPase
17233	9390 at	NUP133	AF052123		
17243	1724 32850 at	NUP153	Z25535		nuclear pore complex protein hnup153
17253	725 39024 at	NUP98	AF042357		
1726 571	71 at	NAP1L1	M86667		nucleosome assembly protein 1-like 1
1727 7	43 at	NAP1L3	D50370		nucleosome assembly protein
17283	12575 at	NAP1L4	U77456	nucleosome assembly protein 1-like 4	nucleosome assembly protein 2
1729	1729 36127 g at	NBP	U18919		nucleotide binding protein
				nudix (nucleoside diphosphate linked	diphosphoinositol polyphosphate
1730	1730 41584_at	NUDT3	AF062529		phosphohydrolase
1731	37693 at	NUMB	L40393		numb homolog
				ob15e02.s1 NCI_CGAP_Kid3 Homo	
				sapiens cDNA clone IMAGE:1323770 3'	
				similar to SW:ROA3_HUMAN P51991	
				HETEROGENEOUS NUCLEAR	
				RIBONUCLEOPROTEIN A3:, mRNA	
1732	1732 35916 s at	INHBC	AA877215	sequence.	
1733	1733 34169 s at	OCRL	U57627	oculocerebrorenal syndrome of Lowe	ocrl1
				olfactory receptor; Human olfactory	
1734	1734 31921 at	OLF3	U56421	receptor (OLF3) gene, complete cds.	HsOLF3
				O-linked N-acetylglucosamine (GlcNAc)	
				transferase (UDP-N-	
				acetylglucosamine:polypeptide-N-	
1735	1735 39507 at	OGT	AL050366	acetylglucosaminyl transferase)	hypothetical protein
1736		OGFR	AF109134	opioid growth factor receptor	09-InC
1737	1737 39745 at	OPA1	AB011139	optic atrophy 1 (autosomal dominant)	KIAA0567 protein
1738	1738 41744 at	OPTN	AF070533	optineurin	optineurin
				OR11-3; offactory receptor; Homo sapiens	
		-		OR7E12P pseudogene, complete	
1739	1739 34539_at	OR7E12P	AF065854	sequence.	

Fig.21

	A	a	٥	2	7 9 diamino-polargonic acid
740	AFEV BioCo of		104423	ORF 1	aminotransferase
<u> </u>	1/40 AFFX-5100-5_at 510A				7,8-diamino-pelargonic acid
1271	1741 AEEY, BioB.M. athioA		.104423	OBF 1	aminotransferase
	ייין מייין אייין אייין				7,8-diamino-pelargonic acid
1742	1742 AFEX-BioDn-5 abjoA		J04423	ORF 1	aminotransferase
					7,8-diamino-pelargonic acid
1743	1743 AFEX-BioDn-3 abioA		J04423	ORF 1	aminotransferase
2					7,8-diamino-pelargonic acid
1744	1744 AFFX-BioC-5 at bioA		J04423	ORF 1	aminotransferase
				ORF; putative; Human ribosomal protein	V.S. diotora Jomesodia richard
1745	1745 32412_at	RPS14	M13934	S14 gene, complete cds.	unknown proteint, riposofitial protein 514
				ORF1; ORF 2; no start codon; Human	
				mRNA for ornithine decarboxylase	to contract the second
1746	1746 1315_at	OAZ1	D78361	antizyme, ORF 1 and ORF 2.	ominine decarboxylase armzylije i
				OBE-3: Human retinoid X receptor	
4747	1747	DYBA: NB2B1	1166306	alpha mRNA, 3' UTR, partial sequence.	retinoid X receptor, alpha
<u>}</u>	32000_at	יספיואי לעוואין	2000	origin recognition complex, subunit 5-like	origin recognition complex subunit 5
1748	1748 38155 at	ORCSL	U92538	(yeast)	homolog
	is - 22			ornithine aminotransferase (gyrate	
1749	1749 36636_at	OAT	M12267	atrophy)	ornithine aminotransferase
1750	17E0 19E9 of	NIZAC	D88674	ornithine decarboxylase antizyme inhibitor antizyme inhibitor	antizyme inhibitor
3	1333_at				
1751	1751 33367_s_at	OAZIN	D88674	ornithine decarboxylase antizyme inhibitor	antizyme inhibitor
				ornithine decarboxylase; Human ornithine	1 asebyodasa 1
1752	1752 1081_at	00001	M33764	decarboxylase gene, complete cus.	$\neg$
				orphan G protein-coupled receptor; Homo sapiens G protein-coupled receptor	
1753	1753 31700_at	GPR35	AF027957	(GPR35) gene, complete cds.	G protein-coupled receptor
1754	1754 1451 s. at	OSF-2	D13666	osteoblast specific factor 2 (fasciclin I-like) osteoblast specific factor 2	osteoblast specific factor 2
1	1756 30774 21	0.841	XB0695	oxidase (cytochrome c) assembly 1-like	oxidase (cytochrome c) assembly 1-like
ř -	0 03/ /4_al	JONNIE JO	22222	,	

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17563	756 39136 at	OSR1	AB017642	oxidative-stress responsive 1	oxidative-stress responsive 1
1757 4		870			oxysterol-binding protein-like protein 8
17583	758 34329 at			p21 (CDKN1A)-activated kinase 2	
17593					P311 HUM
17603			115	protein	Pig11
17614	1761 40441 a at	BP1	AL080119	PAI-1 mRNA-binding protein	hypothetical protein
17624	762 40440 at		AL080119	PAI-1 mRNA-binding protein	hypothetical protein
1763	1763 32001 e at		M80482	paired basic amino acid cleaving system 4 subtilisin-like protease	subtilisin-like protease
	2001				paired box gene 8, isoform PAX8A; paired
	-				box gene 8, isoform PAX8B; paired box
	•				gene 8, isoform PAX8C; paired box gene 8,
					isoform PAX8D; paired box gene 8, isoform
1764	1764 121 at	PAX8	66969X	paired box gene 8	PAX8E
1765	1765 40127 at		M95929	paired mesoderm homeo box 1	homeobox protein
1,00		992	AB023209	palladin	KIAA0992 protein
1767	767 40504 at		AF001601	paraoxonase 2	paraoxonase
				partially supported by FGENES and	
1768	1768 36032 at	dJ167A19.1	AL031427	GENSCAN	hypothetical protein
1769	1769 39243 s at	PSIP2	U94319	PC4 and SFRS1 interacting protein 2	DFS70
1770	∦ਲ	PCF11	AB020631	PCF11p homolog	KIAA0824 protein
1771	1771 38758 at	PDAP1	R98910	PDGFA associated protein 1	
1772	772 36937 s at	PDLIM1	U90878	PDZ and LIM domain 1 (elfin)	carboxyl terminal LIM domain protein
				PDZ domain containing guanine	PDZ domain containing guanine nucleotide
1773	1773 32026_s_at	PDZ-GEF1	AB002311	nucleotide exchange factor(GEF)1	exchange factor(GEF)1
				PDZ domain containing guanine	
1774	1774 34745_at	PDZ-GEF1	AF070570	nucleotide exchange factor(GEF)1	
				PEDF: Human pigment epithelium-derived	
1775	1775 40856_at	SERPINF1; PEDF	DF U29953	factor gene, complete cds.	pigment epithelium-derived factor
				pentaxin-related gene, rapidly induced by	
1776	1776 1491_at	PTX3	M31166	IL-1 beta	tumor necrosis factor
				peptidylglycine alpha-amidating	peptidylglycine alpha-amidating
1777	1777 38465_at	PAM	M37721	monooxygenase	monooxygenase
1778	1778 35823 at	Bldd	M63573	peptidylprolyl isomerase B (cyclophilin B)	secreted cyclophilin-like protein

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1779	1779 37422 at	PPIC	S71018	peptidylprolyl isomerase C (cyclophilin C)	cyclophilin C
1780	1780 37385 at	PPIG	U40763	peptidyl-prolyl isomerase G (cyclophilin G)	CARS-Cyp
1781		PER1	AF022991		Rigui
1782		PDL-108	AB019409	periodontal ligament fibroblast protein	
				peripheral benzodiazepine receptor;	peripheral benzodiazapine receptor;
				Human peripheral benzodiazepine	peripheral benzodiazapine receptor short
1783	1783 32806 at	BZRP; MBR; PBR	R M36035	ds.	form
1784	784 38653 at	PMP22	D11428	peripheral myelin protein 22	PMP-22(PAS-II/SR13/Gas-3)
1785	785 41213 at	PRDX1	X67951	peroxiredoxin 1	peroxiredoxin 1
	1				Aop1_Human, MER5(Aop1_Mouse)-like
1786	1786 36631 at	PRDX3	D49396	peroxiredoxin 3	protein
1787		PRDX4	U25182	peroxiredoxin 4	antioxidant enzyme AOE37-2
1788		PEX11B	AF093670	peroxisomal biogenesis factor 118	peroxisomal biogenesis factor
1789	36864	PEX3	AJ001625	peroxisomal biogenesis factor 3	Pex3 protein
				peroxisomal long-chain acyl-coA	peroxisomal long-chain acyl-coA
1790	1790 36625 at	ZAP128	L40401	thioesterase	thioesterase
				peroxisomal membrane protein 3 (35kD,	
1791	1791 33265 at	PXMP3	M86852	Zellweger syndrome)	peroxisome assembly factor-1
1792		PFTK1	AB020641	PFTAIRE protein kinase 1	KIAA0834 protein
1793		PHF3	D87685	PHD finger protein 3	PHD finger protein 3
1707	1704 30381 21	XAD135	AF055030	PHD zinc finger protein XAP135	PHD Zinc finger protein XAP 135, isoform by PHD zinc finger protein XAP 135, isoform b
5/-		201			
				phosphatase and tensin homolog	
1795	1795 1434_at	PTEN	U92436	(mutated in multiple advanced cancers 1)	MMAC1
			1		type-2 phosphatidic acid phosphatase alpha-
1796	1796 34797_at	PPAP2A	AF014402	phosphatidic acid phosphatase type 2A	
1797	1797 33862 at	PPAP2B	AF017786	phosphatidic acid phosphatase type 2B	phosphatidic acid phosphonydrolase homolog
	13333			phosphatidylinositol 4-kinase, catalytic,	
1798	1798 40783_s_at	PIK4CA	L36151	alpha polypeptide	phosphatidylinositol 4-kinase
		7	2017	phosphatidylinositol binding clathrin	2
	1/99/3/685_at	IFICALIVI	045976	assembly protein	

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	A	9			
		(		phosphatidylinositol glycan, class A	PIG.A protein
1800);	1800 39993_at	PIGA		(B)	
1801	1801 314_at	PIGB	D42138	phosphatidylinositol glycan, class B	PIG-B
3	,	C C	067.40	O sach dender of the original report	phosphatidylinositol-dlycan-class C (PIG-C)
1802	1802 / 51_at	rigo			1 0 10
1803 776	776_at	PIGF	D13435		PIG-F
1804		PIGH	L19783	phosphatidylinositol glycan, class H	phosphatidylinositol glycan, class H
				phosphatidylinositol transfer protein,	homologue of Drosphila retinal degeneration
1805	1805 38297 at	PITPNM	X98654		B gene
				phosphatidylinositol-4-phosphate 5-	phosphatidylinositol-4-phosphate 5-kinase
1806	1806 35741 at	PIP5K2B	U85245	kinase, type II, beta	type II beta
1807	1807 37320 at	PTDSS1	D14694	phosphatidylserine synthase 1	phosphatidylserine synthase 1
				phosphodiesterase 4B, cAMP-specific	
				(phosphodiesterase E4 dunce homolog,	
1808	1808 33705 at	PDE4B	L20971	Ďrosophila)	phosphodiesterase
				phosphodiesterase 4D interacting protein	
1809	1809 39422 at	PDE4DIP	AB007923	(myomegalin)	KIAA0454 protein
1810	1810 37676 at	PDE8A	AF056490	phosphodiesterase 8A	cAMP-specific phosphodiesterase 8A
				phosphoenolpyruvate carboxykinase 2	
1811	37188 at	PCK2	X92720	(mitochondrial)	phosphoenolpyruvate carboxykinase (GTP)
1812	1812 39175 at	PFKP	D25328	phosphofructokinase, platelet	platelet-type phosphofructokinase
1813	1813 32210 at	PGM1	M83088	phosphoglucomutase 1	phosphoglucomutase 1
1814	36963 at	PGD	U30255	phosphogluconate dehydrogenase	phosphogluconate dehydrogenase
1815	1815 37677 at	PGK1	V00572	phosphoglycerate kinase 1	phosphoglycerate kinase 1
1816	1816 41221 at	PGAM1	J04173	phosphoglycerate mutase 1 (brain)	phosphoglycerate mutase 2
1817	II _	PIK3C3	Z46973	phosphoinositide-3-kinase, class 3	phosphatidylinositol 3-kinase
				phosphoinositide-3-kinase, regulatory	
1818	1818 1269 at	PIK3R1	M61906	subunit, polypeptide 1 (p85 alpha)	
				phosphoinositide-3-kinase, regulatory	
1819	1819 37961 at	PIK3R3	1090907	subunit, polypeptide 3 (p55, gamma)	
1820	1820 32775 r at	PLSCR1	AB006746	phospholipid scramblase 1	phospholipid scramblase 1
3	1 0000	D 1946	×86800	ahoenhonrotein enriched in astrocytes 15	
702	32200 al	2 5	200000	or solice in solice in solice in the solice of a solic	phosphoribosyl pyrophosphata synthetasa
1822	1822 36489 at	PRPS1	D00860	phosphoribosyl pyrophosphate synthetase	phosphoribosyl pyrophosphate symmetase phosphoribosyl pyrophosphate symmetase

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$\dagger$				phosphoribosyl pyrophosphate synthetase phosphoribosypyrophosphate synthetase-	phosphoribosypyrophosphate synthetase-
203	1823 37338 at	PRPSAP1	D61391	associated protein 1	associated protein 39
				phosphoribosylaminoimidazole	
					phosphoribosylaminolinidazole carpoxylase,
				phosphoribosylaminoimidazole	phosphoribosylaminoribosylaminolimidazole
7,00	20056 24	PAICS	X53793	succinocarboxamide synthetase	succinocarboxamide synthetase
2 2	1624 39030 at	DUIN I	XBAGOR	phosphorylase kinase, beta	phosphorylase kinase
272	1825 37392 at	מאנים	1147025	phosphorylase dycoden; brain	glycogen phosphorylase B
928	1826 36667_at	רושם	04100	hydanovi. CoA hydroxylase (Refsum	peroxisomal phytanoyl-CoA alpha-
- 1	1000	מתאת	A E023462	disease)	hydroxylase
	1827 32724 at	NINO	1177718	pinin, desmosome associated protein	pinin
828	1828 33543 S. at	LIMIN	2	printer, tumor-transforming 1 interacting	
000	1000 30003	PTTG11P	Z50022	protein	putative surface glycoprotein
1830	1830 34793 s at	PLS3	M22299	plastin 3 (T isoform)	T-plastin polypeptide
3					
			1	platelet-activating factor acetylhydrolase,	Miller-Dieker lissencephaly protein
1831	1831 32569_at	PAFAH1B1	L13385	ISOIOITI ID, aipila sabaili (1919)	platelet-derived growth factor receptor A
				platelet-derived growin factor receptor,	plateier delived grown recent
1832	1832 1731_at	PDGFRA	M21574	alpha polypeptide	_
			001.01	pleckstrin homology, Sec/ and colled/coll	cytoliesiii i, isoloiii i, oyoloolii i, oyol
1833	1833 38666_at	PSCD1	R91C8M	dolinatiles (cytolics)	
				pleckstrin homology, sec/ and collegion	2.40hosip-2
1834	1834 38741 at	PSCD2	U70728	domains 2 (cytonesin-2)	Collo Ling finant protein DI AGI 1
1835	1835 36943 r at	PLAGL1	U81992	pleiomorphic adenoma gene-like 1	CZHZ ZIIIC IIIIgei pioteiii i cocci
1836	1836 34780 at	PLXNB2	AB002313	plexin B2	plexiii 52
1837	1837 32193 at	PLXNC1	AF030339	plexin C1	VESTRI 
1838	1838 38270 at	PARG	AF005043	poly (ADP-ribose) glycohydrolase	poly(AUF-fluose) glycoflydiolaso
1830	1839 31951 s at	PABPC1	Z48501	poly(A) binding protein, cytoplasmic I	polyadellylate biliding protein in
184	1840 31950 at	PABPC1	Y00345	poly(A) binding protein, cytoplasmic 1	poly(A) piriaing protein, cytopiasing
				poly(A)-specific ribonuclease	
184	1841 36003 at	PARN	AJ005698	(deadenylation nuclease)	poly(A)-specific fiboriuciease
186	1842 34305 at	PCBP1	Z29505	poly(rC) binding protein 1	sub2.3
18	1843 35746 r at	PCBP2	X78136	poly(rC) binding protein 2	TOTAL TO
18	1844 35745 f at	PCBP2	X78136	poly(rC) binding protein 2	חחאואריהי
184	ט וי	PCBP3	AL046394	poly(rC) binding protein 3	

Fig. 21

$\vdash$	A	В	S	lemosotile) C coccit F.: 1	
$\vdash$		,	0000	polycystic Kidney disease z (autosoffiai	polycystin 2
8463				e (DNA directed) sigma	LAK-1
8473	1847 33380_at	POLS		n 3	polymerase (DNA directed), epsilon 3 (p17
		67 170	A E070640		subunit)
848	1848 38702_at			polymerase (RNA) II (DNA directed)	
		ACR 100	X63564	polypeptide A (220kD)	RNA polymerase II largest subunit
843	1848 40781 at	,		polymerase (RNA) II (DNA directed)	
850	1850 39746 at	POLR2B	X63563	polypeptide B (140kD)	RNA polymerase II 140 KDa subunit
				polymerase (RNA) II (DNA directed)	
851	1851 36027 at	POLR2F	AA418779	polypeptide F	
		חים ועם	137689	polymerase (RNA) II (DNA directed) polypeptide H	RNA polymerase II subunit
1852	1852 35631_at	rornan		Solumorase (BNA) II (DNA directed)	
070	10531248 at	POLR2H	U37689	polymerase (****) ** (*****) polypeptide H	RNA polymerase II subunit
200				polymerase (RNA) II (DNA directed)	BNA polymerase    subunit
1854	1854 503_at	POLR2L	U37690	polypeptide L (7.5kU)	
	1 7700	00 00	N24355	polymerase (KNA) II (DNA directed) polypeptide L (7.6kD)	
1855	1855 35841_at	FOLDEL	2004341	, , , , , , , , , , , , , , , , , , , ,	
1856	at	PTRF	AL050224	polymerase I and transcript release factor	Dokmeric imminoalobulin receptor
1857	at	PIGR	X73079	polymeric immunogiobulin receptor	purclear ribonic leoprofein
1858	1858 40593_at	PTBP1	X66975	polypyrimidine tract binding protein i	
1050	1950 31600 c at	PMS21.1	D38435	postmeiotic segregation increased 2-like 1	
3	B-5-0010			pot. ORF1 (aa 1-73); ORF2, put. cre	
				protein (aa 1-343); Bacteriophage P1 cre	
1860	1860 AFFX-CreX-5 at		X03453	gene for recombinase protein.	
				pot. ORF1 (aa 1-73); OHF2, put. cre	
				protein (aa 1-343); Bacteriophage P1 cre	
1861	1861 AFFX-CreX-3_at		X03453	gene for recombinase protein.	
1862	1862 315 at	PRDM2	D45132	PR domain containing 2, with ZNF domain zinc-finger DNA-binding protein	n zinc-finger DNA-binding protein
				and laukemia transcription factor 3	homeobox protein
1863	1863 32696_at	PBX3	X59841	pre-b-cell leuvelling ugilscription sector	

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	A	8	၁	O	Ŭ.
T				precursor; Human prolyl 4-hydroxylase	
				beta-subunit and disulfide isomerase	
				lene, exon 11, clones 68-	-
864	1864 36666 at	P4HB	M22806	(1,3,5,6).	prolyl 4-hydroxylase beta-subunit
865	1865 34321 i at	GS3786	D87120	predicted osteoblast protein	GS3786
998	11003 at	PFDN4	U41816	prefoldin 4	C-1
	1867/38698 at	PREIS	AL080070	ation protein 3	hypothetical protein
89	1868 40269 at	PRP18	U51990	ctor 18	hPrp18
				preproenkephalin (; Human enkephalin	
869	1869 38291 at	PENK	J00123	gene: exon 3 and 3'flank.	proenkephalin
870(	1870 641 at	PSEN1	L76517	presenilin 1 (Alzheimer disease 3)	presenilin 1
871	10621 at	PAWR	U63809	PRKC, apoptosis, WT1, regulator	prostate apoptosis response protein par-4
872	1872/41773 at	PCOLN3	U58048	procollagen (type III) N-endopeptidase	PRSM1
873	1873 31609 s at	PCOLCE	L33799	procollagen C-endopeptidase enhancer	procollagen C-proteinase enhancer protein
Γ				procollagen-lysine, 2-oxoglutarate 5-	
1874	1874 34795 at	PLOD2	U84573	dioxygenase (lysine hydroxylase) 2	lysyl hydroxylase isoform 2
				procollagen-lysine, 2-oxoglutarate 5-	
				dioxygenase (lysine hydroxylase, Ehlers-	
1875	1875 36184 at	PLOD	L06419	Danlos syndrome type VI)	lysyl hydroxylase
				procollagen-proline, 2-oxoglutarate 4-	procollagen-proline, 2-oxoglutarate 4-
				dioxygenase (proline 4-hydroxylase),	dioxygenase (proline 4-hydroxylase), alpha
1876	1876/37037 at	P4HA1	M24486	alpha polypeptide l	polypeptide l
	12 - 120 12			procollagen-proline, 2-oxoglutarate 4-	
				dioxygenase (proline 4-hydroxylase),	
1877	1877 34390 at	P4HA2	U90441	alpha polypeptide II	prolyl 4-hydroxylase alpha (II) subunit
				-	
				procollagen-proline, 2-oxoglutarate 4-	
		•		dioxygenase (proline 4-hydroxylase), beta	
				polypeptide (protein disulfide isomerase;	
1878	1878 691 a at	P4HB	J02783	thyroid hormone binding protein p55)	thyroid hormone binding protein p55)
1879	1879 38840 s at	PFN2	L10678	profilin 2	profilin II
1880	1880 38839 at	PFN2	AL096719	profilin 2	profilin 2 isoform b; profilin 2 isoform a
				progesterone receptor membrane	:
1881	1881 38802 at	PGRMC1	Y12711	component 1	putative progesterone binding protein
	 			progesterone receptor membrane	:
1882	1882 38821_at	PGRMC2	AJ002030	component 2	progresterone binding protein

15. A

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	A	8	ပ	Q	1
18833	39035 at	DDS	AF006010	progestin induced protein	progestin induced protein
1884 39036	11	DDS	AF006010		progestin induced protein
885.3	<del> </del>   <del> </del>	PDCD10	AF022385	programmed cell death 10	TFAR15
1886 37569	37569 at	PDCD6	AF035606		calcium binding protein
				(apoptosis-	•
8873	1887 32212 at	PDCD8	AL049703		hypothetical protein
888	1888 36592 at	PHB	S85655	prohibitin	prohibitin
889	1889 1884 s at	PCNA	M15796		proliferating cell nuclear antigen
1890 41600	, I 🛰	PA2G4	U59435	S	cell cycle protein p38-2G4 homolog
				c acid)	
1891	1891 35978 at	PRRG1	AF009242		proline-rich Gla protein 1
1892	1892 36023 at	PRH1	AI864120	proline-rich protein Haelll subfamily 1	
				pro-oncosis receptor inducing membrane	pro-oncosis receptor inducing membrane
1893	1893 40803 at	PORIMIN	AL050161		
				propionyl Coenzyme A carboxylase, alpha	
1894	1894 1348 s at	PCCA	S79219	polypeptide	polypeptide precursor
	1			propionyl Coenzyme A carboxylase, beta	
1895	1895 36561 at	PCCB	X73424	polypeptide	propionyl-CoA carboxylase
			1	proprotein convertase subtilisin/kexin type	DC6 isoform A
1896	1896 41032_at	PCSK5	U56387	5	plotease Lociscioni S
				prosaposin (variant Gaucher disease and	prosaposin (variant Gaucher disease and
1897	1897 36795_at	PSAP	J03077	variant metachromatic leukodystrophy)	variant metachromatic leukodystrophy)
1808	1898 38406 f at	PTGDS	A1207842	prostaglandin D2 synthase (21kD, brain)	
3	•:1			prostaglandin E receptor 2 (subtype EP2),	
1899	1899 828 at	PTGER2	U19487	53kD	prostaglandin E2 receptor
1900	1900 1890 at	PLAB	AB000584	prostate differentiation factor	TGF-beta superfamily protein
190	1901 32611 at	PBP	X75252	prostatic binding protein	phosphatidylethanolamine binding protein
1002	1902 719 n at	PRSS11	D87258	protease, serine, 11 (IGF binding)	serin protease with IGF-binding motif
100	1903 718 at	PRSS11	D87258	protease, serine, 11 (IGF binding)	serin protease with IGF-binding motif
1904	1904 33368 at	PRSS15	X76040	protease, serine, 15	Lon protease-like protein
1905	1905 40078 at	SPUVE	AF015287	protease, serine, 23	serine protease
1906	1906 39845 at	PRSS25	AF020760	protease, serine, 25	serine protease
100	1907 688 at	PSMC1	1.02426	proteasome (prosome, macropain) 26S subunit, ATPase, 1	26S protease (S4) regulatory subunit
200	000 at	1 0110	21. 221		

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	4. 0.00	20400	011004	proteasome (prosome, macropain) 26S	MSS1 profein
808	1908 35353_at	PSIMICE	011034	Т	moorphis (moorphis moorphis) 960
				ne, macropain) zes	proteasome (prosome, macropain) zos
1909	1909 592_at	PSMC3	M34079	subunit, ATPase, 3	subunit, ATPase, 3
				proteasome (prosome, macropain) 26S	
1910	1910 37766_s_at	PSMC5	AF035309	subunit, ATPase, 5	
				proteasome (prosome, macropain) 26S	
1911	1911 949_s_at	PSMC6	D78275	subunit, ATPase, 6	proteasome subunit p42
				proteasome (prosome, macropain) 26S	
1912	1912 1314_at	PSMD1	D44466	subunit, non-ATPase, 1	proteasome subunit p112
				proteasome (prosome, macropain) 26S	
1913	1913 1192 at	PSMD12	AB003103	subunit, non-ATPase, 12	26S proteasome subunit p55
				proteasome (prosome, macropain) 26S	proteasome (prosome, macropain) 26S
1914	1914 32240_at	PSMD5	D31889	subunit, non-ATPase, 5	subunit, non-ATPase, 5
				professome (prosome macropain) 26S	
1015	1015 045 at	PSMD7	D50063	subunit. non-ATPase, 7 (Mov34 homolog) proteasome subunit p40 / Mov34 protein	proteasome subunit p40 / Mov34 protein
2					
				proteasome (prosome, macropain) 26S	
1916	1916 40276_at	PSMD7	D50063	subunit, non-ATPase, 7 (Mov34 homolog)	proteasome subunit p40 / Mov34 protein
				proteasome (prosome, macropain) 26S	
1917	1917 32584_at	PSMD8	D38047	subunit, non-ATPase, 8	26S proteasome subunit p31
				proteasome (prosome, macropain) 26S	
1918	1918 36492_at	PSMD9	AI347155	subunit, non-ATPase, 9	
				proteasome (prosome, macropain)	
1919	1919 41171_at	PSME2	D45248	activator subunit 2 (PA28 beta)	proteasome activator hPA28 suunit beta
				proteasome (prosome, macropain)	
1920	1920 1184_at	PSME2	D45248	activator subunit 2 (PA28 beta)	proteasome activator hPA28 suunit beta
				proteasome (prosome, macropain)	
1921	36974_at	PSMF1	D88378	inhibitor subunit 1 (PI31)	proteasome inhibitor hPI31 subunit
				proteasome (prosome, macropain)	
1922	1922 38371_at	PSMA1	M64992	subunit, alpha type, 1	prosomal protein P30-33K
				proteasome (prosome, macropain)	proteasome (prosome, macropain) subunit,
1923	1923 1446_at	PSMA2	D00760	subunit, alpha type, 2	alpha type, 2
				proteasome (prosome, macropain)	proteasome (prosome, macropain) subunit,
1924	1924 1448 at	PSMA3	D00762	subunit, alpha type, 3	laipna type, o



C proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, alpha type, 5 proteasome (prosome, macropain) subunit, alpha type, 6 proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 2 proteasome (prosome, macropain) subunit, beta type, 4 proteasome (prosome, macropain) subunit, beta type, 4 proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 4 proteasome (prosome, macropain) subunit, beta type, 4 proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 5 proteasome (prosome, macropain) subunit, beta type, 5 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional proteasome) protein inhibitor of activated STAT3 protein kinase (CAMP-dependent, AB019517 catalytic) inhibitor gamma protein kinase C, iota L33881 protein kinase C, iota protein kinase C, iota L33881 protein kinase C, iota L33881 protein kinase C, iota L33881						
PSIMA4 D00763 subunit, alpha type, 4  PSIMA4 D00763 subunit, alpha type, 4  PSIMA4 D00763 subunit, alpha type, 4  PSIMA5 A1246726 subunit, alpha type, 6  PSIMB1 D00761 subunit, alpha type, 6  PSIMB2 D26699 subunit, beta type, 1  PSIMB4 D26600 subunit, beta type, 1  PSIMB4 D26600 subunit, beta type, 6  PSIMB4 D26600 subunit, beta type, 6  PSIMB5 D29011 subunit, beta type, 6  PSIMB5 D29012 subunit, beta type, 6  PSIMB7 D38048 subunit, beta type, 6  PSIMB7 D38048 subunit, beta type, 6  PSIMB7 D38048 subunit, beta type, 6  PSIMB7 D38048 subunit, beta type, 6  PSIMB7 D38048 subunit, beta type, 6  PSIMB7 D38048 subunit, beta type, 7  POTGB820TH proteasome (prosome, macropain)  PSIMB7 D38048 subunit, beta type, 7  POTGB820TH proteasome (prosome, macropain)  PSIMB7 D38048 subunit, beta type, 7  POTGB820TH proteasome (prosome, macropain)  PSIMB7 D38048 subunit, beta type, 7  POTGB820TH proteasome (prosome, macropain)  PSIMB7 D49489 protein disultide isomerase-related protein type, 7  POTGB820TH protein disultide isomerase-related protein type, 7  PRICE AB019517 catalytic) inhibitor gamma  at PRKCBP1 W22296 protein kinase C, lota  BAB019517 catalytic) inhibitor gamma  at PRKCBP1 W22296 protein kinase C, lota  BAB01951 protein kinase C, lota  BAB01951 protein kinase C, lota  BAB01951 protein kinase C, lota  BAB01951 protein kinase C, lota  BAB01951 protein kinase C, lota		A	8	O		T.
PSMA4   D00763   subunit, alpha Vpe, 4						oroteasome (prosome, macropain) subunit,
PSMA4   D00763   Subunit, alpha type, 4	1925	1450 g at	PSMA4	D00763		alpha type, 4
PSMA4 D00763 subunit, alpha type, 4  proteasome (prosome, macropain) PSMA6 X59417 proteasome (prosome, macropain) PSMB6 X59417 subunit, alpha type, 6 proteasome (prosome, macropain) PSMB1 D00761 subunit, beta type, 1 proteasome (prosome, macropain) PSMB2 D26599 subunit, beta type, 4 proteasome (prosome, macropain) PSMB4 D26600 subunit, beta type, 4 proteasome (prosome, macropain) PSMB4 D26600 subunit, beta type, 4 proteasome (prosome, macropain) PSMB5 D29011 subunit, beta type, 5 proteasome (prosome, macropain) PSMB6 D29012 subunit, beta type, 5 proteasome (prosome, macropain) PSMB7 D38048 subunit, beta type, 5 proteasome (prosome, macropain) PSMB7 D38048 subunit, beta type, 5 proteasome (prosome, macropain) PSMB9 D4808961 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 6 proteas						proteasome (prosome, macropain) subunit,
PSMA5   Al246726   Subunit, alpha type, 5   Proteasome (prosome, macropain)	1926	1449 at	PSMA4	D00763		alpha type, 4
PSMA5   Al246726   Subunit, alpha type, 5					proteasome (prosome, macropain)	
PSMA6   X59417   Subunit, alpha type, 6	1927	37046 at	PSMA5	AI246726	subunit, alpha type, 5	
PSMA6   X59417   Subunit, alpha type, 6						
PSMB1 D00761 subunit, beta type, 1  PSMB2 D26599 subunit, beta type, 2  proteasome (prosome, macropain)  proteasome (prosome, macropain)  proteasome (prosome, macropain)  proteasome (prosome, macropain)  proteasome (prosome, macropain)  psMB4 D26600 subunit, beta type, 4  proteasome (prosome, macropain)  psMB5 D29011 subunit, beta type, 5  proteasome (prosome, macropain)  psMB7 D38048 subunit, beta type, 6  proteasome (prosome, macropain)  psMB7 D38048 subunit, beta type, 6  proteasome (prosome, macropain)  proteasome (pro	1928	36122 at	PSMA6	X59417		prosomal P27K protein
PSMB1   D00761   Subunit, beta type, 1   Proteasome (prosome, macropain)					e, macropain)	proteasome (prosome, macropain) subunit,
PSMB2   D26599   Subunit, beta type, 2	1929	1447 at	PSMB1	D00761		beta type, 1
PSMB2   D26599   Subunit, beta type, 2						
PSMB4   D26600   Subunit, beta type, 4	1930	1310 at	PSMB2	D26599		proteasome subunit HsC7-I
at         PSMB4         D26600         subunit, beta type, 4         proteasome (prosome, macropain)         proteasome (prosome, macropain)           at         PSMB4         D26600         subunit, beta type, 4         profeasome (prosome, macropain)           at         PSMB5         D29011         subunit, beta type, 5         profeasome (prosome, macropain)           at         PSMB6         D29012         subunit, beta type, 6         profeasome (prosome, macropain)           at         PSMB7         D38048         subunit, beta type, 7         profeasome (prosome, macropain)           at         PSMB7         D38048         subunit, beta type, 7         profeasome (prosome, macropain)           at         PSMB7         D38048         subunit, beta type, 7         profeasome (prosome, macropain)           at         PSMB7         D38048         subunit, beta type, 7         profeasome (prosome, macropain)           at         PSMB9         profeasome (prosome, macropain)         profeasome (prosome, macropain)           at         PSMB9         profeasome (prosome, macropain)           at         PSMB9         profeasome (prosome, macropain)           at         PSMB9         profeasome (prosome, macropain)           at         PSMB9         profeasome (prosome, macropain)						
PSMB4   D26600   Subunit, beta type, 4	1931		PSMB4	D26600		proteasome subunit HsN3
at         PSMB4         D26600         subunit, beta type, 4         It         PSMB5         D29011         proteasome (prosome, macropain)         It           at         PSMB5         D29012         subunit, beta type, 6         proteasome (prosome, macropain)         proteasome (prosome, macropain)           at         PSMB7         D38048         subunit, beta type, 7         proteasome (prosome, macropain)           at         PSMB7         D38048         subunit, beta type, 7           at         PSMB7         D38048         subunit, beta type, 7           proteasome (prosome, macropain)         subunit, beta type, 7           proteasome (prosome, macropain)         subunit, beta type, 7           proteasome (prosome, macropain)         subunit, beta type, 7           proteasome (prosome, macropain)         subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional protease 2)           at         PSMB9         protein disulfide isomerase-related protein with the protein inhibitor of activated STAT3           at         PRKCBP1         W22296         protein kinase (cAMP-dependent, at the protein kinase (cather)           at         PRKCI         L33881         protein kinase C, iota           at         PRKCI         L33881         protein kinase C, iota           at <t< th=""><td></td><td></td><td></td><td></td><td></td><td></td></t<>						
at PSMB5 D29011 subunit, beta type, 5 proteasome (prosome, macropain) proteasome (prosome, macropain) subunit, beta type, 6 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional subunit, beta type, 9 (large multifunctional protein inhibitor of activated STAT3 at PRKCBP1 W22296 protein kinase (cAMP-dependent, at PRKCI L33881 protein kinase C binding protein 1 protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C-like 2	1932		PSMB4	D26600		proteasome subunit HsN3
at         PSMB5         D29011         subunit, beta type, 5         f           proteasome (prosome, macropain)         proteasome (prosome, macropain)         proteasome (prosome, macropain)         proteasome (prosome, macropain)           at         PSMB7         D38048         subunit, beta type, 7           proteasome (prosome, macropain)         proteasome (prosome, macropain)           at         PSMB7         D38048         subunit, beta type, 7           proteasome (prosome, macropain)         subunit, beta type, 7         proteasome (prosome, macropain)           at         PSMB9         AA808961         proteasome (prosome, macropain)           at         PSMB9         protein type, 7         protein type, 7           proteasome (prosome, macropain)         subunit, beta type, 7         protein type, 7           proteasome (prosome, macropain)         subunit, beta type, 7         protein type, 9 (large multifunctional protein           at         PSMB9         protein disultide isomerase-related protein         protein inhibitor of activated STAT3           at         PRKCBP1         W22296         protein kinase C binding protein 1           at         PRKCI         L33881         protein kinase C, iota           at         PRKCI         protein kinase C, iota           at						
proteasome (prosome, macropain)  at PSMB6 D29012 subunit, beta type, 6 proteasome (prosome, macropain)  at PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type	1933		PSMB5	D29011		proteasome subunit X
PSMB6   D29012   Subunit, beta type, 6   Professome (prosome, macropain)					proteasome (prosome, macropain)	
proteasome (prosome, macropain) at PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) at PSMB7 D38048 subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) subunit, beta type, 7 proteasome, macropain) proteasome, macropain, proteasome, macropain) proteasome, macropain, proteasome, macropain, proteasome, proteasome, proteasome, proteasome, proteasome,	1934	941 at	PSMB6	D29012	subunit, beta type, 6	proteasome subunit Y
at         PSMB7         D38048         subunit, beta type, 7           at         PSMB7         D38048         subunit, beta type, 7           rat         PSMB7         D38048         subunit, beta type, 7           proteasome (prosome, macropain)         proteasome (prosome, macropain)           subunit, beta type, 7         nacropain)           proteasome (prosome, macropain)         nacropain)           proteasome (prosome, macropain)         nultifunctional           proteasome (prosome, macropain)         nultifunctional           proteasome (prosome, macropain)         nultifunctional           proteasome (prosome, macropain)         nultifunctional           proteasome (prosome, macropain)         nultifunctional           proteasome (prosome, macropain)         nultifunctional           protein disultide isomerase-related protein         protein kinase (cAMP-dependent, catalytic) inhibitor of activated STAT3           protein kinase (cAMP-dependent, macropain)         nultifunctional           protein kinase (colorance)         protein kinase (colorance)           protein kinase (colorance)         protein kinase (colorance)           protein kinase (colorance)         protein kinase (colorance)           protein kinase (colorance)         protein kinase (colorance)					proteasome (prosome, macropain)	
at         PSMB7         D38048         subunit, beta type, 7 proteasome (prosome, macropain) subunit, beta type, 7           7_at         PSMB9         AA808961         proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2)           3_at         P5         D49489         protein disulfide isomerase-related protein protein inhibitor of activated STAT3           6_at         PKIG         AB019517         catalytic) inhibitor gamma           7_at         PRKCBP1         W22296         protein kinase (cAMP-dependent, catalytic) inhibitor gamma           at         PRKCI         L33881         protein kinase C binding protein 1           g_at         PRKCI         L33881         protein kinase C, iota           g_at         PRKCI         L33881         protein kinase C, iota           g_at         PRKCI         L33881         protein kinase C, iota           g_at         PRKCI2         D433052         protein kinase C-like 2	1935	39060_at	PSMB7	D38048	subunit, beta type, 7	proteasome subunit z
at         PSMB7         D38048         subunit, beta type, 7           proteasome (prosome, macropain)         proteasome (prosome, macropain)           7_at         PSMB9         AA808961         protease 2)         ,           2_at         P5         D49489         protein disulfide isomerase-related protein           8_at         PIAS3         AB021868         protein inhibitor of activated STAT3           6_at         PKIG         AB019517         catalytic) inhibitor gamma           7_at         PRKCBP1         W22296         protein kinase C binding protein 1           at         PRKCI         L33881         protein kinase C, iota           g_at         PRKCI         L33881         protein kinase C, iota           g_at         PRKCI         L33881         protein kinase C, iota           g_at         PRKCI         L33881         protein kinase C, iota					proteasome (prosome, macropain)	
T_at         PSMB9         AA808961         protease 2)         I           D_at         PS         D49489         protein disulfide isomerase-related protein protein inhibitor of activated STAT3           B_at         PIAS3         AB021868         protein inhibitor of activated STAT3           Feat         PKIG         AB019517         catalytic) inhibitor gamma           7_at         PRKCBP1         W22296         protein kinase C binding protein 1           at         PRKCI         L33881         protein kinase C, iota           g_at         PRKCI         L33881         protein kinase C, iota           g_at         PRKCI         L33881         protein kinase C, iota           g_at         PRKCI         L33881         protein kinase C, iota	1936	1313 at	PSMB7	D38048	subunit, beta type, 7	proteasome subunit z
PSMB9   AA808961   protease 2)   AA808961   protease 2)   AA808961   protease 2)   AA808961   protein disulfide isomerase-related protein at PIAS3   AB021868   protein inhibitor of activated STAT3   protein kinase (cAMP-dependent, at PRKCBP1   W22296   protein kinase C binding protein 1   PRKCI   L33881   protein kinase C, iota   protein kinase C, iota   protein kinase C, iota   protein kinase C, iota   protein kinase C, iota   protein kinase C, iota   protein kinase C, iota   protein kinase C, iota   protein kinase C, iota   protein kinase C, iota   protein kinase C, iota   protein kinase C, iota   protein kinase C, iota   protein kinase C, iota   protein kinase C-like 2		1			proteasome (prosome, macropain)	
PSMB9         AA808961         protease 2)         .           t         P5         D49489         protein disulfide isomerase-related protein inhibitor of activated STAT3           t         PIAS3         AB021868         protein kinase (cAMP-dependent, at PRKCBP1           t         PRKCBP1         W22296         protein kinase C binding protein 1           pRKCI         L33881         protein kinase C, iota           protein kinase C, iota         protein kinase C, iota           protein kinase C, iota         protein kinase C, iota					subunit, beta type, 9 (large multifunctional	
P5 D49489 protein disulfide isomerase-related protein and inhibitor of activated STAT3 PIAS3 AB021868 protein inhibitor of activated STAT3 protein kinase (cAMP-dependent, at PRKCBP1 W22296 protein kinase C binding protein 1 PRKCI L33881 protein kinase C, iota at PRKCI L33881 protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C- like 2	1937	38287_at	PSMB9	AA808961	protease 2)	
t         PIAS3         AB021868         protein inhibitor of activated STAT3           t         PKIG         AB019517         catalytic) inhibitor gamma           t         PRKCBP1         W22296         protein kinase C binding protein 1           pRKCI         L33881         protein kinase C, iota           at         PRKCI         L33881         protein kinase C, iota           t         PRKCI         U33052         protein kinase C-like 2	1038	141750 at	55	D49489	protein disulfide isomerase-related protein	human P5
PKIG AB019517 catalytic) inhibitor gamma PRICBP1 W22296 protein kinase C binding protein 1 PRKCI L33881 protein kinase C, iota at PRKCI L33881 protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota	38	132558 at	PIAS3	AB021868	protein inhibitor of activated STAT3	protein inhibitor of activatied STAT3
PRIG AB019517 catalytic) inhibitor gamma PRKCBP1 W22296 protein kinase C binding protein 1 PRKCI L33881 protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C, iota protein kinase C- like 2					protein kinase (cAMP-dependent,	
PRKCBP1 W22296 protein kinase C binding protein 1 PRKCI L33881 protein kinase C, iota It PRKCI L33881 protein kinase C, iota PRKCI L33881 protein kinase C-like 2	1940	34376 at	PKIG	AB019517	catalytic) inhibitor gamma	protein kinase inhibitor gamma
PRKCI L33881 protein kinase C, iota  11 PRKCI L33881 protein kinase C, iota  PRKCL2 U33052 protein kinase C-like 2	194	1 36957 at	PRKCBP1	W22296	protein kinase C binding protein 1	
at PRKCI L33881 protein kinase C, iota	194	2 1602 at	PRKCI	L33881	protein kinase C, iota	protein kinase C iota
at PRKCL2 U33052 protein kinase C-like 2	194		PRKCI	L33881	protein kinase C, iota	protein kinase C iota
	194		PRKCL2	U33052	protein kinase C-like 2	PRK2

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				cAMP-dependent, e I, alpha (tissue specific	cAMP-dependent protein kinase type I-alpha
1945	1945 41768_at	PRKAR1A	M33336		Subunit
				cAMP-dependent, e I, alpha (tissue specific	cAMP-dependent protein kinase type I-alpha
1946	1946 227 q at	PRKAR1A	M33336		Subunit
				I, alpha (tissue specific	cAMP-dependent protein kinase type I-alpha
1947	1947 226_at	PRKAR1A	M33336	extinguisher 1)	subunit
				protein kinase, interferon-inducible double protein activator of the interferon-induced	protein activator of the interferon-induced
1948	1948 32205 at	PRKRA	AF072860	stranded RNA dependent activator	protein kinase
	1			protein phosphatase 1, catalytic subunit,	serine /threonine specific protein
1949	1949 37725 at	PPP1CC	X74008		phosphatase
				protein phosphatase 1, regulatory	
1950	1950 40438 at	PPP1R12A	D87930	(inhibitor) subunit 12A	myosin phosphatase target subunit 1
				protein phosphatase 1, regulatory	
1951	1951 39366_at	PPP1R3C	N36638	(inhibitor) subunit 3C	
				protein phosphatase 1, regulatory subunit	
1952	1952 41540_at	PPP1R7	Z50749	7	yeast sds22 homolog
				protein phosphatase 1A (formerly 2C),	
1953	1953 857 at	PPM1A	S87759	magnesium-dependent, alpha isoform	protein phosphatase 2C alpha
				protein phosphatase 1A (formerly 2C),	
1954	1954 36501 at	PPM1A	S87759	magnesium-dependent, alpha isoform	protein phosphatase 2C alpha
				protein phosphatase 1D magnesium-	
1955	1955 37107_at	PPM1D	U78305	dependent, delta isoform	Wip1
				protein phosphatase 2 (formerly 2A),	
1956	1956 924 s at	PPP2CB	J03805	catalytic subunit, beta isoform	
	1			protein phosphatase 2 (formerly 2A),	
				regulatory subunit B (PR 52), alpha	
1957	1957 41167 at	PPP2R2A	M64929	isoform	protein phosphatase-2A subunit-alpha
				protein phosphatase 2 (formerly 2A),	
				regulatory subulin B (Fr. 52), alpha	and a state of the
1958	1958 1383_at	PPPZHZA	IM64929	ISOIOIIII	שומים לו משומים בי ממים בי היים של היים של היים בי היים בי היים בי היים בי היים בי היים בי היים בי היים בי היים
1959	1959 32734 at	PPP2R5E	L76703	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	protein phosphatase B56-epsilon
	1011				



	4	В	၁	_	Vicinity of Plaints 1 regulatory
			01010	protein phosphatase 2, regulatory subunit	Subunit
1960	960 40786_at	PPP2R5C	03/352	anilatory subunit	profein phosphatase 2A B'alpha1 regulatory
		0	1197959	Protein priospriatase 2, regulatory superior RF6) damma isoform	subunit
1961	1961 1 / 6_at	rrizh30	200100	regulatory	•
000	100000000000000000000000000000000000000	PPP2R4	X73478		phosphotyrosyl phosphatase activator
1362	3912/ 1 at	11711		protein phosphatase 3 (formerly 2B),	protein phosphatase 3 (formerly 2b),
	•			catalytic subunit, beta isoform (calcineurin	catalytic subunit, beta isoform (calcineurin   catalytic subunit, beta isoform (calcineurin A
1002	1069 28977 at	PPP3CB	M29550	A beta)	beta)
3	30211_al	300		protein phosphatase 3 (formerly 2B),	
				catalytic subunit, gamma isoform	
7007	1004 20541 21	DEPERC	S46622	(calcineurin A gamma)	calcineurin A catalytic subunit
200				protein phosphatase 4, regulatory subunit	
1965	34371 at	PPP4R1	U79267		
	70	Connec	X02072	protein phosphatase 6, catalytic subunit	protein phosphatase 6
	1900 3/301 - 81	PEOS.	M15036	protein S (alpha)	protein S (alpha)
	196/ 33/32_s_all	F1001	A A D R 3 1 2 9	Inrotein translocation complex beta	
1965	1968 32564 at	SECOID	11006001	protein tyrosine kinase 9	protein tyrosine kinase
1985	1969 1064_at	FIRS	005500	protein tyrosine phosphatase type IVA,	
	9	БТБАА1	1148296	member 1	protein tyrosine phosphatase PTPCAAX1
	1970 045 at			protein tyrosine phosphatase type IVA,	
	074	DTD/A2	1114603	member 2	protein-tyrosine phosphatase
<u> </u>	1 304 13 at	7Vr 11 1		protein tyrosine phosphatase type IVA,	•
107	070 1041 04	PTPAA2	U14603	member 2	protein-tyrosine phosphatase
	11			protein tyrosine phosphatase, non-	protein tyrosine phosphatase, non-receptor
107	1073 40137 at	PTPN1	M31724	receptor type 1	lype 1
	5-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0			protein tyrosine phosphatase, non-	-
107	107/ 1/63 at	PTPN12	M93425	receptor type 12	protein tyrosine phosphatase
	5 1			protein tyrosine phosphatase, non-	
				receptor type 13 (APO-1/CD95 (Fas)-	
107	107E 3/108 at	PTPN13	U12128	associated phosphatase)	protein tyrosine priospiratase 15
	100110				protein tyrosine phosphatase, receptor type,
					A, isotorm 1 precursor; protein tyrosine
				protein tyrosine phosphatase, receptor	phosphatase, receptor type, A, isotorm 2
197	1976 1496_at	PTPRA	M34668	ltype, A	Diegraphical Company

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	А	Я	၁	Ŋ	U
				protein tyrosine phosphatase, receptor	
1977	1977 36204_at	PTPRF	Y00815		put. LAR preprotein (AA -16 to 1881)
Г				protein tyrosine phosphatase, receptor	
				PRF), interacting	
1978	1978 41780_at	PPFIA1	U22816	protein (liprin), alpha 1	LAR-interacting protein 1b
				protein tyrosine phosphatase, receptor	
1979 1488	1488_at	PTPRK	L77886	type, K	protein tyrosine phosphatase
				tyrosine phosphatase, receptor	
1980	1980 995_g_at	PTPRM	X58288		protein-tyrosine phosphatase
				protein tyrosine phosphatase, receptor	
1981	31892_at	PTPRM	X58288	type, M	protein-tyrosine phosphatase
				protein-kinase, interferon-inducible double	
				stranded RNA dependent inhibitor,	
1982	1982 41141 at	PRKRIR	AL049970	repressor of (P58 repressor)	hypothetical protein
				protein-L-isoaspartate (D-aspartate) O-	
1983	1983 37737 at	PCMT1	D25547	methyltransferase	PIMT isozyme I
Γ		-		protein-L-isoaspartate (D-aspartate) O-	
1984	1984 37736 at	PCMT1	D13892	methyltransferase	carboxyl methyltransferase
1985	1985 32227_at	PRG1	X17042	proteoglycan 1, secretory granule	proteoglycan 1, secretory granule
1986	38590 r at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
1987	38589 i_at	PTMA	M14630	prothymosin, alpha (gene sequence 28)	prothymosin, alpha (gene sequence 28)
1988	37936_at	HPRP4P	Al184802 ·	PRP4/STK/WD splicing factor	
				pseudoferritin H protein; Human ferritin H	
1989	1989 31697_s_at	FTHP1	J04755	processed pseudogene, complete cds.	
1990	1990 36117_at	PTK2	L13616	PTK2 protein tyrosine/kinase 2	focal adhesion kinase
1991	1991 40048_at	PUM1	D43951	pumilio homolog 1 (Drosophila)	KIAA0099 protein
1992	1992 35359_at	PUM2	D87078	pumilio homolog 2 (Drosophila)	KIAA0235 protein
1993	1993 35221_at	PURA	X91648	purine-rich element binding protein A	
				put. ORFX (AA 1-75); beta subunit (AA 1-	
				340); Human liver mRNA for beta-subunit	
			•	signal transducing proteins Gs/Gi (beta-	guanine nucleotide-binding protein, beta-1
1994	1994 33341_at	GNB1	X04526	G).	subunit
1995	1995 33720_at	LOC56902	L48692	putatative 28 kDa protein	
1996	1996 39363 at	BC-2	AF042384	putative breast adenocarcinoma marker (32kD)	BC-2 protein
	Jan 20000	1 0 2			

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1997	1997 39884 g at	HSA9761	AF091078	$\neg$	putative dimethyladenosine transferase
	-6-, 222			<u>.</u>	putative glialblastoma cell differentiation-
1998	1998 38841 at	GDBR1	AF068195		related protein
1000	1999 41188 at	LC27	W28186	putative integral membrane transporter	
				putative L-type neutral amino acid	
2000	2000 38984 at	KIAA0436	AB007896	transporter	
2001	2001 39116_at	LOC54499	AF070626	putative membrane protein	
6006	2002 25286 r at	BV1	X76302	putative nucleic acid binding protein RY-1	nucleic acid binding protein
3	00500-1-at			Putative prostate cancer tumor	
2003	2003 36852 at	N33	U42349	suppressor	-
				putative protein similar to nessy	
2004	2004 33710 at	C3F	U72515		C3f
2005	2005 40203 at	SUI	AJ012375	٥٢	putative translation initiation factor
2006	2006 37678 at	NMA	U23070		putative transmembrane protein
				putative transmembrane protein; homolog	
				of yeast Golgi membrane protein Yif1p	
2007	2007 35326 at	54TM	AF004876	(Yip1p-interacting factor)	54TMp
				putative; Homo sapiens PTS gene,	
2008	2008 35697 at	PTS	L76259	complete cds.	6-pyruvoyttetrahydropterin synthase
	1			putative; originaly identified as an	
				oncogene', product renamed by NCBI	
				staff; Homo sapiens longation factor 1-	•
2009	2009 40887 g at	PTI-1	L41498	alpha 1 (PTI-1) mRNA, complete cds.	longation factor 1-alpha 1
				putative; originaly identified as an	
				oncogene', product renamed by NCBI	
_				staff; Homo sapiens longation factor 1-	
2010	2010 40886 at	PTI-1	L41498	alpha 1 (PTI-1) mRNA, complete cds.	longation factor 1-alpha 1
				pVHL-interacting deubiquitinating enzyme	
2011	2011 33219 at	VDU1	AB029020		KIAA1097 protein
				Pyruvate dehydrogenase complex, lipoyl-	Y righter volumes contracts of the state of
				containing component X; E3-binding	pyluvate delijulogeriase complex protein x
2012	2012 36164_at	PDX1	U82328	protein	suburint precursor
2013	2013 32378_at	PKM2	M26252	pyruvate kinase, muscle	pyruvate Kinase, muscie
2014	2014 260_at	adpr	M16447	quinoid dihydropteridine reductase	quinoid dinydropteridine reductase

Fig. 21

f			C	Q	F
$\dagger$	₹		,	R3H domain (binds single-stranded	
2015 36610	86610 at	R3HDM	D21852		KIAA0029 protein
016	2016 39030 at	RABAC1	AJ133534	ed)	prenylated hab acceptor ( ( )
		0.00	700007	Rab geranylgeranyltransferase, beta	rab geranylgeranyl transferase
2017[3	2017 37703_at	HABGGIB	10001	continu factor	guanine nucleotide exchange factor mss4
2018	2018 38264_at	RABIF	074324	HAB Interacting factor	
2010	2010 3EE0 at	RAB11A	AF000231		rab11a
	20000 5000	BAB14	AF052113	RAB14, member RAS oncogene family	
	33323 at	DAB1A	AI 050268		hypothetical protein
	2021 34333 I at	V 1000	AI 050268		hypothetical protein
7700	2022 34392_s_at	RAB21	D42087		RAB21, member RAS oncogene family
		DA007A	1157094		Rab27a
2024 2024	_	LADZ/A	1 150977	Г	low-Mr GTP-binding protein Rab31
2025	2025 33371_s_at	HABSI	M28215		GTP-binding protein
2020	2026 36 1 10_at	TAGON I	21.20.	rahe GTPase activating protein (GAP and	
7000	25.000.00	GAPCENA	AJ011679	centrosome-associated)	Rabe GTPase activating protein, GAPCenA
7707	2027 33209 at	RARGA	AF052130	RAB6A, member RAS oncogene family	
2020	2020 0000	DAROA	AI671547	RAB9A, member RAS oncogene family	
2022	2029 39020 at	BC3	AB020663	rabconnectin-3	KIAA0856 protein
200	41710 01	3		Rac/Cdc42 quanine nucleotide exchange	
2021	275/3 at	ARHGEF6	D25304	factor (GEF) 6	
200	20057 at	RAD1	AF084513	RAD1 homolog (S. pombe)	DNA repair exonuclease
4000	2002 30001 _at	RAD21	D38551	RAD21 homolog (S. pombe)	RAD21 homolog
3	3011 <del>1</del> at	1			XP-C repair complementing protein
2034	2034 1874_at	RAD23B	D21090	RAD23 homolog B (S. cerevisiae)	(desunn/sed)
200	207E7 et	BAE1	U84720	RAE1 RNA export 1 homolog (S. pombe)	mRNA export protein
3	32/3/_at	5		RAGE-4 ORF2; one of 2 possible coding	
				regions; RAGE-4 ORF3; one of 2 possible	
				coding regions; Human renal cell	
				carcinoma antigen HAGE-4 IIIniva,	
2036	2036 1524_at		046194	Complete putative cus.	RI IP76 protein
203,	2037 36628_at	RALBP1	L42542	Tary Dilitaring Protein 1	KIAA0959 protein
2038	2038 37539_at	RGL	AB023176	Haid Do-line gene	

Fig. 2

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2039 41342	11342_at	RANBP1	D38076		Han-BP I(Han-binding protein I)
2040	2040 40824 at	RANBP16	AB018288	91	KIAA0745 protein
2041	2041 41174 at	RANBP2L1	AF012086	lke 1	Ran binding protein 2
2042	2042 35255_at	RANBP7	AF098799		RanBP7/importin 7
2043	2043 32602 at	RAP1GDS1	X63465	RAP1, GTP-GDP dissociation stimulator 1 smg GDS	smg GDS
2044	2044 1848 at	RAP1A	M22995	RAP1A, member of RAS oncogene family ras-related protein	ras-related protein
2045	2045 40146 at	RAP1B	AL080212	RAP1B, member of RAS oncogene family hypothetical protein	hypothetical protein
	I.			Ras association (RalGDS/AF-6) domain	
2046	2046 39601_at	RASSF1	AF061836	一	putative tumor suppressor protein
				Ras association (RalGDS/AF-6) domain	Ras association (RalGDS/AF-6) domain
2047	2047 37598_at	RASSF2	D29990		family 2
2048	2048 1659_s_at	RHEB2	D78132		ras-related GTP-binding protein
2049	2049 37309 at	ARHA	L09159	ras homolog gene family, member A	multidrug resistance protein
2050	2050 1394_at	ARHA	L25080		GTP-binding protein
2051	2051 35803 at	ARHE	S82240	ras homolog gene family, member E	RhoE
				RAS p21 protein activator (GTPase	
2052	2052 36935 at	RASA1	M23379	activating protein) 1	GTPase-activating protein
				RAS p21 protein activator (GTPase	
2053	2053 1675 at	RASA1	M23379	activating protein) 1	GTPase-activating protein
				Ras-GTPase activating protein SH3	
2054	2054 35793 at	G3BP2	AB014560	domain-binding protein 2	KIAA0660 protein
				ras-related C3 botulinum toxin substrate 1	
				(rho family, small GTP binding protein	
2055	2055 40864_at	RAC1	D25274	Rac1)	
				ras-related C3 botulinum toxin substrate 1	ras-related C3 botulinum toxin substrate 1 ras-related C3 botulinum toxin substrate 1
				(rho family, small GTP binding protein	isoform Rac1; ras-related C3 botulinum toxin
2056	2056 2050 s at	RAC1	M29870	Rac1)	substrate 1 isoform Rac1b
2057	2057 35316 at	RAGA	U41654	Ras-related GTP-binding protein	adenovirus E3-14.7K interacting protein 1
2058	2058 33234 at	BCAA	AA887480	RBP1-like protein	
2059	2059 41407_at	RDBP	L03411	RD RNA-binding protein	RD protein
	10070	BECOI	1 26140	Oco Ontolin-like (ONA helicase O1-like)	DNA belicase
7007	2000 34084 at	וחבוכתר	1530140	There is a construction of the construction of	

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2061	2061 34685_at	RECOL	AI685944	RecQ protein-like (DNA helicase Q1-like)	
				regulated at the translational level; contains I-mfa domain: untilizes unique	
					machosi niedova Old. Oba machosi niedova Old
2062	2062 37842 at	SH	AF054589	protein isolorm p40 and hit protein isolorm p32 mRNAs, complete cds.	p32
	1			regulator of G-protein signalling 19	
2063	2063 35756_at	RGS19IP1	AF089816		RGS-GAIP interacting protein GIPC
2064	2064 37701_at	RGS2	L13463	24kD	helix-loop-helix phosphoprotein
2065	2065 35722_at	RENT2	AL080198		hypothetical protein
				related RAS viral (r-ras) oncogene	
2066	2066 32827_at	RRAS2	Al365215	homolog 2	
				remainder of gene in clone 549K18	
2067	2067 34845_at	dJ796117.4	AL035398	(AL023654)	CGI-51 protein
2068	2068 1055 g at	BFC4	M87339	replication factor C (activator 1) 4 (37kD)	replication factor C, 37-kDa subunit
2069	2069 38481 at	RPA1	M63488		replication protein A, 70-kDa subunit
2070	2070 652 g at	RPA3	L07493	replication protein A3 (14kD)	replication protein A 14kDa subunit
2071	2071 37651_at	RCOR	D31888	REST corepressor	REST corepressor
				restin (Reed-Steinberg cell-expressed	
2072	2072 34350_at	RSN	X64838	intermediate filament-associated protein)	restin
2073	2073 31851_at	RFP2	AJ224819	ret finger protein 2	tumor suppressor
				reticulocalbin 1, EF-hand calcium binding	
2074	2074 40556_at	RCN1	D42073	domain	reticulocalbin
				reticulocalbin 2, EF-hand calcium binding	, T
2075	2075 37727_1_at	HCNZ	A/8669	domain	Er-mand protein
2076	40 4 00220	DCNO	Y78660	reliculocalbin 2, Er-hand calcium binding	EE-hand protein
2077	2077 31536 at	RTN4	AB020693	reticulon 4	KIAA0886 protein
2078	2078 39964 at	RP2	AJ007590	refinitis pigmentosa 2 (X-linked recessive) XRP2 protein	XRP2 protein
2079	38164	RPGR	U57629	retinitis pigmentosa GTPase regulator	retinitis pigmentosa GTPase regulator
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Č	M15400	retinoblastoma 1 (including	retinoplactoma 1 (including octoocarcoma)
7 7 7 7	2080 2044_s_at	HBI	10401	Usteusarculla)	Teurobiasionia i (metading estectationia)

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RBBPB   Digital   Digita	ŀ			ر	. 0	<b>u</b>
ABBNS   ABBNS   AB007931   retinoblastoma-associated factor 600   Karan   ABBNS   AL049432   retinoblastoma-associated factor 600   Tall   RBAF600   X76061   retinoblastoma-like 2 (p130)   Telepseudogene   ABNS   AL049432   retinoblastoma-like 2 (p130)   Telepseudogene   ABNS   A		- 1	n			XBP interacting protein CtIP
BARGETO   ABOUT 531   retinoblastoma-like 2 (p130)   11	0813			07200	009	(IAA0462 protein
RBL2	082 3	3860_at	200	AB00/931		30K protein
BANSTP   AL049432   retinoce action induces   retropseudogene MSSP-1 DNA, complete   retropseudogene MSSP-1 DNA, complete   retropseudogene MSSP-1 DNA, complete   retropseudogene MSSP-1 DNA, complete   retropseudogene MSSP-1 DNA, complete   retropseudogene MSSP-1 DNA, complete   retropseudogene MSSP-1 DNA, complete   retropseudogene MSSP-1 DNA, complete   retropseudogene MSSP-1 DNA, complete   retropseudogene MSSP-1 DNA, complete   retropseudogene MSSP-1 DNA, complete   retropseudogene MSSP-1 DNA, complete   retropseudogene MSSP-1 DNA, complete   reversion-inducing-cysteine-rich protein   reversion-inducing	0833	2597_at		X/6061	Tellifolasionia mo E (F. C.)	
REV3L	A800	5848 at		AL049432	retinoic acid illunced 17	
REV3L   D82351   Cds   REV3L   D82351   Cds   REV3L   D82351   Cds   REV3L   D82351   Cds   REV3L   D82351   Cds   REV3L   D823E   D91ymerase zeta (yeast)   D823E   D91ymerase zeta (yeast)   D825E   With kazal motifs   reversion-inducing-cysteine-rich protein   reversion-inducing-cysteine-rich protein   with kazal motifs   reversion-inducing-cysteine-rich protein   RECK   D5040E   With kazal motifs   With kazal motifs   Reck   D5040E   With kazal motifs   With kazal motifs   Reck   D6340E   Rho GTPase activating protein 1   ARHGAP1   A961929   Rho GTPase activating protein 1   ARHGAP1   A961929   Rho GTPase activating protein 1   ARHGEF1   A8002292   GEE) 10   Rho guanine nucleotide exchange factor   GEF) 10   Rho guanine nucleotide exchange   F114-RHO-GEF   A8011093   factor (GEF) 2   Rho-specific guanine nucleotide exchange   RNASE4   D37931   ribonuclease P (38kD)   RNASE4   D37931   ribonuclease Rangiogenin inhibitor   RPL11   X79234   ribonuclease Rangiogenin inhibitor   RPL12   AF037843   ribosomal protein L13   RPL13   X68032   ribosomal protein L13   RPL13   X68032   ribosomal protein L13   RPL14   D87735   ribosomal protein L13   RPL14   D87735   ribosomal protein L13   RPL14   D87735   ribosomal protein L14   RPL14   D87735   ribosomal protein L14   RPL14   D87735   ribosomal protein L14   RPL14   D87735   ribosomal protein L14   RPL14   D87735   ribosomal protein L14   RPL14   D87735   ribosomal protein L14   RPL14   D87735   ribosomal protein L14   RPL14   D87735   ribosomal protein L14   RPL14   D87735   ribosomal protein L14   RPL14   D87735   ribosomal protein L14   RPL14   D87735   ribosomal protein L14   RPL14   D87735   ribosomal protein L14   RPL14   D87735   ribosomal protein L14   RPL14   D87735   ribosomal protein L14   RPL14				-	retropseudogene; Human	
REV3L						MSSP-1
REV3L	2085 3	:1672_g_at	RBMS1P; MSSP1	U82351	ANO for the city of DNA	
RECK AA099265 with kazal motifs reversion-inducing-cysteine-rich protein with kazal motifs reversion-inducing-cysteine-rich protein reversion-inducing-cysteine-rich protein reversion-inducing-cysteine-rich protein reversion-inducing-cysteine-rich protein reversion-inducing-cysteine-rich protein reversion-inducing-cysteine-rich protein reversion-inducing-cysteine-rich protein reversion-inducing-cysteine-rich protein reversion-inducing-cysteine-rich protein reversion-inducing-cysteine-rich protein 1  ARHGAP1 D02570 Rho GTPase activating protein 1  ARHGAP1 A961929 Rho GTPase activating protein 1  ARHGEF10 AB002292 Rho guanine nucleotide exchange factor (GEF) 7  ARHGEF7 D63476 (GEF) 7  ARHGEF7 D63476 (GEF) 7  ARHGEF7 D63476 (GEF) 7  ARHGEF7 D63476 (GEF) 7  ARHGEF7 D63476 (GEF) 7  ARHGEF7 D63476 (GEF) 7  ARHGEF7 D63476 (GEF) 7  ARHGEF7 D63476 (GEF) 7  ARHGEF10 RhO11093 factor p114  ARHGEF7 D637931 ribonuclease, RNase A family, 4  ARMASE4 X13973 ribonuclease, RNase A family, 4  ARPL11 X792343 ribonuclease/angiogenin inhibitor ribonuclease/angiogenin L11  ARPL13 X64707 ribosomal protein L13  ARPL13 X64707 ribosomal protein L13  ARPL13 X66302 ribosomal protein L13  ARPL13 X66302 ribosomal protein L13  ARPL13 X66302 ribosomal protein L13  ARPL13 X66902 ribosomal protein L14  ARPL134 D87735 ribosomal protein L14		10000	DEV3	AI 096744		hypothetical protein
RECK         AA099265         with kazal motifs           RECK         AA099265         reversion-inducing-cysteine-rich protein           RECK         AA099265         with kazal motifs           RECK         D50406         with kazal motifs           RECK         D02570         Rho GTPase activating protein 1           ARHGAP1         AI961929         Rho GTPase activating protein 1           ARHGAP1         AB002292         Rho GTPase activating protein 1           ARHGEF10         AB002292         Rho GTPase activating protein 1           ARHGEF7         AB002292         Rho GTPase activating protein 1           ARHGEF7         AB002292         Rho GTPase activating protein 1           ARHGEF7         AB002292         Rho GTPase activating protein 1           ARHGEF7         AB002292         Rho GTPase activating protein 1           ARHGEF7         AB002292         Rho GTPase activating protein 1           ARHGEF7         D63476         Rho guanine nucleotide exchange factor (GEF) 7           RPP38         U77664         Irbonuclease P (38kD)           RPP38         U77664         Irbonuclease R (38kD)           RRM1         X13973         Irbonuclease Angiogenin inhibitor MAD00000           RPL10         M64241         Irbosomal pro	20807	8808_s_at	ne voe		reversion-inducing-cysteine-rich protein	
RECK	-6000	15005 a at	BECK	AA099265	with kazal motifs	
RECK   AA099265   with kazal motifs		33230 g_a			reversion-inducing-cysteine-rich protein	
RECK   D50406   with kazal motifs   ARHGAP1   U02570   Rho GTPase activating protein 1	- 0000	to 36 of	BECK	AA099265	with kazal motifs	
ARHGAP1   U02570   Rho GTPase activating protein 1		33533 at			reversion-inducing-cysteine-rich protein	
ARHGAP1         U02570         Rho GTPase activating protein 1           ARHGAP1         Al961929         Rho GTPase activating protein 1           ARHGAP1         Al961929         Rho guanine nucleotide exchange factor           Rho guanine nucleotide exchange factor         Rho guanine nucleotide exchange factor           ARHGEF7         D63476         (GEF) 10           Rho guanine nucleotide exchange factor         Rho guanine nucleotide exchange factor (GEF) 2           RPHGEF2         U72206         Rho guanine nucleotide exchange factor (GEF) 2           RPHGEF2         U77664         Rho-specific guanine nucleotide exchange factor (GEF) 2           RPP38         U77664         Rho-specific guanine nucleotide exchange factor (GEF) 2           RP RNASE4         U77664         Rho-specific guanine nucleotide exchange factor (GEF) 2           RR RNASE4         U77664         Inbonuclease RNASE Atamily, 4           RR RNASE4         U379331         Inbonuclease RNASE Atamily, 4           AR RNASE4         U379331         Inbonuclease Angiogenin inhibitor           AR RPL10         M64241         Inbosomal protein L10           AR RPL11         X79234         Inbosomal protein L13           AR RPL12         AF037643         Inbosomal protein L13           AR RPL13         X56932         Inbosomal	SORO!	35234 at	RECK	D50406	with kazal motifs	RECK protein precursor
ARHGAP1   Al961929   Rho GTPase activating protein 1   ARHGEF10   AB002292   (GEF) 10   ARHGEF10   AB002292   (GEF) 10   ARHGEF7   D63476   (GEF) 7   Informac guanine nucleotide exchange factor (GEF) 7   Informac guanine nucleotide exchange factor (GEF) 2   Informac guanine nucleotide exchange factor (GEF) 2   Informac guanine nucleotide exchange factor (GEF) 2   Informac guanine nucleotide exchange factor p114   Informac guanine nucleotide exchange factor p1	2000	553 d at	ARHGAP1	U02570	Rho GTPase activating protein 1	מוסיל שנו מיסי מיייש אלייים
ARHGEF10   AB002292   (GEF) 10   Rho guanine nucleotide exchange factor	200	20700	APHGAP1	A1961929	Rho GTPase activating protein 1	
ARHGEF10         AB002292         (GEF) 10           ARHGEF7         D63476         (GEF) 7           ARHGEF2         U72206         tho/rac guanine nucleotide exchange factor (GEF) 2           ARHGEF2         U72206         factor (GEF) 2           Rho-specific guanine nucleotide exchange factor (GEF) 2         Rho-specific guanine nucleotide exchange factor p114           RPP38         U77664         ribonuclease P (38kD)           RNASE4         D37931         ribonuclease A family, 4           RNM         X13973         ribonuclease, RNase A family, 4           RNH         X59543         ribonuclease/angiogenin inhibitor           RPL10         M64241         ribosomal protein L10           RPL11         X79234         ribosomal protein L12           RPL12         AF037643         ribosomal protein L12           RPL13         X64707         ribosomal protein L13           RPL13         X56932         ribosomal protein L13           RPL14         D87735         ribosomal protein L14	1802	39700 at			Rho guanine nucleotide exchange factor	10 rotae enactions object 10
ARHGEF7   D63476   (GEF) 7   rho/rac guanine nucleotide exchange factor (GEF) 7   rho/rac guanine nucleotide exchange factor (GEF) 2   rho/rac guanine nucleotide exchange factor (GEF) 2   Rho-specific guanine nucleotide exchange factor p114   RPP38   U77664   ribonuclease P (38kD)   RNASE4   D37931   ribonuclease/RNase A family, 4   RNASE4   D37931   ribonuclease/angiogenin inhibitor RRM1   X59543   ribonuclease/angiogenin inhibitor   RPL10   RPL10   M64241   ribosomal protein L11   RPL11   X79234   ribosomal protein L11   RPL12   AF037643   ribosomal protein L13   RPL13   X64707   ribosomal protein L13   RPL13   RPL13   ribosomal protein L13   RPL13   RPL13   ribosomal protein L13   RPL13   RPL13   ribosomal protein L13   RPL13   RPL13   ribosomal protein L13   RPL13   RPL13   ribosomal protein L13   RPL13	1000	04400	ABHGEF10	AB002292	(GEF) 10	Rho guanine nucleotide excitatige factor to
ARHGEF7         D63476         (GEF) 7         rho/rac guanine nucleotide exchange factor (GEF) 2         rho/rac guanine nucleotide exchange factor (GEF) 2         restor (GEF) 2         factor (GEF) 2         factor (GEF) 2         factor (GEF) 2         factor p114         fac	2032	34 100 at	מון מון		Rho guanine nucleotide exchange factor	ated refer open change and a second
ARHGEF2	000	10000	ARHGEF7	D63476	(GEF) 7	PAK-Interacting excitating factor both
ARHGEF2         U72206         factor (GEF) 2           P114-RHO-GEF         AB011093         factor p114           RPP38         U77664         ribonuclease P (38kD)           RNASE4         D37931         ribonuclease, RNase A family, 4           RNH         X13973         ribonuclease/angiogenin inhibitor           RNH         X59543         ribonucleotide reductase M1 polypeptide           RRM1         X59543         ribosomal protein L10           RPL10         M64241         ribosomal protein L12           RPL11         X79234         ribosomal protein L12           RPL12         AF037643         ribosomal protein L13           RPL13         X64707         ribosomal protein L13           RPL13         X56932         ribosomal protein L13           RPL13         X56932         ribosomal protein L13           RPL14         D87735         ribosomal protein L13	283	40020 at			rho/rac guanine nucleotide exchange	
Rho-specific guanine nucleotide exchange	7000	40100 24	ARHGEF2	U72206	factor (GEF) 2	guanine nucleotide regulatory factor
P114-RHO-GEF         AB011093         factor p114           RPP38         U77664         ribonuclease P (38kD)           RNASE4         D37931         ribonuclease, RNase A family, 4           RNA         X13973         ribonuclease, angiogenin inhibitor           RNH         X59543         ribonucleotide reductase M1 polypeptide           RPL10         M64241         ribosomal protein L10           RPL11         X79234         ribosomal protein L11           RPL12         AF037643         ribosomal protein L13           RPL13         X64707         ribosomal protein L13           RPL13A         X56932         ribosomal protein L13           RPL14         D87735         ribosomal protein L14	78	40100 at			Rho-specific guanine nucleotide exchange	
RPP38         U77664         ribonuclease P (38kD)           RNASE4         D37931         ribonuclease, RNase A family, 4           RNH         X13973         ribonuclease/angiogenin inhibitor           RNH         X59543         ribonucleotide reductase M1 polypeptide           RPL10         M64241         ribosomal protein L10           RPL11         X79234         ribosomal protein L11           RPL12         AF037643         ribosomal protein L12           RPL13         X64707         ribosomal protein L13           RPL13A         X56932         ribosomal protein L13a           RPL14         D87735         ribosomal protein L14	2000	200007 04	D114.RHO.GEF	AB011093	factor p114	$\rightarrow$
RNASE4         D37931         ribonuclease, RNase A family, 4           RNH         X13973         ribonuclease/angiogenin inhibitor           RNH         X59543         ribonucleotide reductase M1 polypeptide           RPL10         M64241         ribosomal protein L10           RPL11         X79234         ribosomal protein L12           RPL12         AF037643         ribosomal protein L12           RPL13         X64707         ribosomal protein L13           RPL13A         X56932         ribosomal protein L13a           RPL13A         RPL14         D87735         ribosomal protein L14	CSO O	30337 at	пррзя	U77664	ribonuclease P (38kD)	HNaseP protein P36
RNH         X13973         ribonuclease/angiogenin inhibitor           RRM1         X59543         ribonucleotide reductase M1 polypeptide           RPL10         M64241         ribosomal protein L10           RPL11         X79234         ribosomal protein L11           RPL12         AF037643         ribosomal protein L12           RPL13         X64707         ribosomal protein L13           RPL13A         X56932         ribosomal protein L13a           RPL13A         RPL14         D87735           RPL14         D87735         ribosomal protein L14	0802	41040 at	BNASEA	D37931	ribonuclease, RNase A family, 4	RNase 4
RRM1   X59543   ribonucleotide reductase M1 polypeptide	202	32004_al	TACK!	X13973	ribonuclease/angiogenin inhibitor	ribonuclease/anglogenin immbilor
RRM1         X59543         ribonitoreolide octorida           RPL10         M64241         ribosomal protein L10           RPL11         X79234         ribosomal protein L11           RPL12         AF037643         ribosomal protein L13           RPL13         X64707         ribosomal protein L13a           RPL13A         X56932         ribosomal protein L14           RPL14         D87735         ribosomal protein L14	2098	3618/_at	LINIU		and profite reductase M1 polypeptide	M1 subunit of ribonucleotide reductase
RPL10   M64241   ribosomial protein L10   X79234   ribosomal protein L11   RPL12   AF037643   ribosomal protein L12   RPL13   X64707   ribosomal protein L13   RPL13A   X56932   ribosomal protein L14   RPL14   D87735   ribosomal protein L14   RPPL14   RPPPL14   RPPPL14   RPPPL14   RPPPL14   RPPPL14   RPPPL14	2099	34314_at	RRM1	X59543	Thousand broken 10	Wilm's tumor-related protein
RPL11   X79234   ribosomal protein L1     RPL12   AF037643   ribosomal protein L12     RPL13   X64707   ribosomal protein L13     RPL13A   X56932   ribosomal protein L14     RPL14   D87735   ribosomal protein L14	2100	2016 s_at	RPL10	M64241	ribosomal protein L.10	ribosomal protein L11
RPL12   AF037643   ribosomal protein L12   RPL13   X64707   ribosomal protein L13   RPL134   X56932   ribosomal protein L14   RPL14   D87735   ribosomal protein L14	2101	41178 at	RPL11	X79234	ribosomai proteili Li i	
RPL13	2102	33668 at	RPL12	AF037643	ribosomal protein L12	ribosomal protein L13
RPL13A   X56932   ribosomal protein L13a   RPL14   D87735   ribosomal protein L14	2103	131509_at	RPL13	X64707	ribosomai protein L.13	23 kD highly basic protein
RPL14 D87735 Indosonial processing	210	135119_at	RPL13A	X56932	ribosomal protein Liba	ribosomal protein L14
	210	31907 at	RPL14	D87735	ribosomai proteili L 14	

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2106 32432_f_at	It RPL15	L25899	ribosomal protein L15	ribosomal protein L10
2107 32440 at	RPL17	X53777	ribosomal protein L17	ribosomal protein L17
2108 31546 at	RPL18	L11566	ribosomal protein L18	ribosomal protein L18
2109 33614_at	RPL18A	X80822	ribosomal protein L18a	ribosomal protein L18a
2110 32435 at	RPL19	X63527	ribosomal protein L19	ribosomal protein L19
2111 32337_at	RPL21	U25789	ribosomal protein L21	ribosomal protein L21
33451_s	at RPL22	AI526079	ribosomal protein L22	
2113 32395 r a	at RPL23	X55954	ribosomal protein L23	HL23 ribosomal protein
2114 32394 s at	at RPL23	X55954	ribosomal protein L23	HL23 ribosomal protein
	at RPL23A	U37230	ribosomal protein L23a	ribosomal protein L23a
33677 a		M94314	ribosomal protein L24	ribosomal protein L30
	RPL26	X69392	ribosomal protein L26	ribosomal protein L26
2118 39830 at	RPL27	AA044823	ribosomal protein L27	
2119 32436 at	RPL27A	U14968	ribosomal protein L27a	ribosomal protein L27a
2120 31708 at	RPL30	L05095	ribosomal protein L30	ribosomal protein L30
2121 33676_at	RPL31	X15940	ribosomal protein L31	ribosomal protein L31
2122 32276 at	RPL32	X03342	ribosomal protein L32	ribosomal protein L32
2123 33657 at	RPL34	L38941	ribosomal protein L34	ribosomal protein L34
2124 41765_at	RPL35	AI541285	ribosomal protein L35	,
2125 41152 1	at RPL36A	T89651	ribosomal protein L36a	
2126 33656 at	RPL37	D23661	ribosomal protein L37	ribosomal protein L37
2127 31962 at	RPL37A	L06499	ribosomal protein L37a	ribosomal protein L37a
2128 34085 at	RPL38	Z26876	ribosomal protein L38	ribosomal protein
2129 33485 at	RPL4	D23660	ribosomal protein L4	ribosomal protein
				human homologue to yeast ribosomal
2130 32466_at	RPL41	Z12962	ribosomal protein L41	protein YL41
2131 33660_at	RPL5	U14966	ribosomal protein L5	ribosomal protein L5
2132 31952_at	RPL6	X69391	ribosomal protein L6	ribosomal protein L6
2133 36333 at	RPL7	X57958	ribosomal protein L7	ribosomal protein L7
2134 31505 at	RPL8	Z28407	ribosomal protein L8	ribosomal protein L8
2135 31568_at		U14972	ribosomal protein S10	ribosomal protein S10
2136 32330_at		X06617	ribosomal protein S11	ribosomal protein S11
2137 33116_f_al	at	AA977163	ribosomal protein S12	
2138 33619_at	RPS13	L01124	ribosomal protein S13	ribosomal protein S13
2139 34317_g	at RPS15A	W52024	ribosomal protein S15a	ribosomal protein S15a
2140 38061_at	RPS16	Al541256	ribosomal protein S16	

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21413	2141 34593 g at	RPS17	M13932		ribosomal protein S17
21423	2142 34592 at	RPS17	M13932	ribosomal protein S17	ribosomal protein S17
21433	2143 31330 at	RPS19	M81757		S19 ribosomal protein
2144 3	2144 31527 at	RPS2	X17206		ribosomal protein S2
21453	32438_at	RPS20	L06498	ribosomal protein S20	ribosomal protein S20
21463	347 s at	RPS23	D14530	ribosomal protein S23	ribosomal protein
2147	2147 32315 at	RPS24	M31520	ribosomal protein S24	ribosomal protein S24
2148	2148 31573 at	RPS25	M64716	ribosomal protein S25	ribosomal protein
				ribosomal protein S27 (metallopanstimulin	
2149	2149 32748_at	RPS27	AI557852	1)	
2150	2150 34570_at	RPS27A	S79522	ribosomal protein S27a	ubiquitin carboxyl extension protein
2151	39798_at	RPS28	R87876	ribosomal protein S28	
2152	34645_at	RPS3	X55715	ribosomal protein S3	ribosomal protein S3
2153 1	1653 at	RPS3A	M84711	ribosomal protein S3A	v-fos transformation effector protein
2154	34643 at	RPS4X	M58458	ribosomal protein S4, X-linked	ribosomal protein S4X isoform
2155 32437	32437 at	RPS5	U14970	ribosomal protein S5	ribosomal protein S5
2156 31511	31511 at	RPS9	U14971	ribosomal protein S9	ribosomal protein S9
2157	31538	RPLP0	M17885	ribosomal protein, large, P0	ribosomal protein P0
2158	31956 f at	RPLP1	M17886	ribosomal protein, large, P1	ribosomal protein P1
2159	31957 1	RPLP1	M17886	ribosomal protein, large, P1	ribosomal protein P1
				ribosome binding protein 1 homolog	
2160	33213 g at	RRBP1	AF006751	180kD (dog)	ES/130
				Ric-like, expressed in many tissues	.:
2161	38331_at	RIT	Y07566	(Drosophila)	Ric-like, expressed in many tissues
2162	2162 35656_at	RNF6	AJ010346	ring finger protein (C3H2C3 type) 6	RING-H2
2163	2163 39150_at	RNF11	U69559	ring finger protein 11 ·	
2164	2164 35811_at	RNF13	AF037204	ring finger protein 13	RING zinc finger protein
2165	2165 33343_at	RNF14	AB022663	ring finger protein 14	ring finger protein 14
2166	2166 33484 at	RNF2	Y10571	ring finger protein 2	ring finger protein 2
2167	37964 at	RNF3	W25793	ring finger protein 3	
2168	2168 35777 at	RNF4	AB000468	ring finger protein 4	zinc finger protein
				ring zinc-finger protein; escapes X	
				chromosome inactivation; Human ring zinc	~
				finger protein (ZNF127-Xp) gene and 5'	
2169	2169 37650_at	ZNF127-Xp	U41315	flanking sequence.	ZNF127-Xp
2170	2170 37732_at	RYBP	AL049940	RING1 and YY1 binding protein	

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	∢	В	င		Ш
21713	38073_at	RNMT	1	sferase	RNA (guanine-7-) methyltransferase
21724	2172 41460 at	RBM14	AF080561	RNA binding motif protein 14	SYT interacting protein SIP
21734	2173 41741 at		U28686		RNPL
21743	2174 35351_at	RBM4	U89505		Hlark
21753	2175 32804 at	RBMS	AF091263		RNA binding motif protein 5
21764	2176 40870 g at		AF069517		RNA binding protein DEF-3
21774	2177 40260 g at		AL009266		hypothetical protein
2178	2178 39731 at	RBMX	Z23064	RNA binding motif protein, X chromosome hnRNP G protein	hnRNP G protein
	į.			RNA binding motif, single stranded	RNA binding motif, single stranded
2179	2179 33867_s_at	RBMS1	X77494		interacting protein 1, isotorm a
				RNA binding protein S1, serine-rich	
2180	2180 36186_at	RNPS1	L37368		RNA-binding protein
				RNA guanylyltransferase and 5'-	
2181	2181 35202_at	RNGTT	AF025654	phosphatase	mRNA capping enzyme
2182	2182 33237_at	KIAA0801	AB018344	RNA helicase	KIAA0801 protein
2183	2183 36045_at	RNAH	AJ223948	RNA helicase family	RNA helicase
2184	2184 38762 at	RNAHP	AF083255	RNA helicase-related protein	RNA helicase-related protein
				RNA-binding protein gene with multiple	
2185	2185 38049 g_at	RBPMS	D84110	splicing	RBP-MS/type 4
				RNA-binding protein gene with multiple	
2186	2186 38047_at	RBPMS	D84109	splicing	RBP-MS/type 3
2187	2187 38974_at	DJ-1	AF021819	RNA-binding protein regulatory subunit	RNA-binding protein regulatory subunit
				RNA-binding region (RNP1, RRM)	
2188	2188 39725_at	RNPC2	L10910	containing 2	splicing factor
2189	2189 38011_at	RMP	AB006572	RPB5-mediating protein	RPB5 meidating protein
2190	2190 35195_at	RTCD1	Y11651	RTC domain containing 1	phosphate cyclase
				runt-related transcription factor 1 (acute	
2191	2191 943 at	RUNX1	D43968	myeloid leukemia 1; aml1 oncogene)	AML1b protein
					erythrocyte cytosolic protein of 54 kDa, ECP-
2192	2192 40124_at	RUVBL1	Y18418	RuvB-like 1 (E. coli)	54
2193	2193 35758 at	RUVBL2	AB024301	RuvB-like 2 (E. coli)	RuvB-like DNA helicase TIP49b
				S100 calcium binding protein A10	
				(annexin Il ligand, calpactin I, light	
2194	2194 39338_at	S100A10	AI201310	polypeptide (p11))	



			Ĭ		
	A	n	ر	٠.١	
				ntaining inositol	
2195	2195 36089 at	SAC2	AB023183	phosphatase 2	KIAA0966 protein
				ntaining inositol	
2196	2196 41101_at	SAC3	D87464	-+	KIAA0274 gene product
				SAC1 suppressor of actin mutations 1-like	
2197	2197 36511_at	SACM1L	AB020658	(yeast)	KIAA0851 protein
2198	2198 34792 at	AHCYL1	AL049954	S-adenosylhomocysteine hydrolase-like 1	hypothetical protein
2199	2199 41302_at	AHCYL1	R59606	S-adenosylhomocysteine nydrolase-like i	
2200	2200 36685_at	AMD1	W63793	S-adenosylmethionine decarboxylase 1	
2201	22011263 a at	AMD1	M21154	S-adenosylmethionine decarboxylase 1	S-adenosylmethionine decarboxylase 1 precursor
2202	2202 41449 at	SGCE	AJ000534	sarcoglycan, epsilon	epsilon-sarcoglycan
2203	2203 36083 at	SAS	U01160	sarcoma amplified sequence	SAS
2204	2204 36536 at	SCHIP1	AF070614	otein 1	schwannomin interacting protein 1
2205	2205 33423 g at	SEC13L1	AF052155	SEC13-like 1 (S. cerevisiae)	SEC13 (S. cerevisiae)-like 1
2206	2206 33422_at	SEC13L1	AF052155	SEC13-like 1 (S. cerevisiae)	SEC13 (S. cerevisiae)-like 1
2207	2207 36207_at	SEC14L1	D67029	SEC14-like 1 (S. cerevisiae)	SEC14 (S. cerevisiae)-like 1
2208	2208 39099 at	SEC23A	X97064	Sec23 homolog A (S. cerevisiae)	Sec23 protein
				SEC24 related gene family, member A (S.	
2209	2209 34199 at	SEC24A	AJ131244	cerevisiae)	Sec24A protein
				SEC24 related gene family, member B (S.	
2210	2210 35845 at	SEC24B	AJ131245	cerevisiae)	Sec24B protein
				SEC24 related gene family, member D (S.	
2211	2211 32770 at	SEC24D	AB018298	cerevisiae)	KIAA0755 protein
2212	2212 34349 at	SECESL	AJ011779	SEC63 protein	SEC63 protein
2213	2213 32521 at	SFRP1	AF056087	secreted frizzled-related protein 1	secreted frizzled related protein
				secreted phosphoprotein 1 (osteopontin,	
				bone sialoprotein I, early T-lymphocyte	;
2214	2214 34342 s at	SPP1	AF052124	activation 1)	osteopontin
L				secreted protein, acidic, cysteine-rich	secreted protein, acidic, cysteine-rich
221	2215 671_at	SPARC	J03040	(osteonectin)	
3	2216 34265 at	SGNE1	Y00757	secretory granule, neuroendocrine protein 1 (7B2 protein)	secretory granule, neuroendocrine protein i (7B2 protein)
3 6	2210 34203_dt	SEI ENBP1	1129091	Selenium binding protein 1	selenium-binding protein
3	/ 3/403_at	י וכוניייים	253231		

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2218	39078_at	SPS2	U43286	selenophosphate synthetase 2	selenophosphate synthetase 2
2219;		SEPP1	211793	selenoprotein P, plasma, 1	selenoprotein P
				sema domain, immunoglobulin domain	
				(lg), short basic domain, secreted,	
2220 377	377_g_at	SEMA3C	AB000220	(semaphorin) 3C	semaphorin E
				sema domain, immunoglobulin domain	
				(lg), short basic domain, secreted,	
2221	2221 376 at	SEMA3C	AB000220	(semaphorin) 3C	semaphorin E
				sema domain, immunoglobulin domain	
				(lg), short basic domain, secreted,	
2222	2222 35666_at	SEMA3F	U38276	(semaphorin) 3F	semaphorin III family homolog
2223	2223 38826_at	2-Sep	2-Sep D50918	septin 6	septin 2
		1			phosphotyrosine independent ligand for the
2224	2224 40898_at	SQSTM1	U46751	sequestosome 1	Lck SH2 domain p62
				serine (or cysteine) proteinase inhibitor,	
2225	2225 34789_at	SERPINB6	S69272	clade B (ovalbumin), member 6	cytoplasmic antiproteinase
				serine (or cysteine) proteinase inhibitor,	serine (or cysteine) proteinase inhibitor,
				clade E (nexin, plasminogen activator	clade E (nexin, plasminogen activator
2226	2226 38125_at	SERPINE1	M14083	inhibitor type 1), member 1	inhibitor type 1), member 1
				serine (or cysteine) proteinase inhibitor,	,
	-	: : : : : : : : : : : : : : : : : : : :		ciade n (lieat shock protein 47), member	
2227	2227 39167_r_at	SERPINH2	D83174	2	collagen binding protein 2
				serine palmitoyltransferase, long chain	-
2228	2228 38818_at	SPTLC1	Y08685	base subunit 1	serine palmitoyitransterase, subunit I
				serine threonine kinase 39 (STE20/SPS1	
2229	2229 40966_at	STK39	AF099989	homolog, yeast)	Ste-20 related kinase SPAK
2230	2230 41737 at	SRRM1	AF048977	serine/arginine repetitive matrix 1	Ser/Arg-related nuclear matrix protein
2231	2231 36019_at	STK19	L26260	serine/threonine kinase 19	RP protein
				serine/threonine kinase 24 (STE20	
2232	2232 40473_at	STK24	AF024636	homolog, yeast)	STE20-like kinase 3
				serine/threonine kinase 3 (STE20	
2233	2233 32142_at	STK3	U26424 .	homolog, yeast)	MST2
2234	2234 32784 at	PBP4	AB011108	serine/threonine-protein kinase PRP4 homolog	KIAA0536 protein
2	W=10130				



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1			serum response factor (c-fos serum serum response element-binding transcription	serum response factor (c-los serum response element-binding transcription
	na c	303161		factor)
T			response factor (c-fos serum	serum response factor (c-tos serum
			se element-binding transcription	response element-binding transcription factor)
		103161		serum-inducible kinase
	SNK	AF059617		cond tDNA evinthetase
	SARS	X91257	1	Serying Symmotory (myeloid leukemia-
	SET	M93651	SET translocation (myelold leukerilla- associated)	associated)
	SIAH1	U76247	seven in absentia homolog 1 (Drosophila) hSIAH1	hSIAH1
	SIAH2	U76248	iila)	hSIAH2
	NIFIE14	Y18007	seven transmembrane domain protein	seven transmembrane domain protein
			seventh largest subunit; Human RNA polymerase II seventh subunit (rpb-7)	RNA polymerase II seventh subunit
	rpb-7	U52427	gene, complete cus.	SCMI 2 protein
	SCML2	Y18004	Sex comp on management (Colored men)	
	SH3BGR	AI337192	protein	وكانا طونه المري واستوقيات مينايات
			SH3 domain binding glutamic acid-rich	SH3 domain binding giutariiic acto-rich-iike protein
	SH3BGRL	AF042081	protein like	
	SH3BP5	AB005047	SH3-domain binding protein 5 (511)-associated)	SH3 binding protein
	SH3GI B1	AB007960	SH3-domain GRB2-like endophilin B1	SH3-containing protein SH3GLD I
			SHC (Src homology 2 domain containing)	
	SHC1	U73377	transforming protein 1	peesnc
			sialytransferase 9 (CMP-	
			NeuAc:lactosylceramide alpha-2,3-	GM3 synthase
	SIAT9	AB018356	Signylliansierase, amo grimmer)	
	SPC18	Al357653	signal pepildase compiex (1982)	
	SBP14	A1525652	signal recognition particle 14kD (homologous Alu RNA binding protein)	
	SBD10	X12791	signal recognition particle 19kD	signal recognition particle 19kU
	2000	1154000	signal recognition particle 54kD	signal recognition particle
	SRP54	1031350	פולונים וכככתי ביינים ב	

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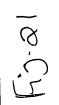
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	∢	8	ပ		ı
2255	2255 33837_at	SRP72	AF069765	signal recognition particle 72kD	signal recognition particle 72
2256	2256 36981 at	SRP9	AF070649		
				ptor	signal recognition particle receptor ('docking
2257	2257 36679_at	SRPR	X06272		protein')
				d activator of	
2258	2258 AFFX-HUMISGF STAT1	STAT1	M97935		transcription factor ISGF-3
				d activator of	
2259	2259 32860 q at	STAT1	M97935		transcription factor ISGF-3
				signal transducer and activator of	
2260	2260 32859_at	STAT1	M97935	transcription 1, 91kD	transcription factor ISGF-3
				signal transducer and activator of	
2261	2261 33338_at	STAT1	M97936	transcription 1, 91kD	
				signal transducer and activator of	
				transcription 3 (acute-phase response	
2262	2262 39708 at	STAT3	L29277	factor)	DNA-binding protein
				signal transducing adaptor molecule (SH3	
2263	2263 160_at	STAM	U43899	domain and ITAM motif) 1	STAM
				similar to Drosophila ash2 gene; Homo	
				sapiens ASH2L gene, complete cds,	
2264	2264 35804_at	ASH2L	AB022785	similar to Drosophila ash2 gene.	
2265	2265 41552 g at	RER1	AW044624	similar to S. cerevisiae RER1	
2266		RER1	AW044624	similar to S. cerevisiae RER1	
2267		DIM1	AF023612	similar to S. pombe dim1+	Dim1p homolog
				similar to SW:GOLI_DROME Q06003	
2268	2268 35083_at	G1L	AL031670	GOLIATH PROTEIN	ring finger protein 24
2269	2269 37178_at	na	M74089	similar to TB1	
				similar to Wiskott-Aldrich syndrome	
2270	2270 40787_at	WIRE	U90911	protein interacting protein	
2271	2271 34705_at	BET3	AJ224335	similar to yeast BET3 (S. cerevisiae)	hBET3 protein
2272	2272 39131 at	UPF3A	N36842	similar to yeast Upf3, variant A	
2273	2273 41277_at	SAP18	AW021542	sin3-associated polypeptide, 18kD	
2274	2274 33859_at	SAP18	U96915	sin3-associated polypeptide, 18kD	sin3 associated polypeptide p18
2275	2275 40992_s_at	SAP30	AF055993	sin3-associated polypeptide, 30kD	mSin3A associated polypeptide p30
				sine oculis homeobox homolog 1	sine oculis homeobox (Drosophila) homolog
2276	2276 40004_at	SIX1	X91868	(Urosopnila)	

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				fascin homolog, sea urchin)	
2277	2277 39070_at	SNL	U03057		actin bundling protein
2278	at	SSBP1	AA768912		
2279	at	SSBP2	AL080076	2	hypothetical protein
2280	2280 35294_at	SSA2	M25077	و چ	60kD Ho/SSA autoantigen
2281	2281 35295_g_at	SSA2	M25077	ribonucleoprotein autoantigen SS-A/Ro)	60kD Ro/SSA autoantigen
				Sjogren syndrome antigen B (autoantigen Sjogren syndrome antigen B (autoantigen	Sjogren syndrome antigen B (autoantigen
2282	2282 38450_at	SSB	X69804	La)	La)
2283	2283 37715 at	SNW1	AF045184	SKI-interacting protein	nuclear receptor coactivator NCoA-62
2284	2284 37389 at	IMAGE145052	Al346580	small acidic protein	
				small nuclear ribonucleoprotein 70kD	
2285	2285 40875_s_at	SNRP70	X06815	polypeptide (RNP antigen)	hU1-70K-like protein (216 AA)
				small nuclear ribonucleoprotein	
2286	2286 38679_g_at	SNRPE	AA733050	polypeptide E	
				small nuclear ribonucleoprotein	
2287	2287 37337_at	SNRPG	A1803447	polypeptide G	
			-	small nuclear ribonucleoprotein	
2288	2288 34842_at	SNRPN	U41303	polypeptide N	small nuclear ribonuleoprotein particle N
				small nuclear RNA activating complex,	į
2289	2289 35247 at	SNAPC5	AI557062	polypeptide 5, 19kD	
				SMART/HDAC1 associated repressor	
2290	2290 32172_at	SHARP	AL096858	protein	hypothetical protein
				SMC1 structural maintenance of	
2291	32849_at	SMC1L1	D80000	chromosomes 1-like 1 (yeast)	
				SMT3 suppressor of mif two 3 homolog 1	
2292	38738_at	SMT3H1	X99584	(yeast)	SMT3A protein
				SMT3 suppressor of mif two 3 homolog 2	
2293	2293 41185 f.at	SMT3H2	AI971724	(yeast)	
2294	2294 38288_at	SNAI2	U69196	snail homolog 2 (Drosophila)	
				soc-2 suppressor of clear homolog (C.	
2295	2295 38659_at	SHOC2	AB020669	elegans)	KIAA0862 protein
2296	2296 40928 at	WSB1	W26496	SOCS box-containing WD protein SWiP-1	
3	140350-at	1001	00:07:1		

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1 20	1000000	SI C143	D26443	solute carrier larmy 1 (gilar right armin) glutamate transporter), member 3	glutamate transporter
2/67	0003_at			belong to the proposed to the proposed	
298	2298 35320 at	SLC11A2	AB004857	solute carrer family 11 (process) member 2 NRAMP2 divalent metal ion transporters), member 2	NRAMP2
				solute carrier family 16 (monocarboxylic	
299 3	2299 33143_s_at	SLC16A3	U81800	acid transporters), member 3	monocarboxylate transporter
		2000	150185	solute carrier family 16 (monocarboxylic acid transporters), member 4	solute carrier family 16 (monocarboxylic acid transporters), member 4
	2300 39260 at	SEC 1984		esoonla per	solute carrier family 2 (facilitated glucose transporter), member 3
2301	2301 36979_at	SLC2A3	M20681	transporter), menucer o	
2	2000 coco	SI C22A5	AF057164	solute carrier family 22 (organic canon transporter), member 5	organic cation transporter OCTN2
2000	25004		10000	solute carrier family 23 (nucleobase	
2303	2303 38122_at	SLC23A1	08/0/2	solute carrier family 25 (mitochondrial	solute carrier family 25 (mitochondrial
				carrier; adenine nucleotide translocator),	carrier; adenine nucleotide translocator),
7000	** 00000	SI C25A4	102966	member 4	member 4
3	2304 32022 at			solute carrier family 25 (mitochondrial	solute carrier family 25 (milocrioridinal
				carrier; adenine nucleotide translocator),	carrier; adenine nucleotide translocator),
2005	220E 27740 r at	SI C25A5	J02683	member 5	member 5
3	31140a			solute carrier family 25 (mitochondrial	
				carrier; adenine nucleotide translocator),	
2306	2306 40436 g at	SLC25A6	J03592	member 6	
	-6-00.01			solute carrier family 25 (mitochondrial	
				carrier; adenine nucleotide translocator),	
2307	2207 40435 at	SLC25A6	J03592	member 6	
3	12-00-04			solute carrier family 25 (mitochondrial	
2308	2308 37675 at	SLC25A3	X60036	carrier; phosphate carrier), member 3	phosphate carrier protein
				solute carrier family 29 (nucleoside	equilibrative nucleoside transporter 1
2309	2309 33901_at	SLC29A1	U813/5	(ransponers), member 1	
5	4006A at	SI Ca1A1	U83460	transporters), member 1	high-affinity copper uptake protein
3	2310 40304_at	GEOOTS!			



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2311	34740 at	SI C31A2	U83461	solute carrier family 31 (copper transporters), member 2	putative copper uptake protein
	74143_all	OCCUPA-		CMP-sialic acid	
2312	2312 37895 at	SLC35A1	D87969		CMP-sialic acid transporter
				solute carrier family 35 (UDP-N-	
	40000	6436713	AB021081	acetylglucosamine (UDF-GictAc)	UDP-N-acetylalucosamine transporter
<u> </u>	2313 30200 at	SECSON	1001300	solute carrier family 4, sodium bicarbonate	
2314	2314 34936 at	SLC4A7	AB012130		sodium bicarbonate cotransporter2
				solute carrier family 6 (neurotransmitter	
2315	2315 34166_at	SLC6A7	S80071	transporter, L-proline), member 7	brain-specific L-proline transporter
				solute carrier family 7 (cationic amino acid solute carrier family 7 (cationic amino acid	solute carrier family 7 (cationic amino acid
2316	2316 32186 at	SLC7A5	M80244	transporter, y+ system), member 5	transporter, y+ system), member 5
	l				from amino acid
1		010	007700	solute carrier family / (callonic allino acid	transporter v+ system), member 6
2317	2317 39533_BI	SLC/A6	D0/432	tidisponer, y+ systemly, member of	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
				solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+,	
2318	2318 32681_at	SLC9A1	S68616	amiloride sensitive)	Na+/H+ exchanger NHE-1 isoform
		·		solute carrier family 9 (sodium/hydrogen	
2319	2319 36542 at	SLC9A6	AF030409	exchanger), isoform 6	sodium-hydrogen exchanger 6
2320	2320 39097_at	SON	X63753	SON DNA binding protein	SON DNA-binding protein
2321	9391 32857 at	SOS2	L13858	son of seventess homotog 2 (Drosophila)	guanine nucleotide exchange factor
2322	2322 41462 at	SNX2	AF065482	sorting nexin 2	sorting nexin 2
2323		SNX3	AF034546	sorting nexin 3	sorting nexin 3
2324	2324 40605 at	SNX4	AA524345	sorting nexin 4	
2325	2325 37808 at	SNX7	AL049989	sorting nexin 7	hypothetical protein
				Source: H.sapiens genes for histones	
2326	33352_at	H2A	X57985	H2B.1 and H2A.	histone H2A
2327	2327 36112_r_at	SC-35	X75755	Source: H.sapiens PR264 gene.	splicing factor, arginine/serine-rich 2
2328	36111_s_at	SC-35	X75755	Source: H.sapiens PR264 gene.	splicing factor, arginine/serine-rich 2
				,	



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	Source: Homo sapie	Source: Homo sapie	Source: Homo sapie	ns chromosome 10	
2329 1173 g at HG172-HT3924 SEQUENCE, 8 unordered pieces.			SEQUENCE, 8 unor	dered pieces.	
	Source: Homo sapie BAC clone CIT987S	Source: Homo sapie BAC clone CIT987S	Source: Homo sapie BAC clone CIT987S	ome 16 plete	
2330 40617_at 44M2.1 AC004381 sequence.	AC004381		sednence.		hypothetical protein FLJ20274
	Source: Homo sapie	Source: Homo sapie	Source: Homo sapie	ins clk2 kinase	
(CLK2), propin1, cote1	(CLK2), propin1, cot	(CLK2), propin1, cot	(CLK2), propin1, cot	e1,	
glucocerebrosidase (GBA), and metaxin	glucocerebrosidase	glucocerebrosidase	glucocerebrosidase	(GBA), and metaxin	÷
genes, complete cds; metaxin	genes, complete cds	genes, complete cds	genes, complete cds	: metaxin	
pseudogene and glucocerebrosidase	pseudogene and glu	pseudogene and glu	pseudogene and glu	cocerebrosidase	
pseudogene; and thrombospondin3	pseudogene; and thi	pseudogene; and thi	pseudogene; and thi		,
2331 33740_at   COTE1   AF023268 (THBS3) gene, partial cds	AF023268		(THBS3) gene, parti	•	chromosome 1 open reading frame 2
		Source: Homo sapie	Source: Homo sapie	ens hJTB gene,	
2332 41834 g at HJTB PAR AB016492 complete cds.	AB016492		complete cds.		jumping translocation breakpoint
		Source: Homo sapi	Source: Homo sapi	ens hJTB gene,	
2333 41833_at HJTB PAR AB016492 complete cds.	AB016492		complete cds.		jumping translocation breakpoint
			Source: Homo sap	iens mRNA for	
2334 32335_r_at UbC2 AB009010 polyubiquitin UbC, complete cds.	AB009010		polyubiquitin UbC,	complete cds.	polyubiquitin UbC
		Source: Homo sap	Source: Homo sap	iens mRNA for	
2335 32334_f_at	AB009010		polyubiquitin UbC,	complete cds.	polyubiquitin UbC
		Source: Human Co	Source: Human Co	CAAT-box-binding	
2336 32194_at   CBF   M37197   factor (CBF) mRNA, complete cds.	M37197		factor (CBF) mRN	A, complete cds.	CCAAT-box-binding transcription factor
		Source: Human Co	Source: Human C(	CAAT-box-binding	
2337 229_at CBF M37197 (CBF) mRNA, complete cds.	M37197		factor (CBF) mRN	A, complete cds.	CCAAT-box-binding transcription factor
	Source: Human Cl	Source: Human Cl	Source: Human Cl	Source: Human Chromosome 16 BAC	
clone CIT987SK-A	clone CIT987SK-A	clone CIT987SK-A	clone CIT987SK-A	clone CIT987SK-A-101F10, complete	
2338/41791 at 101F10.3 AC002550 sequence.	AC002550		sednence.		hypothetical protein
			Source: Human C	Source: Human Chromosome 16 BAC	
clone CIT987SK-A	clone CIT987SK-A	clone CIT987SK-A	clone CIT987SK-A	clone CIT987SK-A-211C6, complete	
2339 41488 at A-211C6.1 AC002394 sequence.	AC002394		sednence.		hypothetical protein A-211C6.1
	Source: Human C	Source: Human C	Source: Human C	Source: Human Chromosome 16 BAC	
			clone CIT987SK-	clone CIT987SK-A-362G6, complete	+ 30030 A minimal principle 4
2340 35742_at A-362G6.1 U95740 sequence.	U95740		sednence.		hypothetical protein A-302.00.1

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T				Source: Human Chromosome 16 BAC	
				clone CIT987SK-A-61E3, complete	
3414	2341 41733_at	61E3.1	AC003007		Unknown gene product (partial)
T				Source: Human DNA sequence from	
				clone RP4-742C19 on chromosome 22,	
342	2342 36894 at		AL031846	complete sequence.	
T				Source: Human mRNA for HLA class I	
343	2343 37383 f at	HLA class I - locus X58536	X58536	locus C heavy chain.	HLA class I heavy chain
				Source: Human N-	
				acetyfglucosaminyltransferase I (GlcNAc-	acetylglucosaminyltransferase I (GlcNAc-  mannosyl (alpha-1,3-)-glycoprotein beta-1,2-
344	2344 39778 at	GLYT1 GLCNAC-	C- M55621	TI) mRNA, complete cds.	N-acetylglucosaminyltransferase
345	2345 41573 at	SP3	X68560	Sp3 transcription factor	
T				spastic ataxia of Charlevoix-Saguenay	
346	2346 32102 at	SACS	AB018273	(sacsin)	KIAA0730 protein
				spastic paraplegia 4 (autosomal dominant;	
347	2347 35171 at	SPG4	AB029006	spastin)	KIAA1083 protein
2348	2348 39423 f at	SPOP	AJ000644	speckle-type POZ protein	SPOP
2349	ט וי	SSH3BP1	AF001628	spectrin SH3 domain binding protein 1	interactor protein AbIBP4
2350	2350 33886 at	SSH3BP1	AF006516	spectrin SH3 domain binding protein 1	e3B1
2351	2351 39556 at	SPTBN1	M96803	spectrin, beta, non-erythrocytic 1	beta-spectrin
	l!				
2352	2352 34304_s_at	SAT	AL050290	spermidine/spermine N1-acetyltransferase	
				sphingomyelin phosphodiesterase 1, acid	
2353	2353 32574 at	SMPD1	X59960	lysosomal (acid sphirtgomyelinase)	sphingomyelin phosphodiesterase
				spinocerebellar ataxia 1	
				(olivopontocerebellar ataxia 1, autosomal	
2354	2354 36142 at	SCA1	X79204	dominant, ataxin 1)	ataxin-1
				spinocerebellar ataxia 2	
				(olivopontocerebellar ataxia 2, autosomal	
2355	2355 36998_s_at	SCA2	Y08262	dominant, ataxin 2)	ataxin 2
				splicing factor 30, survival of motor neuron	
2356	2356 38040_at	SPF30	AF107463	related	splicing factor
2357	2357 36973 at	SF3B2	U41371	splicing factor 3b, subunit 2, 145kD	spliceosome associated protein
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2358	2358 36224 q at	SFPQ	Al827895	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	
2359	2359 40638_at	SFPQ	X70944	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	PTB-associated splicing factor
2360	2360 36098_at	SFRS1	M72709	ctor)	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
2361	2361 140_s_at		U68063	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	transformer-2 beta
2362	32183_at	SFRS11	M74002	splicing factor, arginine/serine-rich 11	arginine-rich nuclear protein
2363	2363 35258_f_at	Ь	AF030234	interacting protein	splicing factor Sip1
2364	2364 40457_at		AF038250		
2365	2365 36991 at	SFRS4 SFRS5	L140/6 U30826	splicing factor, arginine/serine-rich 4	Pre-miniva splicing lactor SRp40-1
2367	2367 40262_at	SRP46	AF031166	16kD	SRp46 splicing factor
2368	2368 35839_at	SOLE	D78130	squalene epoxidase	squalene epoxidase
2369	2369 39047 at	SART3	AB020880	squamous cell carcinoma antigen recognised by T cells 3	squamous cell carcinoma antigen SART-3
2370	2370 41784 at	DKFZp564B0769	_	SR rich protein	hypothetical protein
2371	2371 36091_at	SCAP2	AF051323	src family associated phosphoprotein 2	Src-associated adaptor protein
2372	41354_at	STC1	U25997	stanniocalcin 1	stanniocalcin precursor
2373	32043_at	STC2	AF098462	stanniocalcin 2	stanniocalcin-related protein
2374	2374 41295_at	STARD7	AL041780	START domain containing 7	
2375	2375 38800_at	STMN2	D45352	stathmin-like 2	
2376	2376 41823_at	STAU	AJ132258	staufen, RNA binding protein (Drosophila)	
2377	2377 38669_at	SLK	D86959	Ste20-related serine/threonine kinase	KIAA0204 protein
2378	2378 37147 at	SCGF	AF020044	stem cell growth factor; lymphocyte secreted C-type lectin	lymphocyte secreted C-type lectin precursor
2379	2379 36913_at	SLBP	U75679	stem-loop (histone) binding protein	histone stem-loop binding protein
2380	2380 38034_at	STS	M16505	steroid sulfatase (microsomal), arylsulfatase C, isozyme S	steroid sulfatase (microsomal), arylsulfatase C, isozyme S

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				_	steroid-5-alpha-reductase, alpha polypeptide
				polypeptide 1 (3-oxo-5 alpha-steroid delta	1 (3-oxo-5 alpha-steroid delta 4-
2381	2381 589_at	SRD5A1	M32313	4-dehydrogenase alpha 1)	dehydrogenase alpha 1)
2382	2382 33369 at	SC4MOL	AI535653	sterol-C4-methyl oxidase-like	
				sterol-C5-desaturase (ERG3 delta-5-	
2383	2383 33421_s_at	SCSDL	AB016247	desaturase homolog, fungal)-like	sterol-C5-desaturase
2384	40419 at	EPB72	X85116	stomatin; H.sapiens epb72 gene exon 1.	band 7 integral membrane protein
2385	2385 33322 i at	SFN	X57348	stratifin	stratifin
	!!			stress-associated endoplasmic reticulum	
2386	2386 37035 at	SERP1	A1557272	protein 1; ribosome associated membrane profein 4	
2007	2000	-			stromal cell derived factor receptor 1 isoform
					b; stromal cell derived factor receptor 1
2387	2387 35747_at	SDFR1	AF035287	stromal cell derived factor receptor 1	isoform a
2388	2388 32666 at	SDF1	U19495	stromal cell-derived factor 1	intercrine-alpha
2389	2389 33834 at	SDF1	L36033	stromal cell-derived factor 1	pre-B cell stimulating factor homologue
2390	2390 41627 at	SDF2	D50645	stromal cell-derived factor 2	SDF2
	!			succinate dehydrogenase complex,	succinate dehydrogenase flavoprotein
2391	2391 34826 at	SDHA	L21936	subunit A, flavoprotein (Fp)	subunit
				succinate dehydrogenase complex,	
				subunit C, integral membrane protein,	
2392	2392 34385_at	SDHC	U57877	15kD	integral membrane protein CII-3
				succinate dehydrogenase complex,	:
2393	2393 40467_at	SDHD	AB006202	subunit D, integral membrane protein	cytochrome b small subunit of complex II
				succinate-CoA ligase, ADP-forming, beta	ATP-specific succinyl-CoA synthetase beta
2394	2394 40893_at	SUCLAZ	AF058953	subunit	subunit
2395	2395 35832_at	KIAA1077	AB029000	sulfatase FP	KIAA1077 protein
2396	2396 33712 at	SULT4A1	N63574	sulfotransferase family 4A, member 1	
2397	2397 34814 at	UBA2	AL041443	SUMO-1 activating enzyme subunit 2	
				superkiller viralicidic activity 2-like (S.	
2398	8 37998_at	SKIV2L	U09877	cerevisiae)	helicase-like protein
				superoxide dismutase 1, soluble	superoxide dismutase 1, soluble
2390	2399 36620_at	SOD1	X02317	(amyotrophic lateral sclerosis 1 (adult))	(amyotrophic lateral sclerosis 1 (adult))
2400	2400 40069 at	SVIL	AF051850	supervillin	supervillin
240	2401 36676 at	GHRF GRF	AL031659	supported by FGENESH	growth hormone releasing hormone

Fig. a

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2402	2402 33297_at	CBF-B HAP2 NF-	:-\AL031778	supported by GENEWISE, GENSCAN and FGENES	nuclear transcription factor Y, alpha, isoform
2403	2403 34825_at	TTRAP	AL031775	supported by GENSCAN	TRAF and TNF receptor-associated protein
				suppression of tumorigenicity 13 (colon	6
2404 1640	1640_at	S113	017714	rotein)	putative tumor suppressor 5113
2405	2405 37745_s_at	ST5	U15780	suppression of tumorigenicity 5	p82
2406	2406 37805_at	SRPUL	AF060567		sushi-repeat protein
				sushi-repeat-containing protein, X	
2407	2407 31855_at	SRPX	U61374	chromosome	
2408	2408 31869_at	KIAA0640	AB014540	SWAP-70 protein	KIAA0640 protein
				SWI/SNF related, matrix associated, actin	
				dependent regulator of chromatin,	
2409	2409 40213_at	SMARCA1	M88163	subfamily a, member 1	transcription activator
				SWI/SNF related, matrix associated, actin	
				dependent regulator of chromatin,	
2410	2410 40961_at	SMARCA2	X72889	subfamily a, member 2	HBRM
				SWI/SNF related, matrix associated, actin	
				dependent regulator of chromatin,	
2411	2411 32579_at	SMARCA4	U29175	subfamily a, member 4	transcriptional activator
				SWI/SNF related, matrix associated, actin	
			-	dependent regulator of chromatin,	
2412	2412 39132_at	SMARCA5	AB010882	subfamily a, member 5	hSNF2H
2413	2413 34753_at	SYBL1	X92396	synaptobrevin-like 1	synaptobrevin-like 1
2414	41692_at	SYNJ1	AB020717	synaptojanin 1	KIAA0910 protein
2415	38075_at	SYPL	X68194	synaptophysin-like protein	synaptophysin-like protein
2416	2416 36452_at	KIAA1029	AB028952	synaptopodin	KIAA1029 protein
					synaptosome associated protein of 23
2417	2417 32178_r_at	SNAP23	AJ011915	synaptosomal-associated protein, 23kD	kilodaltons, isoform A
				syndecan 2 (heparan sulfate proteoglycan	
2418	2418 39757 at	SDC2	J04621	1, cell surface-associated, fibroglycan)	
2419	32092_at	SDC3	AB007937	syndecan 3 (N-syndecan)	KIAA0468 protein
2420	2420 38110_at	SDCBP	AF000652	syndecan binding protein (syntenin)	syntenin
2421	2421 38685_at	STX12	AL035306	syntaxin 12	hypothetical protein
2422	38381_at	STX3A	U32315	syntaxin 3A	syntaxin 3



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4233	2423 38774_at	STX7	U77942	syntaxin 7	syntaxın /
4243			AF036715	syntaxin 8	syntaxin 8
4253	2425 33942 s at		AF004563	syntaxin binding protein 1	hUNC18b
4263		STXBP3			unc-18homologue
				ric DNA-binding	
2427 3	2427 33315_at	-	M29204		chimeric DNA-binding factor
				TAF7 RNA polymerase II, TATA box	
				binding protein (TBP)-associated factor,	
2428	2428 192 at	TAF7	U18062		TFIID subunit TAFII55
				TAF9 RNA polymerase II, TATA box	
				binding protein (TBP)-associated factor,	
2429 193 at	193 at	TAF9	U21858		TAFII32 precursor
				TAFII20; contains homology to histone	
				H2B; TFIID subunit; TAFII15; contains	
				homology to histone H2B; TFIID subunit;	
				Human TFIID subunits TAF20 and TAF15	
2430	2430 37620 at	TAF12; TAF2J; TA	TAU57693	mRNA, complete cds.	TAF20; TAF15
2431	32166 at	TLN1	AB028950	talin 1	KIAA1027 protein
2432	2432 39765 at	TLN2	AB002318	talin 2	
2433	2433 41168 at	TAPBP	AF029750	TAP binding protein (tapasin)	tapasin
2434	39779 at	TARBP1	U38847	TAR (HIV) RNA binding protein 1	TAR RNA loop binding protein
2435	32241 at	TARDBP	AL050265	TAR DNA binding protein	hypothetical protein
2436	2436 39416 at	TIP-1	U90913	Tax interaction protein 1	Tax interaction protein 1
				Tax1 (human T-cell leukemia virus type I)	
2437	2437 498_at	TAX1BP1	U33821	binding protein 1	tax1-binding protein TXBP151
				Tax1 (human T-cell leukemia virus type I)	!
2438	2438 35279_at	TAX1BP1	U33821	binding protein 1	tax1-binding protein TXBP151
2439	36702 at	TBX19	AJ010277	T-box 19	TBX19 protein
2440	2440 32196_at	TIP120A	AB020636	TBP-interacting protein	KIAA0829 protein
2441	2441 34791 at	TCP1	X52882	t-complex 1	t-complex 1
				t-complex-associated-testis-expressed 1-	
2442	2442 36921_at	TCTE1L	U02556	like	t-complex-associated-testis-expressed 1-like
				t-complex-associated-testis-expressed 1-	t-complex-associated-testis-expressed 1- it-complex-associated-testis-expressed 1-like
2443	2443 946_at	TCTEL1	D50663	like 1	1

F.5.2

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LLJ		TGFb inducible early protein; early growth response protein alpha		telomeric repeat binding factor 1, isoform 2; telomeric repeat binding factor 1, isoform 1	hypothetical protein	testis enhanced gene transcript (CAA) inhibitor 1)	tetracycline transporter-like protein	nictory toogen deliter	tetratricopeptide repeat protein	IPRU	Zinc Imger transcription factor	TGIF protein					Tooling a rictory anibolity and the	growth factor-binding protein-5 precursor					realization of airpotent and principles	grown factor-billding proteins precursor
	U C C C C C C C C C C C C C C C C C C C	s; EGHa; Homo sapiens Turo cible early protein and early growth onse protein alpha genes, complete	cas.	telomeric repeat binding factor (NIMA- interacting) 1	(SI	testis enhanced gene transcript (BAX inhibitor 1)	tetracycline transporter-like protein	tetraspan 3	tetratricopeptide repeat domain 1	tetratricopeptide repeat domain 3	TGFB inducible early growth response	TGFB-induced factor (TALE family	normeobox)	The AAs encoded by bases 5/26-5/56 and 5917-5926 may be ASN-linked	glycosylation sites; insulin-like precursor;	Homo sapiens growth factor-binding	protein-3 precursor (IGFBP3) gene,	complete cds.	The AAs encoded by bases 5728-5736	and 5917-5926 may be ASN-linked	glycosylation sites; insulin-like precursor;	Homo sapiens growth factor-binding	protein-3 precursor (IGFBP3) gene,	complete cds.
	ပ		LF AF050110	U40705	AL050162	X75861	L11669	M69023	U46570	D83077	S81439		X89750					M35878						M35878
	В		TIEG; EGRA; KLF	TERF1	TES	TOT	TETRAN	TSPAN-3	TTC1	TTC3	TIEG		TGIF					IGFRP3						IGFBP3
	A		2444 38374_at	2445 32255 i at	2446 32134 at		2447 33988_at	2449 38612 at	37321 at	2451 39065 s at	2452 224 at		2453 38805_at					04E4 27310 at						2455 1586_at
	Γ		444	5445	446		448	184	245	245	245,		245					OAE	3					245

Fig. 21

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2456	. at 345 at	ENPP1: M6S1: N	PD12485	The first in-frame ATG codon is located at nucleotides 17-19, followed by a second ATG codon 52 codons downstream. And the second ATG codon is potential initiation point for translation of NPPase.; Human mRNA for nucleotide pyrophatase, complete cds.	NPPase
2457	2457 36992 at			thioredoxin	
2458	2458 34768_at	TXNDC	AL080080	thioredoxin domain-containing	hypothetical protein
2459	2459 31508_at	TXNIP	S73591	thioredoxin interacting protein	brain-expressed HHCPA78 homolog VDUP1
2460	2460 39425_at	TXNRD1	X91247	thioredoxin reductase 1	thioredoxin reductase (NADPH)
2461	2461 32214_at	TXNL	AF003938		thioredoxin-like protein
2462	2462 38473_at		M63180	threonyl-tRNA synthetase	threonyl-tRNA synthetase
2463	2463 659_g_at	THBS2	L12350	thrombospondin 2	thrombospondin 2
2464	2464 658_at	THBS2	L12350	thrombospondin 2	thrombospondin 2
					G/T mismatch-specific thymine DNA
2465	2465 40865_at	TDG	U51166	thymine-DNA glycosylase	glycosylase
2466	2466 31557_at	TMSB4X	M17733	thymosin, beta 4, X chromosome	thymosin, beta 4
				thyroid hormone receptor coactivating	
2467	2467 32654_g_at	SMAP	AW020536	protein	
2468	2468 39699_at	TRIP12	D28476	thyroid hormone receptor interactor 12	thyroid hormone receptor interactor 12
2469	2469 41251 at	TRIP3	L40410	thyroid hormone receptor interactor 3	thyroid receptor interactor
2470	2470 39341_at	TRIP6	AJ001902	thyroid hormone receptor interactor 6	TRIP6
2471	2471 37348_s_at	TRIP7	AA845349	thyroid hormone receptor interactor 7	
2,0	1- 10077	TD & DO 40	A BO11166	thyroid hormone receptor-associated	KIAA0593 protein
2/4/2	24/2 4 1023 at	TRIPIE	AE084260	thyroid receptor interacting protein 15	signalosome subunit 2
2	01020_dl	2		TIA1 cytotoxic granule-associated RNA	TIA1 protein, isoform 1; TIA1 protein,
2474	33852_at	TIA1	M77142	binding protein	isoform 2
				TIA1 cytotoxic granule-associated RNA	
2475	2475 41763_g_at	TIAL1	D64015	binding protein-like 1	T-cluster binding protein
2476	36655_at	TJP2	L27476	tight junction protein 2 (zona occludens 2)	tight junction protein 2 (zona occludens 2) tight junction protein 2 (zona occludens 2)
2477	2477 37801_at	TJ6	AF112972	TJ6 protein	TJ6

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∢	В	0		TOACE
2478 35238 at	TRAF5	AB000509	TNF receptor-associated factor 5	IHAFD
2479 33243 at	GG2-1	AF099935	ein	MDC-3.13 isoform 2
2480 40310 at	TLR2	AF051152		Toll/interleukin-1 receptor-like protein 4
2481 1030 s at	T0P1	U07806	NA) I	DNA topoisomerase I
2482 36571 at	TOP2B	X68060	II beta (180kD)	DNA topoisomerase II
2483 32233 at	TOR18	AF007872		torsinB
2484 32219 at	TLK1	D50927	tousled-like kinase 1	KIAA0137 protein
2485 35321 at	TLK2	AB004884	tousled-like kinase 2	PKU-alpha
			TRAF family member-associated NFKB	
2486 39742 at	TANK	U59863	$\exists$	I-TRAF
2487 40051 at	KIAA0057	D31762		TRAM-like protein
2488 1073 at	TCEA1	M81601		transcription elongation factor SII
			transcription elongation factor A (SII)-like	
2489 38317 at	TCEAL1	M99701		transcription elongation factor A (SII)-IIKe I
in			transcription elongation factor B (SIII),	RNA polymerase II elongation factor SIII,
2490 1399 at	TCEB1	L34587	polypeptide 1 (15kD, elongin C)	p15 subunit
15 - COOL			transcription elongation factor B (SIII),	RNA polymerase II elongation factor-like
2491[41759 at	TCEB1L	247087.	polypeptide 1-like	protein
			transcription elongation regulator 1	
2402 30426 at	TCERG1	AF017789	(CA150)	putative transcription factor CA150
			transcription factor 12 (HTF4, helix-loop-	
2493 33348 at	TCF12	M80627	helix transcription factors 4)	helix-loop-helix protein
			transcription factor 3 (E2A immunoglobulin	
2494 1373 at	TCF3	M31523	enhancer binding factors E12/E47)	
5 0 0			transcription factor 8 (represses	
2405 33440 at	TCF8	U19969	interleukin 2 expression)	ZEB
			transcription factor AP-4 (activating	
2496 39638 at	TFAP4	S73885	enhancer binding protein 4)	AP-4
2497 37757 at	TFDP1	L23959	transcription factor Dp-1	E2F-related transcription factor
2498 32578 at	TCFL4	AW005997	transcription factor-like 4	
			transcription factor-like 5 (basic helix-loop-	
2499 35614 at	TCFL5	AB012124	helix)	
	TANASI	AE069733	franscriptional adaptor 3-like	ADA3-like protein



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	A	B	ပ	O	1
					KIAA1080 protein; Golgi-associated, gamma- adaptin ear containing, ARF-binding protein
2501	2501 35297_at	GGA2 VEAR	AC002400	Transcriptional coactivator P15 like	2
				transcriptional co-activator with PDZ-	
2502	2502 33876_at	TAZ	AL050107	binding motif (TAZ)	nypotnetical protein
				transcriptional co-repressor; Human	
				silencing mediator of retinoid and thyroid	
				ө	silencing mediator of retinoid and thyroid
2503	2503 39358_at	SMRT	U37146	cds.	hormone action
				transcriptional regulator interacting with	
2504	2504 37312_at	TRIP-Br2	D50917	the PHS-bromodomain 2	KIAA0127 gene product
2505	2505 40631 at	T081	D38305	transducer of ERBB2, 1	Tob
2506	2506 32554 s at	TBL1	Y12781	transducin (beta)-like 1	transducin (beta) like 1 protein
2507	2507 37324_at	TFRC	X01060	transferrin receptor (p90, CD71)	transferrin receptor (p90, CD71)
2508	2508 39344_at	HSU53209	U53209	transformer-2 alpha (htra-2 alpha)	transformer-2 alpha
				transforming growth factor beta-stimulated	
2509	2509 39032_at	TSC22	AJ222700	protein TSC-22	TSC-22
				transforming growth factor, beta 1	transforming growth factor, beta 1 (Camurati-
2510	2510 41445_at	TGFB1	X02812	(Camurati-Engelmann disease)	Engelmann disease)
				transforming growth factor, beta receptor	-
2511	2511 1815_g_at	TGFBR2	D50683	II (70-80kD)	TGF-betallR alpha
				transforming growth factor, beta receptor	
2512	2512 1814_at	TGFBR2	D50683	II (70-80kD)	TGF-betallR alpha
	•			transforming growth factor, beta-induced,	
2513	2513 1385_at	TGFBI	M77349	68kD	transforming growth factor induced protein
				transforming, acidic coiled-coil containing	
2514	2514 40841_at	TACC1	AF049910	protein 1	TACC1
				transforming, acidic coiled-coil containing	
2515	2515 38816 at	TACC2	AF095791	protein 2	TACC2 protein
2516	2516 36931 at	TAGLN	M95787	transgelin	smooth muscle protein
2517	2517 36678 at	TAGLN2	D21261	transgelin 2	transgelin 2
2518	2518 31829 r at	TGOLN2	AF027515	trans-golgi network protein 2	hTGN48
				transient receptor potential cation channel	
2519	2519 39124_r_at	TRPC1	X89066	subfamily C, member 1	TRPC1 protein
25.20	2520 30123 c at	TBBC1	Хяалее	transient receptor potential cation channel	TRPC1 protein
2262	39 123_s_at	5	20000	Sablaning O, monibol	

13.2

$\vdash$	A	В	ပ	Q	ш
				RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP): Human homolog of splodingsitTERA_MOUSE TRANSITIONAL ENDOLASMIC ATRANSITIONAL ENDOLASMIC RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP) pirliS25197 transitional endoplasmic reticulum ATPase - mouse gil55217 (214044) murine valosin- containing protein; 99% identical to report protein; 90% identical to report protein; 90% identical to report protein; Most similar to hypothetical protein; Most similar to hypothetical protein; Most similar to hypothetical protein; Most similar to hypothetical protein (AL021766) (Schizosaccharomyces pombe) producing hypothetical protein (AL021766) (Schizosaccharomyces cerevisiae) (Saccharomyces cerevisiae) ginlPIDIe245463 (Z73136) ORF YLL031C (SZA12.9 (Gaenorhabditis elegans); Hypothetical 38.8 kDa putative membrane protein; Most similar to hypothetical more in hypothetical sa.8 kDa putative membrane protein; Most similar to hypothetical protein; PIDIe276130 (Z81072) F30A10.5 TERA_HUMAN; XRCC9; P1.11659_3;	TERA_HUMAN; XRCC9; P1.11659_3;
521	2521 34380_at	XRCC9	AC004472	72655IYB28	P1.11659_4; P1.11659_5
522	2522 33351_at	GC20	AF064607	g	GC20 protein
223	2523 40537_at	IF2	AB018284	translation initiation factor IF2	KIAAU/41 protein
524	2524 32173_at	UK114	X95384	translational inhibitor protein p14.5	14.5 kDa translational inhibitor protein, p14.5

13.2

	A	В	ပ	O	ָר בּייני בייני
2525	2525 41051_at	TSNAX	X95073	translin-associated factor X	I ranslin associated protein X
				translocase of inner mitochondrial	
2526	2526 32831_at	TIMM17A	AA453183	membrane 17 homolog A (yeast)	
25.97	36108 21	TOMM20-PENDIN	IND13641	translocase of outer mitochondrial membrane 20 (veast) homolog	mitochondrial outer membrane protein 19
£3,5,1	m_00100			translocase of outer mitochondrial	
2528	2528 37050 r at	TOMM34	A1130910	membrane 34	
				translocase of outer mitochondrial	
2529	2529 32853_at	TOMM70A	AB018262	membrane 70 homolog A (yeast)	KIAA0719 protein
				translocating chain-associating membrane	
2530	2530 34796 at	TRAM	X63679	protein	TRAM protein
2531	2531 38100 at	TLOC1	D87127	translocation protein 1	translocation protein-1
2532	2532 950_at	TLOC1	D87127	translocation protein 1	translocation protein-1
2533	2533 41531 at	TM4SF1	A1445461	transmembrane 4 superfamily member 1	
2534	2534 39362 r at	TM4SF6	AF043906	transmembrane 4 superfamily member 6	T245 protein
				transmembrane 7 superfamily member 1	•
2535	2535 32083_at	TM7SF1	AF027826	(upregulated in kidney)	putative seven pass transmembrane protein
2536	2536 38835_at	TM9SF1	U94831	transmembrane 9 superfamily member 1	multispanning membrane protein
0	7070	TAMOSES	1 IB400E	transmembrane 9 sunerfamily member 2	920
1007	2337 34307 at	TMEMA	AB015631	transmembrane protein 4	type II membrane protein
2539	2539 37 445 at	TMEM5	AB015633	transmembrane protein 5	type II membrane protein
2540	2540 36128_at	TMP21	L40397	transmembrane trafficking protein	
2541	2541 38982 at	RAP1	W28865	TRF2-interacting telomeric RAP1 protein	
2542	2542 39382 at	TRIM2	AB011089	tripartite motif-containing 2	KIAA0517 protein
2543	2543 36825 at	TRIM22	X82200	tripartite motif-containing 22	gpStaf50
2544	2544 38537 at	TRIM32	U18543	tripartite motif-containing 32	zinc-finger protein
254E	2545 32635 at	TRIM33	AB029036	fripartite motif-containing 33	KIAA1113 protein
2546	2546 33107_at	TRIM37	AB020705	tripartite motif-containing 37	KIAA0898 protein
254,	2547 40461_at	TIX1	AB007855		
2548	2548 36791_g_at	TPM1	M19267		tropomyosin 1 (alpha)
2548	2549 36790_at	TPM1	M19267	tropomyosin 1 (alpha)	rropomyosin i (alpha)

Ris-al

TPM1   E	-					
1267.92 at 17PM1   1247.77   110   140		∢	മ	ပ	<b>O</b> .	T)
1782   1794   1795   1794   1795   1794   1794   1795   1794   1795   1794   1794   1794   1795   1794   1795   1794   1795	2550	36792_at	TPM1	224727	tropomyosin 1 (alpha)	tropomyosin isoform
WRB         Y12478         tryptophan rich basic protein           WARS         X59892         tryptophanyl-IRNA synthetase           TUEN         S75463         Tu translation elongation factor,           TULP3         Al028290         tubbulin, alpha, ubiquitous           TULP3         Al028290         tubbulin, beta polypeptide           TUBB         AF035316         tubulin, beta polypeptide           TUBB         X79535         tubulin, beta polypeptide           TUBG1         M61764         tubulin, peta polypeptide           TUBG1         M61733         tubulin, peta polypeptide           TUBG1         U49188         tubulin, peta polypeptide           TUBG1         U49188         tubulin, peta polypeptide           TUBG1         U49188         tubulin, peta polypeptide           TUBG1         U49188         tubulin, peta polypeptide           TUBG1         U49188         tubulin, peta polypeptide           TUBG1         U49188         tubulin, peta polypeptide           TUBG1         U49188         tubulin, peta polypeptide           TUBG1         U49188         tubulin, peta polypeptide           TUBG1         U49188         tubulin, peta polypeptide           TUBG1         U49188	25513	32313 at	TPM2	M12125	tropomyosin 2 (beta)	tropomyosin 2 (beta)
WARS         X59892         tryptophanyl-tRNA synthetase           TUFM         S75463         Tu translation elongation factor, tubby like protein 3           TULP3         Al028290         tubby like protein 3           TULP3         Al028290         tubby like protein 3           TUBB         X79535         tubulin, beta polypeptide           TUBB         X79535         tubulin, beta polypeptide           TUBB         X79535         tubulin, pera polypeptide           TUBG1         M61764         tubulin, specific chaperone c           TBCC         U61234         tubulin, specific chaperone c           TBCE         U61234         tubulin, specific chaperone c           TBCE         U61234         tubulin, specific chaperone c           TBCE         U61234         tubulin, specific chaperone c           TBCE         U61234         tubulin, specific chaperone c           TBCE         U61234         tubulin, specific chaperone c           TBCE         U61234         tubulin, specific chaperone c           TBCE         U61234         tubulin, specific chaperone c           TBCE         U61234         tubulin, specific chaperone c           TBCE         U61828         tumor crosis factor receptor           TBCE <td>2552</td> <td>32777 at</td> <td>WRB</td> <td></td> <td>tryptophan rich basic protein</td> <td>congenital heart disease 5 protein</td>	2552	32777 at	WRB		tryptophan rich basic protein	congenital heart disease 5 protein
TUFM         S75463         Tu translation elongation factor, and the chondrial and the chondrial structures and the chondrial and the chondrial and the chondrial and the chondrial and the chondrial and the chondrial and the chollenge and th	2553	38121_at	WARS		tryptophanyl-tRNA synthetase	471 aa polypeptide (gamma2)
TUFM         S75463         mitochondrial           TULP3         Al028290         tubby like protein 3           TULP3         Al028290         tubby like protein 3           TUBB         AF035316         tubulin, beta polypeptide           TUBB         AF03535         tubulin, beta polypeptide           TUBB         AF03535         tubulin, beta polypeptide           TUBB         AF03535         tubulin, beta polypeptide           TUBB         AF03535         tubulin, beta polypeptide           TUBB         AF0354         tubulin, beta polypeptide           TUBB         AF0354         tubulin, peta polypeptide           TBCC         U61234         tubulin, specific chaperone c           TBCC         U61232         tubulin, specific chaperone c           TBCC         U61232         tubulin, specific chaperone c           TBCC         U61232         tubulin, specific chaperone c           TBCC         U61232         tubulin, specific chaperone c           TBCC         U61232         tubulin, specific chaperone c           TBCC         U61232         tubulin, specific chaperone c           TBCC         U61232         tubulin, specific chaperone c           TBCC         U61232         tubulin, sp					Tu translation elongation factor,	
TULP3         Al026290         tubby like protein 3           K-ALPHA-1         K00558         tubulin, beta polypeptide           TUBB         X79535         tubulin, beta polypeptide           TUBB         X79535         tubulin, beta polypeptide           TUBB         X79535         tubulin, beta polypeptide           TUBB         X79535         tubulin, perapolypeptide           TBCC         U61234         tubulin-specific chaperone c           TBCE         U61234         tubulin-specific chaperone c           TBCE         U61234         tubulin-specific chaperone c           TBCE         U61234         tubulin-specific chaperone c           TBCE         U61234         tubulin-specific chaperone c           TBCE         U61234         tubulin-specific chaperone c           TBCE         U61234         tubulin-specific chaperone c           TBCE         U61234         tubulin-specific chaperone c           TBC         U49188         tumor necrosis factor receptor           TNFRSF10B         AF016266         superfamily, member 12 (translocating           TNFRSF1         X60592         superfamily, member 5           TNFAIP3         M80783         tumor necrosis factor receptor           TNFAIP3 <t< td=""><td>2554</td><td>39867_at</td><td>TUFM</td><td>S75463</td><td>mitochondrial</td><td>P43</td></t<>	2554	39867_at	TUFM	S75463	mitochondrial	P43
K-ALPHA-1         K00558         tubulin, alpha, ubiquitous         t           TUBB         AF03536         tubulin, beta polypeptide         1           TUBB         X79535         tubulin, beta polypeptide         1           TUBB         X79535         tubulin, beta polypeptide         1           TBCC         U61234         tubulin-specific chaperone c         0           TBCC         U61234         tubulin-specific chaperone c         0           TBC         U61234         tubulin-specific chaperone c         0           TBC         U61234         tubulin-specific chaperone c         0           TBC         U61234         tubulin-specific chaperone c         0           TBC         U61234         tubulin-specific chaperone c         0           TDE1         U49188         tubulin-specific chaperone c         0           TDE1         U49188         tumor necrosis factor receptor         0           TNFRSF10B         AF016266         superfamily, member 10b         0           TNFRSF11         M58286         superfamily, member 12 (translocating than or receptor tumor necrosis factor receptor         0           TNFRSF6         X60592         superfamily, member 5         0           TNFAIP1	2555	31944_at	TULP3	A1028290	tubby like protein 3	
TUBB         AF035316         tubulin, beta polypeptide           TUBB         X79535         tubulin, beta polypeptide           TUBB         X79535         tubulin, beta polypeptide           TUBB         X79535         tubulin, pead polypeptide           TUBB         M61764         tubulin-specific chaperone c           TBCC         U61232         tubulin-specific chaperone c           TDE1         U49188         tumor differentially expressed 1           tumor necrosis factor receptor         tumor necrosis factor receptor           tumor necrosis factor receptor         tumor necrosis factor receptor           tumor necrosis factor receptor         tumor necrosis factor receptor           t         TNFRSF5         X60592         superfamily, member 5           t         tumor necrosis factor, alpha-induced           t         TNFAIP2         M80783         protein 1 (endothelial)           t         TNFAIP2         M59465         protein 2           tumor necrosis factor, alpha-induced           t         TNFAIP2         M59465         protein 2           t         TRABP3         protein 2         tumor protein p53 binding protein, 2           t         TRABP3         tumor protein p53 binding protein, 2           t	2556	32272_at	K-ALPHA-1	K00558	tubulin, alpha, ubiquitous	tubulin, alpha, ubiquitous
at         TUBB         X79535         tubulin, beta polypeptide           at         TUBG1         M61764         tubulin-specific chaperone c           TBCC         U61234         tubulin-specific chaperone c           TBCE         U61232         tubulin-specific chaperone e           TDE1         U49188         tumor differentially expressed 1           TDE1         U49188         tumor necrosis factor receptor           TNFRSF10B         AF016266         superfamily, member 10           t         tumor necrosis factor receptor           t         tumor necrosis factor receptor           t         tumor necrosis factor receptor           t         tumor necrosis factor receptor           t         tumor necrosis factor receptor           t         tumor necrosis factor, alpha-induced           t         tumor necrosis factor, alpha-induced           t         tumor necrosis factor, alpha-induced           t         tumor necrosis factor, alpha-induced           t         tumor necrosis factor, alpha-induced           t         tumor necrosis factor, alpha-induced           t         tumor necrosis factor, alpha-induced           t         tumor necrosis factor, alpha-induced           t         tumor necrosis f	2557	39332 at	TUBB	AF035316	tubulin, beta polypeptide	
TUBG1         M61764         tubulin, gamma 1           TBCC         U61234         tubulin-specific chaperone c           TBCE         U61232         tubulin-specific chaperone e           TBCE         U61232         tumor necrosis factor receptor           TDE1         U49188         tumor necrosis factor receptor           TNFRSF10B         AF016266         superfamily, member 12 (translocating chain-association membrane protein)           TNFRSF12         U83598         chain-association membrane protein)           TNFRSF14         M58286         superfamily, member 12 (translocating tumor necrosis factor receptor tumor necrosis factor receptor           TNFRSF6         X60592         superfamily, member 5           TUMOR NECSIS (actor receptor superfamily, member 5         tumor necrosis factor receptor           TNFAIP1         M80783         tumor necrosis factor receptor           TNFAIP2         M92357         tumor necrosis factor, alpha-induced           TNFAIP3         M59465         protein 2           TNFAIP3         M59465         protein 2           TP53B71         U090477         tumor protein D52-like 2           TP53B72         tumor protein D53 binding protein, 2           TP62B1         tumor protein p53 binding protein, 2           TP62B1         tumo	2558	39331_at	TUBB	X79535	tubulin, beta polypeptide	beta tubulin
TBCC         U61234         tubulin-specific chaperone c           TBCE         U61232         tubulin-specific chaperone e           TDE1         U49188         tumor differentially expressed 1           TDE1         U49188         tumor necrosis factor receptor           tumor necrosis factor receptor         tumor necrosis factor receptor           tumor necrosis factor receptor         tumor necrosis factor receptor           tumor necrosis factor receptor         tumor necrosis factor receptor           tumor necrosis factor receptor         tumor necrosis factor receptor           tumor necrosis factor receptor         tumor necrosis factor receptor           tumor necrosis factor receptor         tumor necrosis factor receptor           tumor necrosis factor receptor         tumor necrosis factor alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           t	2559	33346_r_at	TUBG1	M61764	tubulin, gamma 1	gamma-tubulin
TBCE         U61232         tubulin-specific chaperone e           TDE1         U49188         tumor differentially expressed 1           TDE1         U49188         tumor necrosis factor receptor           tumor necrosis factor receptor         tumor necrosis factor receptor           tumor necrosis factor receptor         superfamily, member 12 (translocating           tumor necrosis factor receptor         tumor necrosis factor receptor           tumor necrosis factor receptor         tumor necrosis factor receptor           tumor necrosis factor receptor         superfamily, member 1A           tumor necrosis factor receptor         tumor necrosis factor receptor           tumor necrosis factor receptor         tumor necrosis factor receptor           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced           tumor necrosis factor, alpha-induced         tumor necrosis factor, alpha-induced	2560	36176 at	TBCC	U61234	tubulin-specific chaperone c	cofactor C
TDE1         U49188         tumor differentially expressed 1           TNFRSF10B         AF016266         superfamily, member 10b           TNFRSF10B         AF016266         superfamily, member 10b           TNFRSF12         U83598         tumor necrosis factor receptor           at         TNFRSF1A         M58286         superfamily, member 12 (translocating chain-association membrane protein)           TNFRSF1A         M58286         superfamily, member 14           TNFRSF6         X60592         superfamily, member 5           TNFRSF6         X63717         superfamily, member 6           TNFAIP1         M80783         tumor necrosis factor receptor           TNFAIP2         M92357         tumor necrosis factor, alpha-induced           TNFAIP2         M92357         protein 2           TNFAIP2         M52465         protein 2           TNFAIP3         M59465         protein 2           TNFAIP3         M59465         protein 2           TNFAIP3         M59465         protein 2           TNFAIP3         U69477         tumor protein D52-like 2           TNF3BP1         U05437         tumor protein D52-like 2           TNF3BP2         tumor protein p53 binding protein, 3           TNF3BP2         tumor	2561	35159_at	TBCE	U61232	tubulin-specific chaperone e	cofactor E
TNFRSF10B AF016266 superfamily, member 10b tumor necrosis factor receptor superfamily, member 12 (translocating tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein) tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor superfamily, member 6 tumor necrosis factor receptor superfamily, member 6 tumor necrosis factor alpha-induced tumor necrosis factor, alpha-induced tumor nec	2562	37007_at	TDE1	U49188	tumor differentially expressed 1	tumor differentially expressed 1
TNFRSF10B   AF016266   Superfamily, member 10b					tumor necrosis factor receptor	
tumor necrosis factor receptor superfamily, member 12 (translocating superfamily, member 12 (translocating superfamily, member 12 (translocating tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor tumor necrosis factor receptor superfamily, member 5 tumor necrosis factor receptor superfamily, member 6 tumor necrosis factor receptor superfamily, member 6 tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor protein 3 tumor protein p53 binding protein, 1 tumor protein p53 binding protein, 2 tumor p10 p10 p10 p10 p10 p10 p10 p10 p10 p10	2563	34892_at	TNFRSF10B	AF016266	superfamily, member 10b	TRAIL receptor 2
11190_at         TNFRSF12         U83598         chain-association membrane protein)           563_s_at         TNFRSF1A         M58286         tumor necrosis factor receptor           15150_at         TNFRSF5         X60592         superfamily, member 1A           15150_at         TNFRSF6         X63717         superfamily, member 5           1563_s_at         TNFRSF6         X63717         superfamily, member 6           1563_at         TNFRSF6         X63717         superfamily, member 6           1563_at         TNFAIP1         M80783         protein 1 (endothelial)           1563_at         TNFAIP2         M92357         protein 2           1563_at         TNFAIP3         M59465         protein 2           1711_at         TPD52L2         AF004430         tumor necrosis factor, alpha-induced           1711_at         TPD53BP1         U09477         tumor protein D52-like 2           1711_at         TPD53BP2         tumor protein D53 binding protein, 1           1753BP2         tumor protein p53 binding protein, 2           1753BP2         tumor protein p53 binding protein, 2           1753BP2         tumor protein p53 binding protein, 2           1753BP2         tumor protein p53 binding protein, 2           1774, at <t< td=""><td></td><td></td><td></td><td></td><td>tumor necrosis factor receptor</td><td></td></t<>					tumor necrosis factor receptor	
TNFRSF12   U83598   Chain-association membrane protein					superfamily, member 12 (translocating	
TNFRSF1A   M58286   Superfamily, member 1A     1563_s_at   TNFRSF5   X60592   Superfamily, member 5     1564_3_at   TNFRSF6   X63717   Superfamily, member 5     1564_3_at   TNFAIP1   M80783   protein 1 (endothelial)     1585_at   TNFAIP2   M92357   protein 2     1711_at   TP53BP1   U09477   tumor protein p53 binding protein, 2     1563_at   TP53BP1   U09477   tumor protein p53 binding protein, 2     1563_at   TP53BP2   U58334   tumor protein p53 binding protein, 2     1563_at   TP53BP2   U58334   tumor protein p53 binding protein, 2     1563_at   TP53BP2   U58334   tumor protein p53 binding protein, 2     1563_at   TP53BP2   U58334   tumor protein p53 binding protein, 2     1563_at   TP53BP2   U58334   tumor protein p53 binding protein, 2     1563_at   TP53BP2   U58334   tumor protein p53 binding protein, 2     1563_at   TP53BP2   U58334   tumor protein p53 binding protein, 2     1563_at   TP53BP2   U58334   tumor protein p53 binding protein, 2     1563_at   TP53BP2   U58334   tumor protein p53 binding protein, 2     1563_at   TP53BP2   U58334   tumor protein p53 binding protein, 2     1563_at   TP53BP2   U58334   tumor protein p53 binding protein, 2     1563_at   TP53BP2   U58334   tumor protein p53 binding protein, 2     1563_at   TP53BP2   U58334   tumor protein p53 binding protein, 2   tumor protein p53 binding protein, 2   tumor protein p53 binding protein, 2   tumor protein p53 binding protein, 2   tumor protein p53 binding protein, 2   tumor protein p53 binding protein, 2   tumor protein p53 binding protein, 2   tumor protein p53 binding protein, 2   tumor protein p53 binding protein, 2   tumor protein p53 binding protein, 2   tumor protein p53 binding protein, 2   tumor protein p53 binding protein, 2   tumor protein p53 binding protein, 2   tumor protein p53 binding protein, 2   tumor protein p53 binding protein, 2   tumor protein p53 binding protein, 2   tumor protein p53 binding protein p53 binding protein p53 binding protein p53 binding protein p53 binding protein p53 binding protein p53 binding pr	2564	41190_at	TNFRSF12	U83598	chain-association membrane protein)	death domain receptor 3 soluble form
1563_s_at					tumor necrosis factor receptor	
150_at         TNFRSF5         X60592         superfamily, member 5           37643_at         TNFRSF6         X63717         superfamily, member 6           38638_at         TNFAIP1         M80783         protein 1 (endothelial)           38631_at         TNFAIP2         M92357         protein 2           40076_at         TNFAIP3         M59465         protein 3           1711_at         TP538P1         U09477         tumor protein p53 binding protein, 1           34822_at         TP63BP2         U58334         tumor protein p53 binding protein, 2           TEGSDDI         tumor protein p53 binding protein, 2         tumor protein p53 binding protein, 2	2565	<i>σ</i> ,	TNFRSF1A	M58286	superfamily, member 1A	tumor necrosis factor receptor
15150_at         TNFRSF5         X60592         superfamily, member 5           17643_at         TNFRSF6         X63717         superfamily, member 6           17643_at         TNFAIP1         M80783         protein 1 (endothelial)           18631_at         TNFAIP2         M92357         protein 2           17076_at         TNFAIP3         M59465         protein 3           1711_at         TP538P1         U09477         tumor protein p53 binding protein, 1           1822_at         TP53BP2         U58334         tumor protein p53 binding protein, 2           1822_at         TP53BP2         tumor protein p53 binding protein, 2           1822_at         tumor protein p53 binding protein, 2           1822_at         tumor protein p53 binding protein, 2           1822_at         tumor protein p53 binding protein, 2           1823A         tumor protein p53 binding protein, 2           1822_at         tumor protein p53 binding protein, 2					tumor necrosis factor receptor	
37643_at         TNFRSF6         X63717         tumor necrosis factor receptor           36988_at         TNFAIP1         M80783         protein 1 (endothelial)           38631_at         TNFAIP2         M92357         protein 2           40076_at         TNFAIP3         M59465         protein 3           1711_at         TP538P1         U09477         tumor protein p53 binding protein, 1           34822_at         TP53BP2         U58334         tumor protein p53 binding protein, 2           1823_at         TP53BP2         tumor protein p53 binding protein, 2           1823_at         tumor protein p53 binding protein, 2           1823_at         tumor protein p53 binding protein, 2           1823_at         tumor protein p53 binding protein, 2           1823_at         tumor protein p53 binding protein, 2           1823_at         tumor protein p53 binding protein, 2           1823_at         tumor protein p53 binding protein, 2           1823_at         tumor protein p53 binding protein, 2	2566	35150_at	TNFRSF5	X60592	superfamily, member 5	CDw40
37643_at         TNFRSF6         X63717         superfamily, member 6           36988_at         TNFAIP1         M80783         tumor necrosis factor, alpha-induced           38631_at         TNFAIP2         M92357         protein 2           40076_at         TNFAIP3         M59465         protein 3           40076_at         TPD52L2         AF004430         tumor protein D52-like 2           1711_at         TP538P1         U09477         tumor protein p53 binding protein, 1           34822_at         TP53BP2         U58334         tumor protein p53 binding protein, 2           4666         tumor protein p53 binding protein, 2         tumor protein p53 binding protein, 2					tumor necrosis factor receptor	:
86988_at         TNFAIP1         M80783         tumor necrosis factor, alpha-induced tumor necrosis factor, a	2567	37643	TNFRSF6	X63717	superfamily, member 6	APO-1 cell surface antigen precursor
36988_at         TNFAIP1         M80783         protein 1 (endothelial)           38631_at         TNFAIP2         M92357         tumor necrosis factor, alpha-induced           595_at         TNFAIP3         M59465         protein 2           4007e_at         TPD52L2         AF004430         tumor protein D52-like 2           1711_at         TP53BP1         U09477         tumor protein p53 binding protein, 1           34822_at         TP53BP2         U58334         tumor protein p53 binding protein, 2           1820ac         tumor protein p53-binding protein, 2         tumor protein p53-binding protein, 2					tumor necrosis factor, alpha-induced	
10076 at The SBP1         The SBP1         MB SBP1         Itemor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor necrosis factor, alpha-induced tumor protein D52-like 2         MS9465         protein 3         protein 3         protein 3         protein 3         protein 3         protein 3         protein 1         protein 1         protein 1         protein 1         protein 1         protein 1         protein 1         protein 1         protein 1         protein 1         protein 1         protein 1         protein 1         protein 1         protein 2         p	2568	36988_at	TNFAIP1	M80783	protein 1 (endothelial)	B12 protein
38631_at         TNFAIP2         M92357         protein 2           595_at         TNFAIP3         M59465         protein 3           40076_at         TPD52L2         AF004430         tumor protein D52-like 2           1711_at         TP53BP1         U09477         tumor protein p53 binding protein, 1           34822_at         TP53BP2         U58334         tumor protein p53 binding protein, 2           182030         tumor protein p53-binding protein, 2         tumor protein p53-binding protein, 2					turnor necrosis factor, alpha-induced	
10076_at         TNFAIP3         M59465         protein 3           1711_at         TP53BP1         U09477         tumor protein p53 binding protein, 1           1822_at         TP53BP2         U58334         tumor protein p53 binding protein, 2           1822_at         TP53BP2         U58334         tumor protein p53 binding protein, 2	2569		TNFAIP2	M92357	protein 2	B94 protein
395_at         TNFAIP3         M59465         protein 3           40076_at         TPD52L2         AF004430         tumor protein D52-like 2           1711_at         TP53BP1         U09477         tumor protein p53 binding protein, 1           34822_at         TP53BP2         U58334         tumor protein p53 binding protein, 2           1823_at         TP53BP2         tumor protein p53 binding protein, 2					tumor necrosis factor, alpha-induced	
40076_at         TPD52L2         AF004430         tumor protein D52-like 2           1711_at         TP53BP1         U09477         tumor protein p53 binding protein, 1           34822_at         TP53BP2         U58334         tumor protein p53 binding protein, 2           1820ac         tumor protein p53-binding protein, 2	2570	595_at	TNFAIP3	M59465	protein 3	A20
1711_at TP53BP1 U09477 tumor protein p53 binding protein, 1 34822_at TP53BP2 U58334 tumor protein p53 binding protein, 2	2571	40076	TPD52L2	AF004430	turnor protein D52-like 2	hD54+ins2 isoform
34822_at TP53BP2 U58334 tumor protein p53 binding protein, 2	2572	1711	TP538P1	U09477	turnor protein p53 binding protein, 1	p53-binding protein
TDESDDI   INDESDDI   INDESDDI   Indian protein p.53-binding protein	2573	34822_at	TP538P2	U58334	tumor protein p53 binding protein, 2	Bbp/53BP2
ווייסים ליייים ווייסים ווייסים לייים ליייים ליייים ליייים ליייים ליייים ליייים ליייים ליייים ליייים ליייים ליים לייים לייים לייים לייים לייים לייים ליים ליים לייים לייים לייים לייים לייים לייים לייים לייים לייים לייים לייים לייים לייים ליים ליים ליים לייים ליים לייים לייים לייים לייים לייים ליים לייים לייים לייים לייים ליים ל	2574	2574 38568 at	TP53BPL	U82939	tumor protein p53-binding protein	p53 binding protein

45.21

<b> </b>	A	В	၁	O	ш
5753	2575 31584 at	TPT1	X16064	lled 1	tumor protein, translationally-controlled 1
2					
2576	2576 21888 c at	TSSC3	AF001294		IPL
2577 147 at	5	-		ptibility gene 101	furnor susceptibility protein
+					
					a ul u DNA hinding profein
2578 4	2578 40328_at	TWIST	X99268	Saethre-Chotzen syndrome) (Urosophilia)	
25792	2579 2086 s at	TYRO3	D17517	Т	Ony
25803	2580 35246 at	TYRO3	U18934	7	receptor tyrosina Kiliasa
3					tyrosine 3-monooxygenase/uyptopilair 3-
_				monooxygenase activation protein, beta	monooxygenase activation protein, beta
25813	2581 32324 at	YWHAB	X57346	polypeptide	polypeptide
				tyrosine 3-monooxygenase/tryptophan 5-	
				monooxygenase activation protein, theta	
2582 409 at	10 PO	WHAO	X56468	polypeptide	14.3.3 protein
2002	, n			tyrosine 3-monooxygenase/tryptophan 5-	
				monooxygenase activation protein, theta	
0500	200000000000000000000000000000000000000	VWHAD	X56468	polypeptide	14.3.3 protein
20027	05,000_at			tyrosine 3-monooxygenase/tryptophan 5-	
				monooxygenase activation protein, zeta	:
7000	103K of	YWHA7	M86400	polypeptide	phospholipase A2
2000	2304 1232 at	TPST1	AF038009	tyrosylprotein sulfotransferase 1	tyrosylprotein sulfotransferase-1
2002	2363 327 10_at	TPST2	AF049891	tyrosylprotein sulfotransferase 2	tyrosylprotein sulfotransferase-2
2507	2300 33172 at	VARS	U89436	tyrosyl-tRNA synthetase	tyrosyl-tRNA synthetase
2007	2021			U2(RNU2) small nuclear RNA auxillary	
258B	2588 36517 at	U2AF1	M96982	factor 1	UZ SUKINP auxiliary factor striail suburint
25.89		UBN1	Al341565	ubinuclein 1	
2590	2590 34824 at	UBQLN2	AB015344	ubiquilin 2	npidnilin z
				ubiquinol-cytochrome c reductase (6.4kD)	
2591	2591 38451 at	Uaca	T58471	subunit	
				ubiquinol-cytochrome c reductase binding	
2592	2592 39427 at	UQCRB	T79616	protein	
				ubiquinol-cytochrome c reductase core	ubiquinol-cytochrome c reductase core
2593	2593 40854 at	UQCRC2	J04973	protein II	protein II
				}	

Fig. 21

	A	B	O	Q	ш
				ubiquinol-cytochrome c reductase hinge	
2594	2594 36104_at	UQCRH	AA526497	protein	
2595 1366	1366_i_at	UBC	M26880	ubiquitin C	ubiquitin C
2596	2596 1367_f_at	UBC	M26880	ubiquitin C	ubiquitin C
				ubiquitin carboxyl-terminal esterase L1	ubiquitin carboxyl-terminal esterase L1
2597	2597 36990_at	UCHL1	X04741	(ubiquitin thiolesterase)	(ubiquitin thiolesterase)
2598	2598 811_at	UFD1L	U64444	ubiquitin fusion degradation 1-like	ubiquitin fusion-degradation 1 like protein
2599	2599 40623_at	UBE3B	AI749193	ubiquitin protein ligase	
				ubiquitin protein ligase E3A (human	
				papilloma virus E6-associated protein,	E6-associated protein E6-AP/ubiquitin-
2600	2600 41205_at	UBE3A	U84404	Angelman syndrome)	protein ligase
2601	2601 34383_at	USP1	AB014458	ubiquitin specific protease 1	ubiquitin specific protease
2602	2602]37683_at	USP10	D80012	ubiquitin specific protease 10	
2603	2603 162_at	USP11	U44839	ubiquitin specific protease 11	UHX1 protein
				ubiquitin specific protease 14 (tRNA-	
2604	2604 36982_at	USP14	U30888	guanine transglycosylase)	tRNA-Guanine Transglycosylase
2605	2605 39866_at	USP22	AB028986	ubiquitin specific protease 22	KIAA 1063 protein
2606	2606 35847_at	USP24	AB028980	ubiquitin specific protease 24	KiAA1057 protein
				ubiquitin specific protease 4 (proto-	
2607	2607 1357_at	USP4	U20657	oncogene)	ubiquitin protease
				ubiquitin specific protease 5 (isopeptidase	
2608	2608 34405_at	USP5	U47927	(T)	isopeptidase T
				ubiquitin specific protease 7 (herpes virus- herpesvirus associated ubiquitin-specific	herpesvirus associated ubiquitin-specific
2609	2609 37672_at	USP7	Z72499	associated)	protease (HAUSP)
2610	2610 39794_at	USP8	D29956	ubiquitin specific protease 8	ubiquitin specific protease 8
				ubiquitin specific protease 9, X	
2611	2611 32572_at	USP9X	X98296	chromosome (fat facets-like Drosophila)	ubiquitin hydrolase
				ubiquitin-activating enzyme E1C (UBA3	
2612	2612 40066_at	UBE1C	AF046024	homolog, yeast)	UBA3
2613	2613 36579 at	UBE4A ·	D50916	ubiquitination factor E4A (UFD2 homolog,	ubiquitination factor E4A (UFD2 homolog,
	:			Uhiquitination factor EAR (LIED2 homolog	
2614	2614 41339_at	UBE4B	AF043117	yeast)	ubiquitin-fusion degradation protein 2
7,00	0.00	200	140010	L	771
2012	2615 36959_at	UBEZVI	049278	ubiquitin-conjugating enzyme Ez variant 1  UEV-1	UEV-1

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C						
at         UBEZA         ubiquitin-conjugating enzyme E2D 1         Indiquitin-conjugating enzyme E2D 1         Indiquitin-conjugating enzyme E2D 1         Indiquitin-conjugating enzyme E2D 2         Indiquitin-conjugating enzyme E2D 2         Indiquitin-conjugating enzyme E2D 2         Indiquitin-conjugating enzyme E2D 2         Indiquitin-conjugating enzyme E2D 3         Indiquitin-conjugati	T	¥	В			E
at         UBEZD1         M74524         homolog)           at         UBEZD1         AF020761         (UBC4/5 homolog, yeast)           at         UBEZD2         Al310002         (UBC4/5 homolog, yeast)           at         UBEZD2         U39317         (UBC4/5 homolog, yeast)           at         UBEZD2         U39318         (UBC4/5 homolog, yeast)           at         UBEZD3         U39318         (UBC4/5 homolog, yeast)           at         UBEZD3         U39318         (UBC4/5 homolog, yeast)           at         UBEZD3         U39318         (UBC4/5 homolog, yeast)           at         UBEZD3         Ubiquilin-conjugating enzyme E2E 3           at         UBEZD3         Ubiquilin-conjugating enzyme E2E 3           at         UBEZD3         Ubiquilin-conjugating enzyme E2I (UBC9)           at         UBEZD3         Ubiquilin-conjugating enzyme E2I 3           at         UBEZD3         Ubiquilin-conjugating enzyme E2I 3           barry barr						ubiquitin-conjugating enzyme E2A (HAD6
at         UBE2D1         AF020761         Ubiquitin-conjugating enzyme E2D 1           at         UBE2D2         Al310002         (UBC4/5 homolog, yeast)           at         UBE2D2         Ubiquitin-conjugating enzyme E2D 2           ubiquitin-conjugating enzyme E2D 2         UBG4/5 homolog, yeast)           ubiquitin-conjugating enzyme E2D 3         UBE2D3           ubiquitin-conjugating enzyme E2D 3         UBE2D3           ubiquitin-conjugating enzyme E2D 3         UBC4/5 homolog, yeast)           at         UBE2D3         U39318           ubiquitin-conjugating enzyme E2D 3         UBC4/5 homolog, yeast)           at         UBE2D3         Ubiquitin-conjugating enzyme E2D 3           at         UBE2D3         Ubiquitin-conjugating enzyme E2D 3           ubiquitin-conjugating enzyme E2D 3         Ubiquitin-conjugating enzyme E2D 3           ubiquitin-conjugating enzyme E2D 4         Ubiquitin-conjugating enzyme E2D 4           ubiquitin-conjugating enzyme E2D 5         Ubiquitin-conjugating enzyme E2D 6           ubiquitin-conjugating enzyme E2D 6         UBC4/5 homolog, yeast)           ubiquitin-conjugating enzyme E2D 6         UBC4/5 homolog, yeast)           ubiquitin-conjugating enzyme E2L 6         UBC4/5 homolog, yeast)           ubiquitin-conjugating enzyme E2L 6         UBC4/5 homolog, yeast)      <	2616 <u> </u>	390_at	UBEZA		homolog)	homolog)
UBEZD1         AF020761         (UBC4/5 homolog, yeast)           UBEZD2         Al310002         (UBC4/5 homolog, yeast)           UBEZD2         Al310002         (UBC4/5 homolog, yeast)           UBEZD2         U39317         (UBC4/5 homolog, yeast)           UBEZD3         U39318         (UBC4/5 homolog, yeast)           UBEZD3         U39318         (UBC4/5 homolog, yeast)           UBEZD3         U39318         (UBC4/5 homolog, yeast)           UBEZD3         U39318         (UBC4/5 homolog, yeast)           UBEZD3         U39318         (UBC4/5 homolog, yeast)           UBEZD3         U39318         (UBC4/5 homolog, yeast)           UBEZD3         U59318         Ubriquitin-conjugating enzyme E2E 3           UBEZD3         U59318         Ubriquitin-conjugating enzyme E2I (UBC9)           UBEZD3         U56867         homolog, yeast)           UBEZD3         U56867         homolog, yeast)           UBEZD3         U56867         homolog, yeast)           UBEZD3         U56867         homolog, yeast)           UBEZD3         U56867         homolog, yeast)           UBEZD3         U56867         U56807           U57122         U56907         U56713           U57122 <td></td> <td></td> <td></td> <td></td> <td>ubiquitin-conjugating enzyme E2D 1</td> <td></td>					ubiquitin-conjugating enzyme E2D 1	
UBEZDZ         Ubiquitin-conjugating enzyme EZD 2         UBEZDZ         UBS317         (UBC4/5 homolog, yeast)         UBEZDZ         U39317         (UBC4/5 homolog, yeast)         (UBC4/5 homolog, yeast)         (UBC4/5 homolog, yeast)         (UBC4/5 homolog, yeast)         (UBC2/	2617 3	37826_at	UBE2D1		(UBC4/5 homolog, yeast)	
UBE2D2         Al310002         (UBC4/5 homolog, yeast)           UBE2D2         US9317         (UBC4/5 homolog, yeast)           UBE2D3         U39318         (UBC4/5 homolog, yeast)           UBE2D3         U39318         (UBC4/5 homolog, yeast)           UBE2D3         U39318         (UBC4/5 homolog, yeast)           UBE2D3         U39318         (UBC4/5 homolog, yeast)           UBE2B3         AB017644         (UBC4/5 homolog, yeast)           UBE2B3         AF032456         (UBC4/5 homolog, yeast)           UBE2B3         AF032456         (UBC4/5 homolog, yeast)           UBE2B3         AF032456         (UBC4/5 homolog, yeast)           UBE2B3         AF032456         (UBC4/5 homolog, yeast)           UBE2B3         AF032456         (UBC4/5 homolog, yeast)           UBE2B4         UA5328         homolog, yeast)           UBE2B4         UA5328         homolog, yeast)           UBE2B4         UA5328         homolog, yeast)           UBE2B4         UA5328         homolog, yeast)           UBE2B4         UA5328         homolog, yeast)           UBE2B4         UBG4011in-conjugating enzyme E2I (UBC9           UBE2B4         UBC413 homolog, yeast)           UBE2B4         UBC413					ubiquitin-conjugating enzyme E2D 2	
UBEZDZ         Ubiquitin-conjugating enzyme E2D 2           UBEZDZ         U39317         (UBC45 homolog, yeast)           UBEZD3         U39318         (UBC45 homolog, yeast)           UBEZD3         U39318         (UBC45 homolog, yeast)           UBEZD3         U39318         (UBC45 homolog, yeast)           UBEZB3         AB017644         (UBC465 homolog, yeast)           UBEZB3         AB017644         (UBC465 homolog, yeast)           UBEZB3         AF032456         (UBC7 homolog, yeast)           UBEZB3         AF032456         (UBC7 homolog, yeast)           UBEZB3         AF032456         (UBC7 homolog, yeast)           UBEZB3         U465867         ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)           UBEZB4         UA5328         homolog, yeast)           UBEZB4         UA5328         homolog, yeast)           UBEZB4         UBG417in-conjugating enzyme E2I (UBC9 homolog, yeast)           UBEZB4         UBG417in-conjugating enzyme E2I (UBC9 homolog, yeast)           UBEZB4         UBG4171in-conjugating enzyme E2I (UBC9 homolog, yeast)           UBL1         UBC122         Ubiquitin-like 1 (sentrin)           UBL397         ubiquitin-like 1 (sentrin)           UBC3         UBC3         UBC3	2618	38705 at	UBE2D2	AI310002	(UBC4/5 homolog, yeast)	
at         UBE2D2         U39317         (UBC4/5 homolog, yeast)           at         UBE2D3         U39318         (UBC4/5 homolog, yeast)           ubiquilin-conjugaling enzyme E2D 3         (UBC4/5 homolog, yeast)           ubiquilin-conjugaling enzyme E2E 3         (UBC4/5 homolog, yeast)           at         UBE2G2         AF032456         (UBC4/5 homolog, yeast)           at         UBE2G2         AF032456         (UBC7 homolog, yeast)           at         UBE2G2         AF032456         (UBC7 homolog, yeast)           at         UBE2L3         U66867         ubiquitin-conjugaling enzyme E2I (UBC9 ubiquitin-conjugaling enzyme E2I (UBC9 ubiquitin-conjugaling enzyme E2I (UBC9 ubiquitin-conjugaling enzyme E2I (UBC9 ubiquitin-conjugaling enzyme E2I (UBC9 ubiquitin-conjugaling enzyme E2I (UBC9 ubiquitin-conjugaling enzyme E2I (UBC9 ubiquitin-conjugaling enzyme E2I (UBC9 ubiquitin-conjugaling enzyme E2I (UBC9 ubiquitin-conjugaling enzyme E2I (UBC9 ubiquitin-conjugaling enzyme E2I (UBC9 ubiquitin-conjugaling enzyme E2I (UBC9 ubiquitin-conjugaling enzyme E2I (UBC9 ubiquitin-conjugaling enzyme E2I (UBC9 ubiquitin-conjugaling enzyme E2I (UBC9 ubiquitin-like I (sentin) (UBC122 ubiquitin-like I (sentin) (UBC122 ubiquitin-like I (sentin) (UBC9 ubiquitin-like I (sentin) (UBC9 ubiquitin-like I (sentin) (UBC9 ubiquitin-like I (sentin) (UBC9 ubiquitin-like I (sentin) (UBC9 ubiquitin-like I (sentin) (UBC9 ubiquitin-like I (sentin) (UBC9 ubiquitin-like I (sentin) (UBC9 ubiquitin-like I (sentin) (UBC9 ubiquitin-like I (sentin) (UBC9 ubiquitin-like I (sentin) (UBC9 ubiquitin-like I (sentin) (UBC9 ubiquitin-like I (sentin) (UBC9 ubiquitin-like I (se		<b>!</b>			ubiquitin-conjugating enzyme E2D 2	
at         UBEZD3         U39318         (UBC4/5 homolog, yeast)           uBEZD3         U39318         (UBC4/5 homolog, yeast)           uBEZD3         (UBC4/5 homolog, yeast)           at         UBEZG2         AF032456           ubiquitin-conjugating enzyme EZE 3         (UBC4/5 homolog, yeast)           at         UBEZG2         AF032456           ubiquitin-conjugating enzyme EZI (UBC9 ubiquitin-conjugating enzyme EZI (UBC9 ubiquitin-conjugating enzyme EZI (UBC9 ubiquitin-conjugating enzyme EZI (UBC9 ubiquitin-conjugating enzyme EZI (UBC9 ubiquitin-conjugating enzyme EZI (UBC9 ubiquitin-conjugating enzyme EZI (UBC9 ubiquitin-conjugating enzyme EZI (UBC9 ubiquitin-conjugating enzyme EZI (UBC9 ubiquitin-conjugating enzyme EZI (UBC9 ubiquitin-conjugating enzyme EZI (UBC9 ubiquitin-like 1 (sentin) at UBL1 UBL1 UBT3           at         UBEZIG         AA883502         ubiquitin-conjugating enzyme EZI (UBC9 ubiquitin-like 1 (sentin) at UBC13           at         UBL1         U67122         ubiquitin-conjugating enzyme EZI (UBC9 ubiquitin-like 1 (sentin) at UBCD2           at         UBL1         U67122         ubiquitin-conjugating enzyme EZI (UBC9 ubiquitin-like 1 (sentin) at UBCD2           at         UBL397         ubiquitin-like 1 (sentin) at UBCD2         UDP-Gal:betaGlcNAc beta 1,4-UBCD2           at         UBCD2         UDP-Gal:betaGlcNAc beta 1,4-UBCD2         UDP-Gal:betaGlcNAc beta 1,4-UBCD2           at         BAGALT2         <	2619 <u> </u> 8	332 at	UBE2D2	U39317	(UBC4/5 homolog, yeast)	UbcH5B
UBE2D3         U39318         (UBC4/5 homolog, yeast)           UBE2D3         U39318         (UBC4/5 homolog, yeast)           UBE2D3         U39318         (UBC4/5 homolog, yeast)           t         UBE2E3         AB017644         (UBC4/5 homolog, yeast)           t         UBE2E3         AF032456         (UBC4/5 homolog, yeast)           t         UBE2E3         AF032456         (UBC4/5 homolog, yeast)           t         UBE2E3         AF032456         (UBC4/5 homolog, yeast)           t         UBE2E3         AF032456         (UBC4/5 homolog, yeast)           t         UBE2E3         AF032456         (UBC4/5 homolog, yeast)           t         UBE2E3         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           t         UBE2E3         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           t         UBE2E3         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           t         UBE2E3         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           t         UBE2E3         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           t         UBE2E4         UBA883502         ubiquitin-conjugating enzyme E2I (UBC9)           t         UBE2N         UBA883502 <td></td> <td></td> <td></td> <td></td> <td>ubiquitin-conjugating enzyme E2D 3</td> <td></td>					ubiquitin-conjugating enzyme E2D 3	
UBE2D3         ubiquitin-conjugating enzyme E2D 3           UBE2D3         U39318         (UBC4/5 homolog, yeast)           t         UBE2E3         AB017644         (UBC4/5 homolog, yeast)           t         UBE2E3         AB017644         (UBC4/5 homolog, yeast)           at         UBE2G2         AF032456         (UBC7 homolog, yeast)           t         UBE2I         U66867         homolog, yeast)           t         UBE2I         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           t         UBE2I         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           t         UBE2IS         S81003         ubiquitin-conjugating enzyme E2I (UBC9)           t         UBE2IS         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           t         UBE2IS         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           t         UBE2IS         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           t         UBE2IS         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           t         UBE2IS         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           t         UBE2IS         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           t	2620	39083 at	UBE2D3	U39318	(UBC4/5 homolog, yeast)	UbcH5C
UBE2D3         U39318         (UBC4/5 homolog, yeast)           at         UBE2E3         AB017644         (UBC4/5 homolog, yeast)           at         UBE2E3         AF032456         (UBC4/5 homolog, yeast)           s_at         UBE2I         AF032456         (UBC7 homolog, yeast)           at         UBE2I         U4532B         ubiquitin-conjugating enzyme E2I (UBC9)           at         UBE2I         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           at         UBE2I         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           at         UBE2I         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           at         UBE2I         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           at         UBE2I         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           at         UBE2I         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           at         UBE2I         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           at         UBE2I         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           at         UBC304         (UBC13 homolog, yeast)           at         UBXD2         D87684         UDP-Gal:betaGIcNAc beta 1,4-	T				ubiquitin-conjugating enzyme E2D 3	
at         UBE2E3         AB017644         (UBC4/5 homolog, yeast)           at         UBE2G2         AF032456         (UBC4/5 homolog, yeast)           s_at         UBE2G2         AF032456         (UBC7 homolog, yeast)           s_at         UBE2I         U66867         ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC1 UBC12)           at         UBE2IG         AA883502         ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC12)           at         UBE2IG         AA883502         ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-like 1 (sentrin))           at         UBL1         UG7122         ubiquitin-like 1 (sentrin)           at         UBL397         ubiquitin-like 3         UDP-Gal:betaGlcNAc beta 1,4-           at         BAGALT1         D29805         UDP-Gal:betaGlcNAc beta 1,4-           at         BAGALT2         AF038661         galactosyltransferase, polypeptide 2           at         BAGALT3	2621	504 at	UBE2D3	U39318	(UBC4/5 homolog, yeast)	UbcH5C
UBE2E3         AB017644         (UBC4/5 homolog, yeast)           UBE2G2         AF032456         (UBC7 homolog, yeast)           UBE2G2         AF032456         (UBC7 homolog, yeast)           ubiquitin-conjugating enzyme E2I (UBC9)         Ubiquitin-conjugating enzyme E2I (UBC9)           UBE2I         U45328         homolog, yeast)           UBE2L3         S81003         ubiquitin-conjugating enzyme E2I (UBC9)           UBE2L6         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           UBE2L6         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           UBE2L6         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           UBE2L6         AA883502         ubiquitin-conjugating enzyme E2I (UBC9)           UBE2L7         UBC132         ubiquitin-like 1 (sentrin)           UBL1         U67122         ubiquitin-like 1 (sentrin)           UBL3         AL080177         ubiquitin-like 1 (sentrin)           UBXD2         D87684         UBP-Gal:betaGlcNAc beta 1.4-           UBP-Gal:betaGlcNAc beta 1.4-         UDP-Gal:betaGlcNAc beta 1.4-           UDP-Gal:betaGlcNAc beta 1.4-         UDP-Gal:betaGlcNAc beta 1.4-           UDP-Gal:betaGlcNAc beta 1.4-         UDP-Gal:betaGlcNAc beta 1.4-           UDP-Gal:betaGlcNAc beta 1.4-         UDP-Gal:betaGlc					ubiquitin-conjugating enzyme E2E 3	
UBE2G2   AF032456   (UBC7 homolog, yeast)   UBE2G2   Ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC1 UBE2L6 ubiquitin-conjugating enzyme E2I (UBC12 ubiquitin-conjugating enzyme E2I (UBC13 homolog, yeast)   UBL1 U67122 ubiquitin-like 1 (sentrin)   UBL1 U61397 ubiquitin-like 1 (sentrin)   UBL1 UBX0177 ubiquitin-like 3   UBX02 D87684 UDP-Gal:betaGIcNAc beta 1,4-	2622	34850_at	UBE2E3	AB017644	(UBC4/5 homolog, yeast)	ubiquitin-conjugating enzyme E2
UBE2G2         AF032456         (UBC7 homolog, yeast)           UBE2I         Ub6867         ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2L 3           UBE2I         U45328         homolog, yeast)           UBE2L6         AA883502         ubiquitin-conjugating enzyme E2L 6           UBE2L6         AA883502         ubiquitin-conjugating enzyme E2L 6           UBE2L         AA883502         ubiquitin-conjugating enzyme E2L 6           UBL1         UB7122         ubiquitin-like 1 (sentrin)           UBL1         U67122         ubiquitin-like 3           UBL3         AL080177         ubiquitin-like 3           UBXD2         D87684         UBX domain-containing 2           UBXD2         D87684         UDP-Gal:betaGlcNAc beta 1,4-           B4GALT1         D29805         galactosyltransferase, polypeptide 1           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           B4GALT2         AF038660         galactosyltransferase, polypeptide 3           UGP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           BAGALT3         AF038661         galactosyltransferase, polypeptide 3           UGP-Gal:betaGlcNAc beta 1,4-         UGP-Gal:betaGlcNAc beta 1,4-           UGP-Gal:betaGlcNAc beta 1,4					ubiquitin-conjugating enzyme E2G 2	
UBE21         Ub66867         Indiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2I (UBC9 ubiquitin-conjugating enzyme E2L 3           UBE21         U45328         homolog, yeast)           UBE2L3         S81003         ubiquitin-conjugating enzyme E2L 3           UBE2L6         AA883502         ubiquitin-conjugating enzyme E2L 6           UBE2L         AA883502         ubiquitin-conjugating enzyme E2L 6           UBE2N         UBC13 homolog, yeast)           UBL1         U67122         ubiquitin-like 1 (sentrin)           UBL1         U61397         ubiquitin-like 3           UBL3         AL080177         ubiquitin-like 3           UBXD2         D87684         UBX domain-containing 2           UBXD2         UDP-Gal:betaGlcNAc beta 1,4-           B4GALT1         D29805         galactosyltransferase, polypeptide 1           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           B4GALT2         AF038660         galactosyltransferase, polypeptide 3           UGP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-	2623	32236_at	UBE2G2	AF032456	(UBC7 homolog, yeast)	ubiquitin conjugating enzyme G2
UBE21         U66867         homolog, yeast)           UBE21         U45328         homolog, yeast)           UBE2L3         S81003         ubiquitin-conjugating enzyme E2L 3           UBE2L6         AA883502         ubiquitin-conjugating enzyme E2L 6           UBE2L6         AA883502         ubiquitin-conjugating enzyme E2L 6           UBE2N         UB2004         (UBC13 homolog, yeast)           UBL1         U67122         ubiquitin-like 1 (sentrin)           UBL1         U61397         ubiquitin-like 3           UBXD2         UBX domain-containing 2           UBXD2         UBX domain-containing 2           UBXD2         UDP-Gal:betaGlcNAc beta 1,4-           B4GALT1         D29805         galactosyltransferase, polypeptide 1           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           BAGALT2         AF038660         galactosyltransferase, polypeptide 3           UGP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UGP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UGP-Gal:betaGlcNAc beta 1,4-         UGP-Gal:betaGlcNAc beta 1,4-           UGP-Gal:betaGlcNAc beta 1,4-         UGP-Gal:betaGlcNAc beta 1,4-           UGP-Gal:betaGlcNAc beta 1,4-         UGP-Gal:betaGlcNAc beta 1,4-      <					ubiquitin-conjugating enzyme E2I (UBC9	
UBE2I         Ubecligation on provided and provided	2624	38480_s_at	UBE2I	U66867	homolog, yeast)	ubiquitin conjugating enzyme 9
UBE2I         U45328         homolog, yeast)           UBE2L3         S81003         ubiquitin-conjugating enzyme E2L 3           UBE2L6         AA883502         ubiquitin-conjugating enzyme E2L 6           UBE2L6         UB3004         (UBC13 homolog, yeast)           UBL1         U67122         ubiquitin-conjugating enzyme E2N           UBL1         U67122         ubiquitin-like 1 (sentrin)           UBL1         U61397         ubiquitin-like 3           UBXD2         D87684         UBX domain-containing 2           UBXD2         D87684         UDP-Gal:betaGlcNAc beta 1,4-           B4GALT1         D29805         galactosyltransferase, polypeptide 1           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1					ubiquitin-conjugating enzyme E2I (UBC9	;
UBE2L3         S81003         ubiquitin-conjugating enzyme E2L 3           UBE2L6         AA883502         ubiquitin-conjugating enzyme E2L 6           UBE2N         UB3004         (UBC13 homolog, yeast)           UBL1         U67122         ubiquitin-conjugating enzyme E2N           UBL1         U67122         ubiquitin-like 1 (sentrin)           UBL3         AL080177         ubiquitin-like 3           UBXD2         D87684         UBX domain-containing 2           UBXD2         D87684         UDP-Gal:betaGlcNAc beta 1,4-           B4GALT1         D29805         galactosyltransferase, polypeptide 1           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:beta	2625	838_s_at	UBE2I	U45328	homolog, yeast)	ubiquitin-conjugating enzyme
UBE2L6         AA883502         ubiquitin-conjugating enzyme E2L 6           UBE2N         D83004         (UBC13 homolog, yeast)           UBL1         U67122         ubiquitin-conjugating enzyme E2N           UBL1         U67122         ubiquitin-like 1 (sentrin)           UBL3         AL080177         ubiquitin-like 3           UBXD2         D87684         UBX domain-containing 2           UBXD2         D87684         UDP-Gal:betaGlcNAc beta 1,4-           B4GALT1         D29805         galactosyltransferase, polypeptide 1           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc b	2626	223 at	UBE2L3	S81003	ubiquitin-conjugating enzyme E2L 3	L-UBC
UBE2N         Ubiquitin-conjugating enzyme E2N           UBL1         U67122         Ubiquitin-like 1 (sentrin)           UBL1         U61397         Ubiquitin-like 3           UBL3         AL080177         Ubiquitin-like 3           UBXD2         D87684         UBX domain-containing 2           UBXD2         D87684         UBX domain-containing 2           UBXD2         D87684         UDP-Gal:betaGlcNAc beta 1,4-           B4GALT1         D29805         galactosyltransferase, polypeptide 1           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc	2627	40505 at	UBE2L6	AA883502	ubiquitin-conjugating enzyme E2L 6	
UBE2N         D83004         (UBC13 homolog, yeast)           UBL1         U67122         ubiquitin-like 1 (sentrin)           UBL1         U61397         ubiquitin-like 3           UBL3         AL080177         ubiquitin-like 3           UBXD2         D87684         UBX domain-containing 2           UBXD2         D87684         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:bet					ubiquitin-conjugating enzyme E2N	:
UBL1         U67122         ubiquitin-like 1 (sentrin)           UBL1         U61397         ubiquitin-like 3           UBL3         AL080177         ubiquitin-like 3           UBXD2         D87684         UBX domain-containing 2           UBXD2         D87684         UBX domain-containing 2           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           B4GALT2         AF038660         galactosyltransferase, polypeptide 2           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-	2628	36604_at	UBEZN	D83004	(UBC13 homolog, yeast)	ubiquitin-conjugating enzyme E2 UbcH-ben
UBL1         U61397         ubiquitin-like 3           UBL3         AL080177         ubiquitin-like 3           UBXD2         D87684         UBX domain-containing 2           UBXD2         D87684         UBX domain-containing 2           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           B4GALT2         AF038660         galactosyltransferase, polypeptide 2           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-	2629	457_s_at	UBL1	U67122	ubiquitin-like 1 (sentrin)	SUMO-1
UBL3         AL080177         ubiquitin-like 3           UBXD2         D87684         UBX domain-containing 2           UBXD2         D87684         UBX domain-containing 2           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           B4GALT2         AF038660         galactosyltransferase, polypeptide 2           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-glacosyltransferase, polypeptide 3         UDP-glucose ceramide           UGCG         D50840         glucosyltransferase	2630	155_s_at	UBL1	U61397	ubiquitin-like 1 (sentrin)	ubiquitin-homology domain protein PIC1
UBXD2         D87684         UBX domain-containing 2           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           B4GALT1         D29805         galactosyltransferase, polypeptide 1           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-Gal:betaGlcNAc beta 1,4-         UDP-Gal:betaGlcNAc beta 1,4-           UDP-glucose ceramide         UDP-glucose ceramide           UGCG         D50840         glucosyltransferase	2631	40839 at	UBL3	AL080177	ubiquitin-like 3	hypothetical protein
UDP-Gal:betaGlcNAc beta 1,4-   B4GALT1   D29805   galactosyltransferase, polypeptide 1     UDP-Gal:betaGlcNAc beta 1,4-   B4GALT2   AF038660   galactosyltransferase, polypeptide 2     UDP-Gal:betaGlcNAc beta 1,4-   UDP-Gal:betaGlcNAc beta 1,4-   UDP-glucose ceramide   UDP-glucose ceramide     UGCG   D50840   glucosyltransferase	2632	37336 at	UBXD2	D87684	UBX domain-containing 2	KIAA0242 protein
BAGALT1 D29805 galactosyltransferase, polypeptide 1 UDP-Gal:betaGlcNAc beta 1,4- BAGALT2 AF038660 galactosyltransferase, polypeptide 2 UDP-Gal:betaGlcNAc beta 1,4- BAGALT3 AF038661 galactosyltransferase, polypeptide 3 UDP-glucose ceramide UDP-glucose ceramide					UDP-Gal:betaGlcNAc beta 1,4-	
B4GALT2 AF038660 galactosyltransferase, polypeptide 2 UDP-Gal:betaGlcNAc beta 1,4- UDP-Gal:betaGlcNAc beta 1,4- B4GALT3 AF038661 galactosyltransferase, polypeptide 3 UDP-glucose ceramide	2633	40960 at	B4GALT1	D29805	galactosyltransferase, polypeptide 1	beta-1,4-galactosyltransferase
B4GALT2 AF038660 galactosyltransferase, polypeptide 2 UDP-Gal:betaGlcNAc beta 1,4- B4GALT3 AF038661 galactosyltransferase, polypeptide 3 UDP-glucose ceramide UGCG D50840 glucosyltransferase					UDP-Gal:betaGlcNAc beta 1,4-	
DEP-Gal:betaGicNAc beta 1,4- B4GALT3 AF038661 galactosyltransferase, polypeptide 3 UDP-glucose ceramide UGCG D50840 alucosyltransferase	2634	34177 at	B4GALT2	AF038660	galactosyltransferase, polypeptide 2	beta-1,4-galactosyltransferase
B4GALT3 AF038661 galactosyltransferase, polypeptide 3 UDP-glucose ceramide UGCG D50840 alucosyltransferase					UDP-Gal:betaGlcNAc beta 1,4-	
UDP-glucose ceramide D50840 alucosyltransferase	2635	39445_at	B4GALT3	AF038661	galactosyltransferase, polypeptide 3	beta-1,4-galactosyltransferase
[UGCG   D50840   Idlucosyltransferase					UDP-glucose ceramide	
2,000	2636	40215_at	Ngcg	D50840	glucosyltransferase	ceramide glucosyliransierase

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2637	2637 35214_at	ПСВН	AF061016	UDP-glucose dehydrogenase	UDP-glucose dehydrogenase
2638	2638 37373_at	UGP2	U27460	UDP-glucose pyrophosphorylase 2	uridine diphosphoglucose pyrophosphorylase
2639 38041	38041_at	GALNT1	U41514	UDP-N-acetyl-alpha-D- galactosamine:polypeptide N- acetylgalactosaminyltransferase 1 (GallNAc-T1)	UDP-GalNAc:polypeptide N- acetylgalactosaminyttransferase
2640	2640 36515_at	GNE	AJ238764	UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase	UDP-N-acetylglucosamine-2-epimerase/N-UDP-N-acetylglucosamine-2-epimerase / N-acetylmannosamine kinase
2641	2641 41242_at	UAP1	AB011004	UDP-N-acteylglucosamine pyrophosphorylase 1	UDP-N-acetylglucosamine pyrophosphorylase
2642	2642 34827_at	ULK1	AF045458	unc-51-like kinase 1 (C. elegans)	serine/threonine kinase ULK1
2643	2643 37315_f_at	ВМозе	A1057607	uncharacterized bone marrow protein BM036	
2644	2644 35750_at	HT010	AL049948	uncharacterized hypothalamus protein HT010	
2645	2645 41058 g at	HT012	A1760162	uncharacterized hypothalamus protein HT012	
2646	2646 41057_at	HT012	AI760162	uncharacterized hypothalamus protein HT012	
2647	2647 38610 s_at	KRT10; KPP	X14487	unnamed protein product; Human gene for acidic (type I) cytokeratin 10.	keratin 10
2648	2648 34402_at	UNRIP	AB024327	unr-interacting protein	WD-40 repeat protein
2649	2649 34372_at	UREB1	AB002310	upstream regulatory element binding protein 1	upstream regulatory element binding protein
2650	2650 37686_s_at	ONG	Y09008	uracil-DNA glycosylase	uracil-DNA glycosylase
				uridine monophosphate synthetase (orotate phosphoribosyl transferase and	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-
2651	33815_at	UMPS	J03626	orotidine-5'-decarboxylase)	decarboxylase)
2652	2652 41859_at	UST	AB020316	uronyl-2-sulfotransferase	dermatan/chondroitin sulfate 2- sulfotransferase
2653	2653 39429_at	UVRAG	X99050	UV Radiation Resistance Associated Gene; H.sapiens mRNA; UV Radiation Resistance Associated Gene.	p63 (processed form)

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_	A	В	၁	O	ב
					v-abl Abelson murine leukemia viral
					oncogene homolog 1 isoform a; v-abl
				v-abl Abelson murine leukemia viral	Abelson murine leukemia viral oncogene
2654		ABL1			homolog 1 isoform b
2655	2655 35779_at		AJ133421		vacuolar protein sorting
				VAMP (vesicle-associated membrane	
2656	2656 38801_at	VAPA	AI742846	protein)-associated protein A (33kD)	
					vascular cell adhesion molecule 1, isoform a
					precursor; vascular cell adhesion molecule
2657	2657 583_s_at	VCAM1	M30257	vascular cell adhesion molecule 1	1, isoform b precursor
2658			AF024710		vascular endothelial growth factor
2659	=		AF022375	vascular endothelial growth factor	vascular endothelial growth factor
					VEGF related factor isoform VRF186
2660	2660 37268_at	VEGFB	U43368	vascular endothelial growth factor B	precursor
					vascular endothelial growth factor related
2661	2661 159_at	VEGFC	U43142	vascular endothelial growth factor C	protein
				VDAC protein; similar to mouse VDAC 3;	
				Homo sapiens voltage dependent anion	
2662	2662 36102 at	VDAC3: HD-VDAG	AF038962	channel protein mRNA, complete cds.	voltage dependent anion channel protein
2663	2663 40147 at	VATI	U18009	vesicle amine transport protein 1	vesicle amine transport protein 1
2664	ш _ ч	RA410	AB020724	vesicle transport-related protein	KIAA0917 protein
				vesicle-associated membrane protein 2	
2665	2665 32254_at	VAMP2	AL050223	(synaptobrevin 2)	
				vesicle-associated membrane protein 3	
2666	2666 35783_at	VAMP3	H93123	(cellubrevin)	
2667	2667 40103_at	VIL2	X51521	villin 2 (ezrin)	villin 2
2668	2668 34091 s at	VIM	Z19554	vimentin	vimentin
					vinculin isoform VCL; VCL isoform meta-
2669	2669 36601_at	VCL	M33308	vinculin	VCL
2670	2670 39091_at	JWA	AF070523	vitamin A responsive; cytoskeleton related JWA protein	JWA protein
				vitamin D (1,25- dihydroxyvitamin D3)	vitamin D (1,25- dihydroxyvitamin D3)
2671	2671 1388_g_at	VDR	J03258	receptor	receptor
				v-Ki-ras2 Kirsten rat sarcoma 2 viral	
2672	2672 1940_at	KRAS2	M54968	oncogene homolog	K-ras oncogene protein

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	V	В	၁	O	U
		L	A 17.01.02.02	fibrosarcoma	short form transcription factor C-MAE
2673 4	2673 41504_s_at	MAF	AFU553/b	T	
	-			v-mar musculoaponeurotic librosarcoma	
2674 3	2674 32835_at	MAFF	AA725102		
2675	2675 40198 at	VDAC1	L06132		voltage-dependent anion channel
2676	2676 37696 at	VDAC2	L06328	voltage-dependent anion channel 2	voltage-dependent anion channel
2677	2677 171 at	VBP1	U56833	von Hippel-Lindau binding protein 1	VHL binding protein-1
				v-raf-1 murine leukemia viral oncogene	
2678	2678 38743 f at	RAF1	X06409	homolog 1	
				v-ral simian leukemia viral oncogene	
				homolog B (ras related; GTP binding	v-ral simian leukemia viral oncogene
2679	2679 32776 at	HALB	M35416	protein)	homolog B
				v-rel reticuloendotheliosis viral oncogene	
				homolog A, nuclear factor of kappa light	
		-		polypeptide gene enhancer in B-cells 3,	
2680	2680 36645 at	RELA	L19067	p65 (avian)	NF-kappa-B transcription factor subunit
				v-rel reticuloendotheliosis viral oncogene	
				homolog A, nuclear factor of kappa light	
				polypeptide gene enhancer in B-cells 3,	
2681	2681 1295 at	RELA	L19067	p65 (avian)	NF-kappa-B transcription factor subunit
				v-yes-1 Yamaguchi sarcoma viral	v-yes-1 Yamaguchi sarcoma viral oncogene
2682	2682 1674 at	YES1	M15990	oncogene homolog 1	homolog 1
	1			v-yes-1 Yamaguchi sarcoma viral related	v-yes-1 Yamaguchi sarcoma viral related
2683	2683 1402 at	Ľ	M16038	oncogene homolog	oncogene homolog
2684	2684 1058 at	WASF3	062698	WAS protein family, member 3	
2685	2685 38736 at	WDR1	AL050108	WD repeat domain 1	hypothetical protein
2686	2686 41430_at	WDR7	AB011113	WD repeat domain 7	KIAA0541 protein
2687	2687 36009_at	C1 683	AF091092	weakly similar to glutathione peroxidase 2	weakly similar to glutathione peroxidase 2
2688	2688136909 at	WFF1	X62048	WEE1+ homolog (S. pombe)	_
3	15-0000				eukaryotic translation initiation factor 4H,
	_			Williams-Beuren syndrome chromosome	isoform 1; eukaryotic translation initiation
2689	2689 41212 r at	WBSCR1	D26068	region 1	factor 4H, isoform 2
2690	2690 41635 at	WTAP	D14661	Wilms' tumour 1-associating protein	Wilms' turnour 1-associating protein
				wingless-type MMTV integration site	wingless-type MMTV integration site family,
2691	2691 31862_at	WNT5A	L20861	family, member 5A	member 5A precursor

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	¥	В	0	D	ш
,	10001	COSTIN	A 5101124		Wolf-Hirschhorn syndrome candidate 2
7697	2692 34225_at	WHSCZ	AF101434	andidate 2	protein
2693	2693 33438_at	WBP2	AL049981	WW domain binding protein 2	
				WW domain binding protein 4 (formin	
2694	2694 35213_at	WBP4	AF071185		formin binding protein 21
2695	2695 39995_s_at	WWOX	U13395	•	oxidoreductase
				WW domain-containing adapter with a	
2696	2696 36822_at	WAC	U51334	coiled-coil region	putative RNA binding protein RBP56
				xeroderma pigmentosum,	
2697	2697 1307_at	XPA	D14533	complementation group A	XPAC protein
Γ				xeroderma pigmentosum,	
2698	2698 1873_at	XPC	D21089	complementation group C	XP-C repair complementing protein (p125)
				XPA binding protein 1; putative ATP(GTP)-	
2699	2699 41756_at	NTPBP	AJ010842	binding protein	ATP(GTP)-binding protein
				X-ray repair complementing defective	
				repair in Chinese hamster cells 5 (double-	
				strand-break rejoining; Ku autoantigen,	
2700	2700 38733_at	XRCC5	M30938	80KD)	ATP-dependant DNA helicase II
				X-ray repair complementing defective	
				repair in Chinese hamster cells 5 (double-	
		-		strand-break rejoining; Ku autoantigen,	
2701 585	585_at	XRCC5	M30938	80KD)	ATP-dependant DNA helicase II
				X-ray repair complementing defective	
				repair in Chinese hamster cells 5 (double-	
				strand-break rejoining; Ku autoantigen,	
2702	2702 2093_s_at	XRCC5	J04977	80kD)	ATP-dependant DNA helicase II
2703	2703 35827_at	KIAA0905	AB020712	yeast Sec31p homolog	KIAA0905 protein
2704	2704 40988_at	YME1L1	AJ132637	YME1-like 1 (S. cerevisiae)	ATP-dependent metalloprotease YME1L
2705	2705 891_at	7771	M77698	YY1 transcription factor	GLI-Krupple related protein
				zb29g04.s1	
				Soares_parathyroid_tumor_NbHPA Homo	
				sapiens cDNA clone IMAGE:305046 3',	
2706	2706 34887_at		N92548	mRNA sequence.	
2707	36308 at	ZIC1	D76435	Zic family member 1 (odd-paired homolog, Drosophila)	Zic protein
2708	2708 35681 r at	ZFHX1B	AB011141	zinc finger homeobox 1b	KIAA0569 protein

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A	В	0	Q	3
2709 34786 at	TSGA	AB018285	zinc finger protein	KIAA0742 protein
2710 39977_at	ZNF-U69274	U69274	zinc finger protein	zinc finger protein
	710400	0.76444	rice finance profesion 103 homology (mostes)	olomot 103 homolog
2712 36205 at	Zrr 103	1100444	zinc finger protein 134 (clone nHZ-15)	zinc finder protein ZNF134
	ZNE144	D13969	zinc finger protein 144 (Mel-18)	Mel-18 protein
11	ZNF146	X70394	zinc finger protein 146	zinc finger protein
2715 41532 at	ZNF151	Y09723	zinc finger protein 151 (pHZ-67)	Miz-1 protein
2716 32628_at	ZNF161	D28118	zinc finger protein 161	DB1
2717 41436_at	ZNF198	AJ224901	zinc finger protein 198	ZNF198 protein
2718 40724_at	ZNF200	Y14443	zinc finger protein 200	zinc finger protein
2719 35368_at	ZNF207	AF046001	zinc finger protein 207	zinc finger protein 207
2720 41542_at	ZNF216	AF062346	zinc finger protein 216	zinc finger protein 216 splice variant 1
2721 840_at	ZNF220	U47742	zinc finger protein 220	monocytic feukaemia zinc finger protein
2722 39762_at	ZNF262	AB007885	zinc finger protein 262	zinc finger protein 262
2723 34299_at	ZNF278	AL096880	zinc finger protein 278	hypothetical protein
2724 39005_s_at	ZNF294	AB018257	zinc finger protein 294	KIAA0714 protein
2725 37860_at	ZNF337	AL049942	zinc finger protein 337	hypothetical protein
			zinc finger protein 36, C3H type, homolog	
2726 40448_at	ZFP36	M92843	(mouse)	zinc finger transcriptional regulator
2727 38740_at	ZFP36L1	X79067	zinc finger protein 36, C3H type-like 1	butyrate response factor 1
2728 36046_at	ZNF363	AL050144	zinc finger protein 363	hypothetical protein
				hypothetical protein, similar to (U06944)
2729 32129_at	ZNF364	AL079314	zinc finger protein 364	PRAJA1 [Mus musculus]
2730 41033_at	ZNF84	M27878	zinc finger protein 84 (HPF2)	DNA binding protein
2731 40610_at	ZFR	AI743507	zinc finger RNA binding protein	
2732 39751_at	ZDHHC3	AF052182	zinc finger, DHHC domain containing 3	
			zinc metalloproteinase (STE24 homolog,	
2733 33912_at	ZMPSTE24	Y13834	yeast)	farnesylated-proteins converting enzyme 1
2734 36521_at	DZIP1	AB023213	zinc-finger protein DZIP1	KIAA0996 protein
2735 35995_at	ZWINT	AF067656	ZW10 interactor	ZW10 interactor Zwint
2736 706_at		HG4582-HT4987		
2737 960_g_at		HG2463-HT2559		
2738 956_at		HG1980-HT2023		
2739 955_at		HG1862-HT1897		
2740 324_f_at		HG1515-HT1515		

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	A	8	0	Q	Е
2741	2741 327_f_at		HG1800-HT1823		
2742	2742 333_s_at		HG2639-HT2735		
2743	2743 1840 g at		HG1112-HT1112		
2744	2744 1664_at		HG3543-HT3739		
2745	2745 1624_at		HG2036-HT2090		
2746	2746 1278_at		HG162-HT3165		
2747	2747 1179_at		HG2855-HT2995		
2748	2748 1180 g_at		HG2855-HT2995		
2749	2749 32243_g_at		AL038340		
2750	2750 311_s_at		HG3044-HT3742		
2751	2751 297_g_at		HG4322-HT4592		
2752	2752 296_at		HG4322-HT4592		
2753	2753 1839_at		HG1112-HT1112		
2754	2754 723 s_at		HG1322-HT5143		
					guanine nucleotide binding protein (G
2755	2755 33300_at	dJ283E3.1	AL031282		protein), beta polypeptide 1
					guanine nucleotide binding protein (G
2756	2756 41249_at	dJ283E3.1	AL031282		protein), beta polypeptide 1

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